

m218.seq

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/q218

			10	20	30	40	50	60					
m218.pep			MVAVDPYTA	KVVSTMPRN	QGWYYTMD	EIHSDMML	GAA GDYLL	ETAASLTI	IMVVSGLYLW				
g218			MVAVDPYTA	KVVNTMPRN	QGWYHTMD	EIHGDMM	LGAAGDYLL	ETAASLTI	IMVVSGLYLW				
			10	20	30	40	50	60					
70	80	90	100	110	120								
m218.pep			WVKRRGIK	AMLLPSK	GXARSW	WRNLHGT	FTGTVV	SLILLF	CLSGIA	WAGIWGG	KFVQAWS		
g218			WAKQRIK	AMLLPPK	SRARSW	WRNLHGA	FTGTVV	SLILLF	CLSGIA	WAGIWGG	KFVQAWN		
			70	80	90	100	110	120					
			130	140	150	160	170	180					
m218.pep			QFPAGKW	GVEPNP	VSVPPT	HGEVLND	GKVK	VEVPV	WLELT	PMPVSG	TTVGKD	GINDP	DEPMT
g218			QFPAGKW	GVEPNP	VSIVPT	HGEVLND	GKVK	VEVP	WILEL	MPMPV	SGTTVG	ENGIN	PTEPNN
			130	140	150	160	170	180					
			190	200	210								
m218.pep			LETVDR	FARXNR	FQAL	SVEFA	QRRGR	RMDF	VAGFYEL				
g218			IGNRRP	FRAGNR	FQAL	SVEFA	QRRGR	GMDF	VAGFYEL				
			190	200	210								

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1   ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTCGAC AGGTGATTAT CTTTGGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GCGCGGCGAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GCGCGCTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGA ACTTGGGTGT CGTTGATTTT ACTGTGTTC
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGAA CCGAACCTTG
401 TTTCACTCGT GCCGACCCAC GCGCAGGTAT TGAATGACGG CAAGGTAAAG
451 GAAGTGCCGT GGGTTTGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAAACCG
551 TCGACCGTTT TGCGCGG.GA AATCGGTTTC AAAGGCGTT ATCAGCTGAA
601 TTTCCCAAAA GCGGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1   MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

m218.pep	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYTMDEIHS DMMLGAAGDYLLETAASLTIIMVVSGLYLW					
a218	: : : :					
	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS DMMLGSTGDYLLLETAASLTIIMIISGLYLW					
m218.pep	70	80	90	100	110	120
	WVKRRGIKAMLLPSKXARSWWRNLHGTFGTWVSLILLFLCLSGIAWAGIWGGKFVQAWS					
a218	: : : :					
	70	80	90	100	110	120
	WVKRRGIKAMLLPPKGRARSWWRNLHGAFGTWVSLILLFLCLSGIAWAGIWGGKFVQAWS					
m218.pep	130	140	150	160	170	180
	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
a218	: : : :					
	130	140	150	160	170	180
	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
m218.pep	190	200	210			
	LETVDRFARXNRFQRLSVEFAQRRGRMDFVAGFYEL					
a218	: :					
	LETVDRFARXNRFQRLSAEFAQRRGRMDFVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
1   atgacggcaa ggtaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt gggtgaaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaccgtc gaccgtttcg cgcgggaaat cggtttcaaa
151 gggcgttatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201 gtgcgaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatattatg gcggcaagca ttgcgctgca
351 tatggggact ttgggctggg ggagcgtgtt ggccaacgtc gtgttctgcc
401 ttgccgtgat tttatcggc atcagcggct gcgtgatgtg gtggaacgc
451 cgtccgtccg gcgtggcggg cattgttcct ccggcgcaaa aaatcaaact
501 gcccgctctg tggcgatgg cattgccgct gctgttgatt gcactgcttt
551 tcccgaaccg gctgcttgcc attgccgtga tttggctgtt ggataccttg
601 ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaat ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
1   MTARLRKCRG FWSLCLCLSQ GRLWVKALT PPSPITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLNV VFCLAVIFIG ISGCVMWKR
151 RPSGVAGIVP PAQIKLPVW WAMALPLLLI ALLEPTALLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
1   ATGACGGCAA GGTTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGaCyGt gGGCAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTGC GCGGnGAAAT CGGTTTCAAA
151 GGGCGTTATC AGTTGAATT GCCCAAAGC GAGGACGGCG TATGGACTTT
201 GTCGAGGAT TCTATGAGT ACGACATGAT CAGCCCGTT GCCGACCGCA
251 CGGTACATAT CGACCACTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGT GCGCAACGTC TTGTTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGACCG GAGCGGTGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGGTTTGG TGGATGATG CATTGCCGCT ATTGGCAATC GCACTGCTCT
551 TCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTGCG GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
1   MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLNV LFCLAVIFIG ISGCVMWKR
151 RPTGAVGIVP PAQVKLPVW WMMALPLLAI ALLEPTSLLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

m219/g219

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
g219	MTARLRKCRGFWSLCLCLSQGRLWVKALTTPSPITLETVDREIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
g219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	: : : : :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMMWKRPSGAVGIVPPAQKIKLPVWWMALPLLII					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : : :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```
a219.seq
1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTCG GCGG.GAAAT CCGTTTCAAA
151 GGGCGTTATC AGCTGAATTG GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCAGTAC AGCGGCAAGA TTCTTGCCGA CATCGTTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GGCGAACGTT TTGTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGTCCG GCGCGGTGGG CATGGTCCG CCGGCGCAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CCGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```
a219.pep
1  MTARLRKCRG FWSLRCLCFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*
```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLCFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	: : : :					
a219	MTARLRKCRGFWSLRCLCFQGRWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	: : : :					
a219	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	: : : :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMMWKRPSGAVGMVPPAQKIKLPVWWMAMAVPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1   atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatgcggcga gccgtaaatc adatcgacgc tgacggattt gaacctgcc
101 tcacgggcgg catcgatgac ttctttggtt tcttcgtagc tttggatgcy
151 gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgtca
201 tgcggttgaa gccgagtctg ccgagcatga ggacggtgct gcggctgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcggcgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgaagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcgccg cggcttttgt ctttgggtgat gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcgg
551 ttgtttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1   MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FGFVVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MFADHAEDTF DLFVAQKGRR AAEEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151 GIGAAFVFGD DFVAAAVVAD GVAKRNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1   ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAA
51  CGACGCTGAC GGATTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTCGATC TGTTCTGTCG TCAAAAAGGt GCGTGCCCGC CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCATT
401 TCTTTTTCAA GATATTCGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451 GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTGTGTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1   MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAHEH GVAADFARVD FDGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAFVFG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng)

from *N. gonorrhoeae*:

m221/g221

```

              10      20      30      40      50
m221.pep      MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE
              ||::||| ||||| ||| :| ||||| ||| |||||
g221          MHDHGAMDRRLPAFGSLMRRVNXIDADGFEPCLTGGIDDFFGFFVVALDAVDCRLHFGVE
              10      20      30      40      50      60

              60      70      80      90      100     110
m221.pep      ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-
              ||||| ||||| ||||| ||||| ||||| ||||| |||||
g221          ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR
              70      80      90      100     110     120

              120     130     140     150     160     170
```

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```

m221.pep  CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
          |||||||
g221      AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
          130      140      150      160      170      180

m221.pep  GKRFVX
          |||||
g221      GKRFVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1  ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGC GGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTTCTTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACC
501 GAATGTGAAT GTAAAGGGAA AGCGGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1  MVVLMRLSLV RQAVNQIDAD GFEPFRFARRI DDFFGFFVTL DAVDRRLHFG
51  VEILNADAHV VEAESAHEHD GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMW S EQFHFFFKF DVGIGAAAFV
151 GDDFVAAAVV ADGVAERNVN VKGKRFV*

```

m221/a221 95.5% identity in 177 aa overlap

```

          10      20      30      40      50      60
m221.pep  MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFFGFFVTLDAVDRRLHFGVEILNADAHV
          |||||
a221      MVVLMRLSLVRQAVNQIDADGFEPFRFARRIDDFFGFFVTLDAVDRRLHFGVEILNADAHV
          10      20      30      40      50      60

          70      80      90      100     110     119
m221.pep  VEAESAHEHDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLFVAQKGA-CPAEVQLG
          |||||||
a221      VEAESAHEHDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLVVAQKGRRAAAEVQLG
          70      80      90      100     110     120

120      130      140      150      160      170
m221.pep  KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGKRFVX
          |||||||
a221      KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGKRFVX
          130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1  atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca
51  tttcgatggc gaattgggtct ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggtc atcgaagccg aaacgggagg gaatcgcgcc
151 cgtggatact tgcaggtcga ggaatgtgat gtagaaagtg aaatcacgta
201 cagcaacgta atcagcgtaa ggagcagctt ggtgtttcca gttttctctg
251 cgcaggtctt tggcaacgtc gagcagctct tgttcaactga tctctttgcg
301 ccagtatatt tcttgggcga atttcaattc acggaaggcg ccgacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..

1 MEFRHQVVVV GVEPFGHFDG ELVFVAARQL EELFQRQVLA IEAETGGNRA
 51 RGYLQVEDVM VESEITYSNV ISVRSSLVFP VFLAQVFGNV EQLLFTDLFA
 101 PVFFLGEFQF TEGADTREAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 789>:

m223.seq
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGGTCA
 51 TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
 101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCCTAC
 201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTCCAG TTTTCTCGC
 251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTTGCGC
 301 CAGTATTTT CTTGTGCGAA TTTCAATTCG CGGAAGGCGC CGACACGCGG
 351 GAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

m223.pep
 1 VEFRHQVVVV GVEPFGHFDS ELVFVTARQL EELFQRQVLA VEAEGGNRA
 51 GGDQVEDV VSEIXYGN IGVGSDLVFP VFLAQVFSNS QQFLADFFA
 101 PVFFLGEFQF AEGADTREAA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

m223/g223

	10	20	30	40	50	60
m223.pep	VEFRHQVVVV	GVEPFGHFD	SELVFVTAR	QLEELFQRQ	VLAVEAEAG	GNRAGGDLQ
	:	:	:	:	:	:
g223	MEFRHQVVVV	GVEPFGHFD	GELVFVAAR	QLEELFQRQ	VLAIEAETG	GNRARGYLQ
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGN	EIGVGS	DLVFPVFL	AQVFSNS	QQFLADFF	APVFFLCE
	:	:	:	:	:	:
g223	VESEITYSN	VISVRSS	LVFPVFL	AQVFGNV	EQLLFTDL	FAFPVFFL
	:	:	:	:	:	:
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

a223.seq
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGGTCA
 51 TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
 101 TCCAAAGATA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCGCCTA
 201 CGGCAACGTA ATCGGCGTTG GCAGCGGCCT GGTGTTTCCA GTTTTCTCG
 251 CGCAAGTCTT TAGCAACAGC CAGCAATTCT TGCTCGCTGA TTTCTTTGCG
 301 CCAAGTATTT TCTTGTGCGA ATTCAATTC GCGGAAGGCA CCGACACGCG
 351 GGAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

a223.pep
 1 VEFRHQVVVV GVEPFGHFDS ELVFVTARQL EELFQR*VLA VEAEGGNRA
 51 GGDQVEDV VSEIAYGNV IGVGSLVFP VFLAQVFSNS QQFLADFFA
 101 PVFFLGEFQF AEGDTREAA*

m223/a223 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
m223.pep	VEFRHQVVVV	GVEPFGHFD	SELVFVTAR	QLEELFQRQ	VLAVEAEAG	GNRAGGDLQ
	:	:	:	:	:	:
a223	VEFRHQVVVV	GVEPFGHFD	SELVFVTAR	QLEELFQRQ	VLAVEAEAG	GNRAGGDLQ
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGN	EIGVGS	DLVFPVFL	AQVFSNS	QQFLADFF	APVFFLCE
	:	:	:	:	:	:
a223	VESEIAYGN	VIGVGS	GLVFPVFL	AQVFSNS	QQFLADFF	APVFFLCE
	:	:	:	:	:	:

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcggtccgc cccgcccttg cgcagcagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttaccc
151 gtcaaccgag ccccgcccg ggcggcgggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcctaacg aacagcccgt tgtacgcgtc aaccgagccn
251 ccgcccggcg ggcgggcaat gccgacaaac tcacgcggcag cgcgatgcgg
301 cttttgggta ttgcttaccg ctacggcggc acatcggtgt ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcg cacgtcggcg gaacaggcgc ggatgggcgc acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgcgcg cagggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgccgcg cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKNDPSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTTCAAACC CGGCAGTTTG GCGGTTTGG TGGCTGAWGT TTGCCGTCCG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTACC CATCAACCGA
151 GCCCCGCCCC GCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCC TTTTACCCGT CAACCGAGTC CCCGCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301 CAGCCCGTTT TACCCGTCAA CCGAGCCCC GCGGCGGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401 ACGGCGGCAC ATCGGTTTCT ACCGGTTTG ACTGCAGCGG CTTATGCAG
451 CACATCTTCA AACGCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATTG CAGCCCGGAG
551 ATATGGTGTT TTTCCGACG CTCGGCGGCA GCCGCATTC CATGTGCGA
601 CTTTATATCG GCAACAACCG CTTATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701 TCGCCCGCCG GGTCAAGAAA AACGACCCGT CCCGCTTCT GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101 QPVLVNRAP ARRAGNADEL IGNAMGLLGI AYRYGGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSABQAR MGPVARSSEL QPGDMVFERT LGGSRISHVG
201 LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

m225/g225

```

              10      20      30      40      50
m225.pep      FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
              | : ||||| | | | | | | | | | | | | | | | | | | | | | | | |
g225           MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPVNRAPARRAG
```

510

	10	20	30	40	50	60
m225.pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
	: :					
g225	NADELIG-----			GAMGLNEQPVVRVNRAXARRAGNA		
		70	80	90		
m225.pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
	: : :					
g225	DKLIGSAMRLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225.pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225.pep	240	249				
	VKKN DPSRFLNX					
g225	VKKN DPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225.seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTACCC
151 ATCAACCGAN CCCC CGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAAGTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCGCCGCCCC GCGGGCGGG CAATGCCGAC
451 GAACATCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCAGCTCG GCGGCAGCCG CATTCCCCT GTCGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR S ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKN DPSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225.pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG				
	:				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG				
	10	20	30	40	50
	60	70	79	80	
m225.pep	NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA				


```

|||||
a225      NADELIGSAMGLNEQPVLVPVNRXPARRAGNADXLIGNAMGLNEQPVLVPVNRVPARRAGNA
          70          80          90          100          110          120

          90          100          110          120          130          140
m225.pep  DELIGNAMGLNEQPVLVPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          |||||||
a225      DELIGNAMGLNEQPVLVPVNRAPARRAGNADDELIGNAMGLLGIAYRYGGTSISTGFDCSGF
          130          140          150          160          170          180

          150          160          170          180          190          200
m225.pep  MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          |||||||
a225      MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFXFRTLGGSRISHVGLYIGNNRF
          190          200          210          220          230          240

          210          220          230          240          249
m225.pep  IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNPDSRFLNX
          |||||||
a225      IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNPDSRFLNX
          250          260          270          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcgctccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag ttgcccgaag acgaacagcc cgttttacc
151  gtcaaccgag ccccgcccg gcgggcgggc aatgccgagc aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251  cgcggcgggc ggcgggcaat gccgacaaac tcacgcggcg cgcgatgcgg
301  cttttgggta ttgcctaccg ctacggcgcg acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgcgcgc cagctcggcg gaacaggcgc ggatgggcgc acccgttgcc
451  cgaagcgaat tgcagcccg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551  acgcgcgcgc caggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgcccgc cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1  MDSFFKPAVAV AVLWLMFAVR PALADELTNL LSSREQILRQ PAEDEQPVLP
51  VNRAFPARRAG NADELIGGAM GLNEQPVVVR NRAXARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNPDSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151  ATCAACCGAG CCCCCGCCCG GCGGGCGGGC AATGCCGAGC AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCCT TTTACCCGTC AACCGAGTCC
251  CCGCCCGGCG GCGGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCGTTT ACCCGTCAAC CGAGCCCCCG CCGGCGGGC
351  GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTGA CTGCAAGCGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCGCA AGCGAATTGC
551  AGCCCGGAGA TATGGTGTG TCCGCACGC TCGGGCGCAG CGGCATTTC
601  CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCACG CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701  AATACGCGTT CGCCCGCCGG GTCAAGAAAA ACGACCCGTC CCGCTTTCTG
751  AACTGA

```

m225-1/g225-1 84.9% identity in 251 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

1	MDSFFKPAVW	AVLWLMFAVR	PALADELTNL	LSSREQILRQ	FAEDEQPVLP
51	INRXPPARRAG	NADELIGSAM	GLNEQPVLPV	NRXPARRAG	ADXLIGNAMG
101	LNEQPVLPVN	RVPARRAGNA	DELIGNAMGL	NEQVLPVNR	APARRAGNAD
151	ELIGNAMGLL	GIAYRYGGTS	ISTGDCSGF	MQHIFKRAMG	INLPR TSAEQ
201	ARMGTTPVARS	ELQPGDMVXF	TRLGGSSRIH	VGLYIGNNRF	IHPARTSGKNI
251	EITSLSHKYW	SGKYAFARRV	RKNDPSRFLN	*	

a225-1/m225-1 88.6% identity in 280 aa overlap

```

      10      20      30      40      50      60
a225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG
          |||
m225-1     MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
          |||

      70      80      90     100     110     120
a225-1.pep NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
          |||
m225-1     NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA
          70                        80      90

     130     140     150     160     170     180
a225-1.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
          |||
m225-1     DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          |||

     190     200     210     220     230     240
a225-1.pep MQHIFKRAMGINLPRSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
          |||
m225-1     MQHIFKRAMGINLPRSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          |||

     250     260     270     280
a225-1.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKNDPSRFLNX
          |||
m225-1     IHAPRTGKNIEITSLSHKYWSGKYAFARRVKNDPSRFLNX
          |||
          220     230     240     250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

```

g226.seq
1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCAGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccgataacc caattctcct tcccgccctg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcggtg tctcccgcca
451 tttctgttgc ctccgcctct cctgcccgcgc ctccggccgc atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cctttctcct Cgggcccctg cccctccccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

```

g226.pep
1  MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
101 GSVTGIVTGM YFAAWLGPDT QSFPPRLQY LLFTPSGIPI HTLYARVLP
151 FLLPPPLLPR LGPHTLRRFT ILPKLRRPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

```

m226.seq
1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCAGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCGGCGGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGTATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep
 1 MNEILRQPSV LLFLTLAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226.pep	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	:					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226.pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226.pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG					
	:					
g226	QFSFPRLQYLLFTPSGIPHTLYARVLPFLLPPLLPRLGPHTLRRFTILPKKLRPFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC
 51 CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAACCC
 251 GCCGTAAAT CTTCAACCAA TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGCATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep
 1 MNEILRQPSI LLFLTLAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep  MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
a226      MNEILRQPSILFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
           10      20      30      40      50      60

           70      80      90      100     110     120
m226.pep  AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
a226      AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
           70      80      90      100     110     120

           130     140     150     160     170     180
m226.pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
a226      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
           130     140     150     160     170     180

           190     200     210     220     230
m226.pep  MSLGTASHAMGIAASLERSRRMAAYAGLGTfNGVLTALIAPLLIPVLGFX
a226      MSLGTASHAMGIAASLERSRRMAAYAGLGTfNGVLTALIAPLLIPVLGFX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctccggtgcc tcgccgccgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccggc agcatcgtcg
101 gcatggcgct gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttcct
201 cgtgccgccc tgcgtggcgg tcatcageta tttggatttg attgccgacg
251 attggttttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1  MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLF LQAGWLKTS
51  WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1  ..ACGTCTTKGC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTG GATTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTA CTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1  ..TSXLQQLTDA LMSNLTFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227

           10      20      30
m227.pep  TSXLQQLTDALMSNLTFLVPPCVAVISYL
           || |||||:|||||
g227      TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTLFLVPPCVAVISYL
           20      30      40      50      60      70

           40      50      60

```

516

```

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||||
g227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
               80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTCCTAG CAGGCATCAA ACTGCCCCGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTGC GCTTTGCAGG CGGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCG TCGTGCGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGTTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLFA LLQAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep      TSXLQQLTDALMSNLTFLVPPPCVAVISYL
               || |||||:|||||
a227          TAVFLAGIKLPGSIVGMGVLFA LLQAGWVKTSWLQQLTDALMANLTFLVPPPCVAVISYL
               20      30      40      50      60      70

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||||
a227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
               80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLTK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

a228.pep
 1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
 101 KMKDAAK*

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

g229.seq
 1 atggctgccg tatcgggcgg cggtgccggtc ttcctgataa tgcttcacaa
 51 tattgcccgc gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
 101 aaatcgccat tgaagccgcc ggcgaaattg tatcggtctc cgcccaagag
 151 gttttgcccc acaaacggca cggtgccgaa cgagcgcgtt accgaacggt
 201 tttgatggcc gaacgacagg cgcaggttct gttcgtgtaa atctttgtta
 251 tccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgccc
 301 gccgcattg atttcgcgcg acacgcccaa gccgtagcgc aaaccgtgtg
 351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat
 401 tcaatcgttt tttcggacga agcgttggtt atagcggatt acaaaaaatc
 451 aggacaagc ggccggccgc aggcagtagc gatggtacg aaccggttcg
 501 cccggtgctt ggacgcctta gggaaaccgt ccctttgagc cggggcgggg
 551 caaccgtac cggttttgtg tcatccgcca tattgtgttg a

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

g229.pep
 1 MAAVSGGGAV FLIMLPHIAR VQRQPPAFAQ ASGEIGIEAA GEIVSAAAE
 51 VLPDKRHGAE RARYRTLMA EROAQVLF AE IFVIPIMHAA ADAAVEEMMP
 101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFFGR SVVYSGLTKE
 151 RTRRRAGST DGTEFVRPVL GRLREFFPLS RGGATRTGFC SSAILC*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

m229.seq (partial)
 1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
 101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
 151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCGC CTGATGCCGC
 201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTGCGCGCA CACGCCTAAG
 251 CCCTAGCGCA AACCGTGTGC CTTTTCGCGC AGGCTGTTCG CGGTTTTTCGT
 301 CCAGCTTCTG CCCGCAAATT CAATCGTTTT TTCGGACGAA GCGTTGTTTA
 351 TAGCGGATTA ACAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
 401 AATAGTACGG AACCGATTCA CTGGTGCTT CAGCACCTTA GAGAATCGTT
 451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

m229.pep (partial)
 1 ..AQALGEIGIE AADEIVSAAA XEVLDDKRHD AERARYRTVF IAERQAQALF
 51 AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTV LRLQAVGGFR
 101 PASARKFNRF FGRSVVYSGL TKIRTRQSA DSTNSTEPIH LVLQHLRESR
 151 SLFCSSAILC *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||||| ||||| ||||| ||| ||| |||
g229      MAVVSGGGAVFLIMLPHIARVQRQPPAFAQASGEIGIEAAAGEIVSAAAEVLDPKRRHGA
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFIPIIMHAAAADAAVEEMMPARIDFARHAXALAQTVCLL
                ||| ||||| :| ||||| :| ||||| ||||| ||||| ||||| ||||| :| |||||
g229      RARYRTVLMARQAQVLF AEIVFIPIIMHAAA-DAVEEMMPARIDFARHAQAVAQTVCLL
                                70      80      90      100     110

                                100     110     120     130     140
m229.pep      RQAVGGFRPASARKFNRFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRE----
                ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g229      RQAVGGFRPASARKFNRFGRSVVYSGLTKIRTRRRRAAGSTDGTEPVRPVLGRLREPFPL
                120     130     140     150     160     170

                                150     160
m229.pep      -----SRSFLCSSLAILCX
                :| :| ||||| |||
g229      SRGGATRTGFCSSAILC
                180     190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

```

a229.seq (partial)
1  ATGGCTGTCTG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51 TATTGCCCAC GTTCAGCGTC AGCCGCCA.. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTTGCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCCGCTGATG TCTCCGTAGA GGAAATGATG
301 CCCGCCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCTGCA
401 AATTCAATCG TTTTTCGGA CGAAGCGTTG TTTATAGCGG ATTAACAAAA
451 ATCAGGACAA GGCACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTAGCACC TTAGAGAATC GTCTCTTTGA GCTAAGGCCG
551 GGCAACGCCG TACTGGTTT TGTTTCATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

```

a229.pep (partial)
1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51  VLLDKRHDAE *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADVSVEEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRFEG RSVVYSGLTK
151 ITRRRRSADS TDSTEPIHLV LQHLRESSL* AKARQRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||||| ||||| ||||| ||| ||| |||
a229      MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFIPIIMHAAAADAAVEEMMPARIDFARHAXALAQTVCLL
                ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a229      XARYXTVFIAERQAQALFAEIVFVILIVHAAAADVSVEEMMPARIDFARHAQAVAQTVCLL
                70      80      90      100     110     120

```


	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
	: : : : :					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
	: :					
a229	AKARQRRTGFCSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```

g230.seq
1  atgttccatt ccatcgaaaa atacagaaca cccgccaag tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttcccatc
101 cggcgccga ctacatcgtc caagtggcg acgaaaaaat cagcgagcac
151 tcaatcaaca acgccatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtcacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtttg
401 tcgaagaaat ccgcgatcag tttgccttgc agaatttggg aagcctcgtc
451 caaaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcagggt
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcatcgccca agtcaaagcg tctgaagccg atttgagaaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tggaaatagt
651 cgccttgaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaacagg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaaa gcggttgccg acttcaacaa ggcaaaagaa aagctgggcg
851 acgatgcgtt caatcatccc tcctcgcttg ccgaagccgc caaaaacagc
901 ggtttgaaag tggaaacca agaaacttgg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaaa acctaataca tgccgtattc agcgcagacg
1001 tattgaagaa aaaacacaaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tccgcgcaa agaagtccgc gaagaaaaaa acctactggt
1101 tgaagaagcc aaagatgcgg tgcgctcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

```

g230.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGA KLMI SVSSEIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEK AAVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKHN SEVL TINSET
351 AWWVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```

m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCC.GACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC

```

```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTC AAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTGTCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAGAA AAATTGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCT.. ...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPDA VFQSLQRAY LKQGA KLMI SVSSEIQKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGD DAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKTLPFMEA KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDH SINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230.pep	ADGGGSPDAVFQSLQRAYLKQGA KLMI SVSSEIQKI IVDDPNFH DANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGA KLMI SVSSEIQKQ MIVDDPNFH DANGKFSHALLS					
	70	80	90	100	110	120
m230.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
g230	QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
	130	140	150	160	170	180
m230.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230.pep	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGD DAVNHP SSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGD DAFNHP SSLAEAAKNS					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDVLLKKHNSVLTINSETAWVVRKEVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDVLLKKHNSVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPPFAEAKDAVRQAYIRTEAAKL					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACAG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGCTTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCCAAA GCGGTCAAAT TGGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TCGGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVSTV VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAQLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKHNS SEVLTINSET
351 AWWVVRKEVR EEKTLPPFAE KDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGPSRDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIIVDDPNFHDANGKFDHALN					
a230	ADGGGPSRDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIIVDDPNFHDANGKFDHALN					
	70	80	90	100	110	120
	130	140	150	160	170	180

m230.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
a230	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
	130 140 150 160 170 180
m230.pep	190 200 210 220 230 240
	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
a230	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
	190 200 210 220 230 240
m230.pep	250 260 270 280 290 300
	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAVNHPSLAEAAKNS
a230	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSLAEAAKNS
	250 260 270 280 290 300
m230.pep	310 320 330 340 350 360
	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDLVKKKHSEVLTINSETAWVVRKEVR
a230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDLVKKKHSEVLTINSETAWVVRKEVR
	310 320 330 340 350 360
m230.pep	370 380
	EEKTLPF AEAKDAVRQAYIRTEAAKL
a230	EEKTLPF AEAKDAVRQAYIRTEAAKL
	370 380

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT  CCATCGAAAA  ATACAGAACA  CCCGCCCAAG  TCTTATTAGG
51  CCTGATTGCA  TTAACCTTTG  TCGGCTTCGG  CGTCAGCAGC  GTTTCCTATC
101 CGGGCGCCGA  CTACATCGTC  CAAGTGGGCG  ACGAAAAAAT  CAGCGAGCAC
151 TCAATCAACA  ACGCCATGCA  GAACGAGCAG  GCGGACGGCG  GCAGCCCTTG
201 GCGCGACGCG  GTGTTCCAAT  CCCTGCTGCA  ACGCGCCTAC  CTGAAACAGG
251 GCGCGAAGCT  GATGGGCATT  TCGGTTTCTT  CCGAACAAAT  CAAGCAGATG
301 ATGTGGACG  ATCCCAATT  CCACGACGCA  AACGGCAAAT  TCAGTCACGC
351 GCTTTTGAGT  CAATACCTGT  CGCAACGCCA  TATGTCTGAA  GACCAGTTTG
401 TCGAAGAAAT  CCGCGATCAG  TTTGCCTTGC  AGAATTGGT  AAGCCTCGTC
451 CAAAACGGCG  TATTGGTCGG  CGACGCGCAG  CGGGAACAGC  TGATCAGGCT
501 GACGCAGGTC  AACCGCACCA  TCCGTTTCGA  CACTTTC AAC  CCCGACGAGT
551 TCATCGCCCA  AGTCAAAGCG  TCTGAAGCCG  ATTTGCAGAA  ATTTTATAAT
601 GCGAACAAAA  AAGACTATCT  GCTGCCGCGA  GCGGTCAAAT  TGGAAATATG
651 CGCCTTGAAT  CTGAAGGATT  TTGCAGACAA  GCAGACCGTC  AGTGAAACGG
701 AAGTGAAAAA  TGCCTTTGAA  GAGCGCGTGG  CGCGTTTGCC  GGCACATGAA
751 GCCAAACCTT  CTTTCGAGCA  GGAAAAAGCC  GCCGTCGAAA  ACGAATTGAA
801 AATGAAAAAG  GCGGTTGCCG  ACTTCAACAA  GGCAAAAGAA  AAGCTGGGCG
851 ACGATGCGTT  CAATCATCCC  TCCTCGCTTG  CCGAAGCCGC  CAAAACAGC
901 GGTTTGAAAG  TGGAAACCCA  AGAACTTGG  CTGAGCAGGC  AGGACGCACA
951 AATGTCCGGC  ATGCCCGAAA  ACCTAATCAA  TGCCGTATTC  AGCGACGACG
1001 TATTGAAGAA  AAAACACAAT  TCCGAAGTGC  TGACCATCAA  CAGCGAAACC
1051 GCGTGGGTCT  TCCGCGCCAA  AGAAGTCCGC  GAAGAAAAAA  ACCTACTGTT
1101 TGAAGAAGCC  AAAGATGCGG  TGGCTCAGGC  CTATATCCGT  ACCGAAGCCG
1151 CCAAACCTTG  CGAAAACAAG  GCAAAAGAAG  TGCTTACCCA  ACTGAACGGC
1201 GGCAAGGCAG  TTGACGTGAA  ATGGTTCGGAA  GTGTCCGTTT  TGGGCGCGCA
1251 GCAGGCAAGG  CAGTCCATGC  CGCCGAGGCG  TTATGCGGAA  CTGCTGAAAG
1301 CAAAACCGGC  AAACGGCAAA  CCCGCCTATG  TCAGACTGAC  CGGTCTGCCG
1351 GCACCCGTGA  TTGTCGAGGC  GCAGGCAGTC  ACGCCTCCGG  AGGATATTGC
1401 CGCACAGCTT  CCTCCTGCGA  AACAGGCTTT  GGGCGAACAG  CAGTCTGCCA
1451 ATACTTTTCA  CCTGCTGATC  CGCTATTTC  ACGGAAAAAT  CAAACAGACT
1501 AAAGGAGCAC  AATCGGTTGA  CAACGGCGAT  GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT  PAQVLLGLIA  LTFVGVGVST  VSHPGADYIV  QVGDEKISEH
51  SINNAMQNEQ  ADGGSPWRDA  VFQSLQRAY  LKQGAKLMI  SVSSEQIKQM
101  IVDDPNFHDA  NGKFSHALLS  QYLSQRHMSE  DQFVEEIRDQ  FALQNLVSLV

```

```
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELMKKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRakeVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPDIDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```
1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACAG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCATCAACA ACGCCATACA GAACGAACAG CGCGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCTTAC CTGAACACAG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG CGCGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAAGT TCTGAAGCCG ATTTGCGAAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCATTTTGA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCGCG CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCCGAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTACGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTTG CGAAACAAG GCAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACGGGC AAACGGCAAA CCCGCCCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTGCAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GGGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGTTGATA CGTTATTTCA ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAALMGI SVSSEQIKQI
101 IVDNPNFHDA NGKFDHALLN RYLSQRHMSD DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRakeVR EEKTLPPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPDIDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*
```

m230-1/g230-1 96.3% identity in 512 aa overlap

```
10 20 30 40 50 60
m230-1.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
|||||
g230-1 MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
10 20 30 40 50 60

70 80 90 100 110 120
m230-1.pep ADGGGPSRDAVFQSLQRAYLKQGAALMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN
|||||
g230-1 ADGGSPWRDAVFQSLQRAYLKQGAALMGISVSSEQIKQIIVDDPNFHDANGKFSHALLS
70 80 90 100 110 120

130 140 150 160 170 180
m230-1.pep RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
```

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 837>:

a230-1.seq

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCCCCACAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACTCTTCG	TCAGGTTTCGG	GGTCAGACAG	GTATCCCATT
101	CGGGTGGCGA	TCACTATCGT	CAAGTGGGCG	ACGAAAAAAT	CAGCGACACC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	CGGGACGGCG	CGGCGCCCTTC
201	CGCGCGACGG	GTGTGTTCAAT	TCCTGGTACA	ACGCGCCTAC	CTGAACACAGG
251	CGCGGAAGCT	GATGGGCATT	CCGTGTTCTT	CCGAACAATA	CAAGCAGAT
301	ATCTGTGGACG	ATCCCAATTT	CCACGACGCA	ACGGCAGAA	TCGACACGCG
351	GCITTTTAAAC	CGCTACCTTT	CCCAACGTCA	TATGTCGTAA	GACCACTTTG
401	TCGAAGAAAT	CCGCGATCAG	TTTGCCTTGC	AGAATTTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTGGTCGG	CGACGGCAG	CGGGAACAGC	GTATCAGGCT
501	GACGCGAGTC	AACCGCACCA	TCGTTTCGCA	CACTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCGTAAGCCG	ATTTGCAGAA	TGTTTATAAC
601	GCAAAACAAA	AAGACTACCT	GCTTCCCAAA	CGGTCAGAA	TTGGAATATGT
651	CGCCTTGAAT	CTGAAGAGCT	TTGCAAGCAA	ACAGACCTTG	AGCGAAACAG
701	AAGTGAAGAA	TGCGTTTGAA	GAGCGCGTGG	CGCGTTTGCC	CGCAAAATGAA
751	GCCAAACCTT	CTTTCGAGCA	GGAAAAAGCC	CGCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	GCGGTTGCGC	ACTTCAATAA	GGCAAAAGAA	AAGCTGGGCG
851	ATGACCGGCT	CAACCATCCT	TGCTCGCTTG	CCGAAGCGCG	CAAAAACAGC
901	GGTTTGAAG	TCGAAACCCA	ACCAACTTGG	CTGACGAGC	AGGATGCGCA
951	AATGTCGGGT	ATGCCCGAAA	ACCTGATCAA	TGCCGTATTC	AGCGACGACG
1001	TATTGAAGAA	AAAACACAAT	TCCGAAGTGC	TGACCATCAA	CAGCGAARCC
1051	CGGTGGGTTCG	TTCCGCGCAA	ACGAGTCCGC	GAGAGATAAA	CCCTGCGGTT
1101	TGCCGAAGCC	AAAGACGCGG	TACGTACAGC	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTTGC	CGAAAAACAG	GCAAAAAGAC	TGTTATCCCA	TGACACGCGC
1201	GCAAGGCTGA	TTGACGTGAA	ATGGTCGGAA	TGCTTCGTTT	TGGCGCGCAA
1251	GCAGGCAAGG	CAGTCCATGC	CGCCCGAGGC	TTATGCGGAA	CTGCTGAAAG
1301	CAAAACCGGC	AGGCGGCAAA	CCCCGCTACG	TCAGGCTGAT	CGGTCGTCCG
1351	GCACCGGTGA	TTTGCGAAGT	ACAGGCTGTA	ACCCCGCCGG	ATGATATTGCG
1401	CGCACAGCTT	CCGCTTTGCA	AACAGGCTTT	GGCGCAACAG	CAGTCTGCCA
1451	ATACTTTCGA	CTTGTTTGATA	CGTTATTCTA	ACGGCAAAAT	CAACACAGACC
1501	AAAGGAGCGC	AATCGGTCGA	CAACGCGCAC	GGTCAAGTAA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFGVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGFSRDA VFQSLQRAY LKQGAKLMI SVSSEIQIKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKHNN SEVLTINSET
351 AWVVRAKEVR EEKTLPPFAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

q231.seq

1	atgtcaaaaac	gaaaatccat	aaaccgtccg	tatcaaaaaac	cggcggaact
51	gcgcgcgttg	caaaataatc	cgccatttta	cgtaaaaaac	cgccgcctga
101	acttttttat	cgcgcgagac	ggcggttgcg	cgtctccgca	aaaatgcagg
151	gcgcgcgggt	ttcagacggc	atttgccgtt	caaggccgtg	cggtgtcttt
201	accaaattgc	caaccattcg	cccacggaat	ccatccaatc	cttattgccc
251	cgcgcgtctc	tgcctgcctc	gcggtcagcc	cacggcgctt	cggagtttgc
301	agctttccac	aatccctttg	gttcccttcc	cgcctgaatt	tgaagctcgg
351	catagtcggc	aaaatccgcc	ttatcctgct	gttctttagc	ataactttta
401	taatgccacg	cgcgcccgtc	ctgcacctgc	atcaggttca	aatcggtttt
451	gccggcggat	acctgcgcca	cttcgcgctg	atagcggtcg	gtttcaaaaca
501	cacgtacact	gactttccta	ccctcccgcc	cgcgcgcgag	gttgctcgcc
551	gaacgtgtac	cgtaagcctg	tttcatctcc	ggtgcgtcga	tatacgccat
601	cgaattttta	tgtttcgcgc	cgtcgccgct	gatgacgtga	agggtatcgc
651	cgtcatagac	tttggaaccc	gtgcctgtgt	agctgtgtgc	ggatttcgcc
701	gatgcccgtc	ggcgaacggg	cgcgtcgaaa	cccacgtccc	ctgcagtgcc
751	gagtacgtcg	agtacggcaa	ccgccgtccg	caccgcctca	ctgtcatatc
801	ccgtataacc	caacgcgccc	aaaagcgaca	gggcgacggg	aagccatttc
851	atgatttttt	taatctgcat	atttttcaaa	tgccgatgcc	gtctgaacat
901	ctctga				

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

q231.pep

1	MSKRKSINRP	YQKPAELPPL	QNNPPFYRKN	RRLNFFIAAD	GGCASPQKCR
51	ARGFQTAFAV	QGRVAVSLNA	QPFFAGHIPI	LIAPAAPACP	AVRPQRRLIRF
101	SFPQSFAFPF	RLNLSVGVIG	KIRLILLFFS	ITFIMPRRPV	LHLHQVQLIRH
151	AGGYLRHFAL	IAVGFKHTYT	DFPTLRRRAQ	VVARTCTVSL	FHLRCVDIRF
201	PNFMFRAVAV	DDVKGIAVID	FGHRACVAVA	GFRRCPSANG	RVETHVPCSA
251	EYVEYGNRRP	HRLTVISRIT	QRAQKRGDGD	KPFHDFFNLI	IFQMPMPSEH
301	L*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

m231.seq (partial)

1 ATGTCAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAT
51 GCCGCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CTCGCGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG GC

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

m231.pep (partial)

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRAVSLPNA OPFG.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

m231/g231

m231.pep 10 20 30 40 50 60
 MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
 |||||
 g231 MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
 10 20 30 40 50 60

m231.pep 70
 QSRVSLPNAQPPG
 |:|||||:|:
 g231 QGRAVSLPNAQPFAGHPIIAPAAPACPAVRPRRLRIFSFQSFAPFRLNLSVGIVG
 70 80 90 100 110 120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

a231.seq (partial)

```

1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTGCG GTGTCGAACA
501 CCGGACGCT GACTTTCCTG CCTTCCGCGC CCGCGCGCAG GTTGTCCGCG
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGGTGCG TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGGCGGG CGGTCGGAA CCGCGTCCC CTGCGCGGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTT
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPOKCR
51  ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFQSFAPFP RLNLVGLIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFENLH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFG					
a231	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFQSFAPFPRLNLVGLIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTCGCGCTG ATAGCGGTG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCCG ccgcgcgCAG GTTgtcgcGC
551 GAACgGTGAC CGTAagcgtg TTtcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTTta tGTTtcgcgc cgtcgcCgtc gATGACGTGA AGGGtatcGC
651 CgtcATAGAC TTTGGACACC Gtgctgcgt AGctGTGGCC GGATTtcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51  ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

101 SFPQSFAFPF RLNLVGVIG KIRLILLEFS ITFIMPRRPV LHLHQVQIGF
 151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSV FHLRCVDIRH
 201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq
 1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCCTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
 151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
 201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCC
 251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTT
 301 AGCTTTCCAC AATCCTTTC GTTCCCTTTC CGCTGAATT TGAGCGTCGG
 351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
 401 TAATGCCACG CCGCCCGTTC CTGCACCTGC ATCAGGTTC AATCGGTTT
 451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTG GTATCGAACA
 501 CGCGCAGCT GACTTTCCTG CCTCCGCGC CCGCGCGCAG GTTGTGCGC
 551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGCTCGA TATACGCCAT
 601 CCGGATTTG TGTTCGCGC CGTCGCGTC GATAACGTGA AGGTGTGCG
 651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
 701 GATGCTCGGC GCGCGGCGGG CGCGTCGGAA CCGCGCTCC CTGCGCGGCC
 751 GAGTACGTCG AGTACGGCAA CCGCGTCCG CACCGCTCG CTGCGGTACC
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
 851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
 901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep
 1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51 ARGFQTAFV QSRAVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
 101 SFPQSFAFPF RLNLVGVIG KIRLILLEFS ITFIMPRRPV LHLHQVQIGF
 151 ADRNLRHFAL VAVGIEHAHA DFPFRRAQ VVARTRAVSL FHLRRVDIRH
 201 PDFVFRVAV DNVKGVAVD FGHRACVAVA GFRCSAAG RVGTRVPCRA
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
 301 IGGFQTAS*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAGHIHPILIAAPACPAVRPRRLRIFSFPQSFAFFRLNLVGVIG					
m231-1	QSRAVSLPNAQPFAGHIHPILIAAPACSAVRPRRLRIFSFPQSFAFFRLNLVGVIG					
	70	80	90	100	110	120
g231-1.pep	KIRLILLEFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILLEFSITFIMPRRPVLHLHQVQIGFADRNLRFALVAVGIEHAHADFPFRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRCSAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq
 1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCCTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTAA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTG GTGTCGAACA
501 CCGGACGCT GACTTTCCTG CCTTCGCCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCCGTC GATAACGTA AGGGTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCCGC
701 GATGCTCGGC GCGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGQTAFQAV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAL VAVGVEHADA DFPAFERRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRC SAAG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQDGD KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGQTAFQAV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGQTAFQAV					
	10	20	30	40	50	60
a231-1.pep	70	80	90	100	110	120
	QSRVSLPNAQPFAGHIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSVGIIG					
m231-1	QSRVSLPNAQPFAGHIHPILIAPAAPACSAVRPRRLRIFSFPQSFAFPFRLNLVSVGIIG					
	70	80	90	100	110	120
a231-1.pep	130	140	150	160	170	180
	KIRLILFFSITFIMPRRPVHLHLQVQIGFADRNLRFHFAVAVGVEHADADFFAFRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVHLHLQVQIGFADRNLRFHFAVAVGIEHAHADFFAFRRRAQ					
	130	140	150	160	170	180
a231-1.pep	190	200	210	220	230	240
	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAIDFGHRACVAVAGFRRC SAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAIDFGHRACVAVAGFRRC SAAGG					
	190	200	210	220	230	240
a231-1.pep	250	260	270	280	290	300
	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQDGDGKPFHDFNLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQDGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300
a231-1.pep	310					
	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatcctggt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctgttt

```

```

151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtgggaatat
201 tgtccgtggt acaaaatccc tgctgcgtga aacgggtgcg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggg attgccgcg
401 gttcgggtact gtgtgccaaag ttcggcaggg aacgggtgat gttggcttgg
451 gtaacgggtg gtgcgttggg ttcgacgggt tgcggcctgg ttttgggtgtg
501 gctgacgcac ggacaccgtt ttgaagggtt gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cggtgatgac gctgatcggc
601 tttttcggcg gatttttctc cgttcgcgtc tatacctggc tgcaaacgc
651 cagcagcgag actttccgcy cccgcgcgtt tgcgcgcaac aatatcggtta
701 acggcatctt tatgggttcc gccgcggtt tgagcgcggt attgctggtt
751 ttggttgaca gcattttcct gctgtatctg attgtcgcct tgggcaatat
801 tccgttgcg gtatttttga ttaagcgca aaggcggtt ttaggcgcg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGNLGI FWFLSQGWAY PMAVMTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NIWNGIFMVS AAVLSAVLLF
251 LFDSISLILYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1 ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTGC CCATCCTGTT
51 CGGTCAGATT TTGGGAACGG CGGTGCGAGG TGTACGCCT TATATTGTGC
101 GGATACTGGT TTGCTGGTGC GCCGTCGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCCTGGC ACAAATCCC TGCTGCGTGA AACGGTGGG CACAAGCCCG
251 TTTTACC GC CATTATCGGT ATTTCGTGGT TTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTC AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCCGCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTGACGGTT TCGGCTTGG TTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CCGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTCTC CGTTCGCTC TATACCT(g)TG CAAACGCCCA
651 TAGCGAGATT TCCGCGCCG GCCGTTGCC CACAATAT CGTTAACGGT
701 ATTTTATGG TTCCGCTGC CGTTTGGAGC GCGGTGTTGC TGTTTTGTG
751 TGACAGCATT TCCTGTGTGT ATCTGATTGT CGCTTTGGGC AATATCCGT
801 TGTCGGTATT TTGATTAAAG CGCGAAAGGC GGTTTTTAGG CGCGCGGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGNLGI FXFLSQGWAY PMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSIISLILYL ALGNIPLSVF LIKRERRFLG AAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

	10	20	30	40	50	60
m232.pep	MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD					
	: : : : :					
g232	MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD					

531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232.pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPNVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	130	140	150	160	170	180
m232.pep	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFGRRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	190	200	210	220	230	
m232.pep	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMV					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMV					
	190	200	210	220	230	240
	240	250	260	270	280	289
m232.pep	AAVLSAVLLFLFDSISLLYLIVLALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIVLALGNIPLAFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232.seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAGCC GCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTCA
101 AAACCGCGCT GTTGTGATG ATTGGGTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAAC TTG GCGCGTTGC TGTATTATT
201 GCCGTATTC CTGTTTTCCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAT GATCATTATG
301 GCGGTGGCGG CACACGGGTT TTATATCCGG TCTGCCCGCG TGCTTTTGGC
351 GTGTCTGTTT TGCATGGGCG CGCAATCGAC GCTGTTTCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTGTGCGC ATCCTGTTCC GTCAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGGTTT
551 TGCTGTCGCG CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGAATATTG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CGGTGCGGCA CAAGCCCGTT TTTACCGCCA
701 TTATCGGTAT TTCGTGTTT TGGTTTGTCC GCGCGGTTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGAA CGGCTGAGGT TGGCTTGGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTG CGGCTTGGT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTCGGCGGGA
1051 TTTTCTCCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACAA TATCGTTAAC GGTATTTTTA
1151 TGGTTTCCCG TGCCGTTTTC AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTGCTTTG GGCAATATTC CGTTGTCGGT
1251 ATTTTGTATT AAGCGCGAAA GCGGTTTTT AGGCGCGGCG GCAATCAGGA
1301 AAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232.pep
1  MYAKKGGLGL VKSRRFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAGQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLLACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFVA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLFMPVS
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIIGISWF WFGAVYTTQ
251 LPTFTQIHLG GNDNVFNLM ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPUMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAVL SAVLLFLFDS
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLFCMGAQSTLFGPLKYAILPDYLDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP						
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
		180	190	200	210	220	230
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSXERLMLAW					
a232		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSRERLRLAW					
		240	250	260	270	280	290
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVLVWLTHGHRFEGNLGIFXFLSQGWAYPUMAVMTLIGFFGGFFSVPL					
a232		VTVGALGLTVCGLVLVWLTHGHRFEGNLGIFWFLSQGWAYPUMAVMTLIGFFGGFFSVPL					
		300	310	320	330	340	350
m232.pep		220	230	240	250	260	
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
a232		YTWLQTASSETFRARAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
		360	370	380	390	400	410
m232.pep		270	280	289			
		VFLIKRERREFLGAAAIRKKPX					
a232		VFLIKRERREFLGAAAIRKKPX					
		420	430				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

1	atgaaacgca	aaaatatcgc	gctgattccc	gccgccggca	tcgggggtgcg
51	tttcggtgcg	gacaaaacca	agcaatatgt	cgaaatcgga	agcaaaaaccg
101	ttttagaaca	tgtacttggg	atttttgaac	ggcatgaggc	cgctcgatttg
151	accgtcgttg	tcgtctcgcc	cgaagacacg	tttgccgata	aggttcagac
201	ggcatttcca	caggttcggg	tgtggaaaaa	cggtggacag	acccgcgccg
251	aaactgtccg	caacggtgtg	gcaaaactgt	tggaaaaccg	tttggcgcg
301	gaaaccgaca	atattctggt	acacgatgcc	gcccgtgctg	gcctgccgtc
351	tgaagctctg	gcgcggttga	tagaacaggc	gggcaacgcc	gccgaaggcg
401	ggattttggc	agttcccgtt	gccgatacgc	tcaagcgcg	agaaaagcgga
451	caaatacagt	caactgtcga	ccgttcgggg	ctttggcagg	cgcaaacgcc
501	gcagcttttt	caagcgggtt	tgctgcaccg	cgcattggct	gcggaaaact
551	tgggcggcat	taccgatgaa	gcgtccgccg	tggaaaaact	gggtgtgctg
601	ccgctactga	tacaggcgga	cgcgcgcaat	ttgaaaactga	cgcagccgca
651	ggacgcatac	atcgctaggc	tgctgctcaa	tgccgtctga	

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

1	MKRKNIALIP	AAGIGVRFGA	DKPKQYVEIG	SKTVLEHVLG	IFERHEAVDL
51	TVVVVSPEDT	FADKVQTAFP	QVRVWNGGQ	TRAETVRNGV	AKLLETGLAA
101	ETDNILVHDA	ARCCLPSEAL	ARLIEQAGNA	AEGGILAVPV	ADTLKRAESG

533

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR
 201 PLLIQGDARN LKLTQPDAY IVRLLLNAV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTGAGAC
 201 GGCATTTCCT CAGGTTCTGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG
 401 GGATTTTGGC AATTCCCAT TCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFP QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA
 101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

m233.pep	10	20	30	40	50	60
	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
m233.pep	70	80	90	100	110	120
	FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
g233	FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	130	140	150			
	TRLIEQAGNAAEGGILAIPIADTLKCADGGNI					
g233	ARLIEQAGNAAEGGILAVPVADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTGAGAC
 201 GGCATTTCCT CAGGTTCTGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACGTGTCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG
 401 GGATTTTGGC AATTCCCGTT GCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATTAGTG CAACCGTCGA GCGGACGAGC CTTTGGCAGG CGCAAACGCC
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAAACT
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC
 601 CCTTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPIV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDVAV*
```

m233/a233 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
a233	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233.pep	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
a233	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
a233	TRLIEQAGNA AEGGILAIPIVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA					
	130	140	150	160	170	180
a233	AENLDGITDEASAVEKLGIRPLLQGDARNLKLTQPQDAYIVRLLLDVAVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg ttccgcgcgc catcgctttt gccgcgcgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgctcga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggccagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccctag cgattgaaa
301 caggaatccg gcatttccgg caaagcgcag aacctgaaag gcgcagatta
351 tgcgttacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcggggcgaat acgcacttcc caaccgcgaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattgcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRFNV LNRNLSALK
101 QESGISGAQ NLKGADYVVT GDVTEFGRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGTSGY DATLNGKVL
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTGA GACTTGCGAA
101 TCCGCGAAGC .gTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

m234.pep (partial)
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIREAVNS LVQAVDNGAW
 51 QPNR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

				10	20	30
m234.pep				GAGEYALSNREI	IGFGGTSGY	DATLNGKVL
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQ	GAGEYALSNREI	IGFGGTSGY	DATLNGKVL		
	140	150	160	170	180	190
		40	50			
m234.pep		DLAIREAVNSLVQAVDNGAWQPNRX				
			::			
g234		DLAIREAVDNLVQAVDNGAWQSNRX				
	200	210	220			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)
 1 AACCGCACCT ATTTGAACGC ATTAAACAG GAATCCGGCA TTTCCGGCAA
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)
 1 NRTYLNALKQ ESGISGAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD
 101 ATLNGKVL DL AIREAVNSLV QAVDNGAWQP NR*

m234/a234 100.0% identity in 54 aa overlap

				10		20
30						
m234.pep				GAGEYALSNREI	IGFGGTSGY	DATLNGKVL
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQ	GAGEYALSNREI	IGFGGTSGY	DATLNGKVL		
	50	60	70	80	90	100
		40	50			
m234.pep		DLAIREAVNSLVQAVDNGAWQPNRX				
			::			
a234		DLAIREAVNSLVQAVDNGAWQPNRX				
	110	120	130			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

```

1  atgaaacctt tgatttttag gcttgccgcc gtgttggtc tgtctgctg
51  ccaagttcga aaagctcccg acctcgacta cagtcattc aaagaaagca
101 aaccggcttc aattttggtg gttccgccgc tgaacgagtc gcctgatgtc
151 aacggcactt ggggatgct ggcttcgacc gccgcgccga tttccgaagc
201 cggctattac gtctttcccg ccgcagtcgt ggaggaaacc ttcaaagaaa
251 acggcttgac caatgccgcc gatattcacg ccgtccgccg ggaaaaactg
301 catcaaattt tcggcaatga tgcggttttg tacattacgg ttaccgaata
351 cggcacttca tatcaaattt tagacagcgt gacgaccgta tccgccaaag
401 cacggctggt cgattcccg caccgggaaag agttgtggtc gggttcggcc
451 agcatccgcg aaggcagcaa caacagcaac agcggcctgt tgggggcttt
501 ggtcggcgca gtggtcaatc agattgccaa cagcctgacc gaccgcggtt
551 atcaggtttc caaaaccgcc gcatacaacc tactgtcgcc ctattcccgcc
601 aacggtatct tgaaaggtcc gagattcgtc gaagagcagc ccaaataa

```

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

```

1  MKPLILGLAA VLALSACQVR KAPDLDTYTSF KESKPASILV VPPLNESPDV
51  NGTWGMLAST AAPISEAGYY VFPAAVVEET FKENGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWGSQA
151 SIREGSNNSN SGLLGALVGA VVNQIANSLT DRGYQVSKTA AYNLLSPYSR
201 NGILKGPRFV EEQPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

```

1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTCCGAAGC
201 CGGCTATTAC GTCTTCCCG CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGCCG GGAAAACTG
301 CATCAGATTT TCGGCAATGA TGCGGTTTGT TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCCTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGTTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAAGCGA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC CAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAGGTCC GAGATTCGTT GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235.pep

```

1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWGSQA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST					
g235	MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
	:					
g235	AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130      140      150      160      170      180

          190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
          190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCGAAGC
201 CGGCTATTAC GTCTTCCCCG CCGCAGTCGT GGAGGAAACC TTCAAACAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGGTTTGT TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAG
401 CACGGCTGGT CGATTCGCCG AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTC TAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

          10      20      30      40      50      60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          10      20      30      40      50      60

          70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          70      80      90      100     110     120

          130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130     140     150     160     170     180

          190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTA ATGCCAGCAG
101 CGTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATT CTCCGGCGC GGTAAATTCG
251 GCTTCCGCCT GCAAggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAAGTC GGCTTCGGCT TTTCGTTGA TGGCCGGGAA CTGGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTGCGCCG TCGCGCGGC GCGCTGTCTG
551 GCTTTGGTGG TGTAGAGGCG GTCTTCAGG ATGTGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGGAAGG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTTGCG CCGCCGCGCC
701 AATACCAAGG CGTAGCGTC GATTTCCACC ATATCCGCCT GTTGACCGC
751 ATCTTCAATC GGATTAAGT CGCTCAAAT GGCAAacag AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcccgt gTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCTG TATAGACTTC CTGCGGCGCG ACGACGTGTC
951 CGATGGATTT CGACATTTTG CGGCCGTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGNGKFI
51 TDFHFCFRHQ QGKAQFFAQs IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFVVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGGRLAAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNV FHEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAG
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTCCGC GCGCAAAGGC TCGATGCGCG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCACCAGT
101 TCGGCTTCGG TTTTTCGTT GATGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCTCTTCGC CGCCCGCGWT GAYGTCCAC GCTTCTTCGC
201 CCGTGAAGCA CAAATCGGT GCAATCAAGA GAACCAAACT GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CCGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACATG TCTTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG AACTCTTGC AGCTGACGTG CCAATACCAC
451 GCGGTAGCGG TCGATTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCG CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCAGT CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GGCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGGFFV DGRELVPMSME
51 EDAVXFAXX DVPRFFAGEA QNRCNQENQT ACDVIQGS LC AAACMAVCFG
101 GVEAVFQDVE VERTQVFAE RNXYFYGKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDFFHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMQQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```

a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGCAGA
51  CGGTTTTCATG GCCTGCAACC GCGCCACAT  CGCGGGTGTA GTGCCAGCAG
101 CGTTCGCATT TTTACCATT  ACTGGCTTTA GCGGCAACGG CAAGTTCGCT
151 GCGTACTTTC ACTTCGCTT  TAGACACGAG CAAGCAATCTT
201 CGCCCAAAGC ATTCAGATAG CGGGCCATTT CTTCCGGCGC GGTAAATTTCG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTCGGCGC GCAAAGGCTC
301 GATGGCGGCG GTTACGCTT  CGCGGCTTC  GCGGATTGCC GTCCATTTTT
351 TCACCAGTTC GGCTTCGGT  TTTTCGTTGA TGGTCGGGAA CTCGTGCCAA
401 GTATGAAAA  GCACGCTGT  TTCTGCGGCC CGCCCGATGA TGTCCCACGC
451 TTCTTCGCGG GTACAGCACA AAATCGGTGC AATCAAGAGA ACACGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTCGCGCG TCGCGCGGGC GCGGCTGTGC
551 GCTTTGTGTG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACCGGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTC TTTACGGCA  AAGTGGAAAG
651 CATAACGCGG ATAAAAATCA CCGGCAACGC GTTCTTGCAG CCGCCTTGCC
701 AACACCAAGG CATAGCGGTC GATTCTCACC ATATCCGCCT GTTGCACGGC
751 ATCTTCAATA GGATTGAAGT CGTCCAAGTT GGCAACAARA AAGTCARAAG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTTGAG GATTTCTTTG
851 GAAATCGCCA ATTCGCGGCT GTAATCGGTG GATCGCGCCC ACAGGCGCAG
901 GATGTCGCGC CCGAACTCGT TATACACTTC TTGCGGCGCG ACGACGTTGC
951 CGATGGATTG CCGACTTTTG CGCCGCTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTTGTATCG CGCGCGACCC ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

```
a236.pep
1 MARFAFSADI LCTAFADGFM ACNRAHIAGV VPAAFAFFTI TGFSGNGKFA
51 AYHFHCFRHO QSKAQFFAQ IGIAGHFFRR GNEFGFLQGR TDCFVGQAQRL
101 DGGGYREAGF ADCRPFPHQF QFGFVFDGRE LVPSMEKHAV FCAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGGRLAAAG AAVGFGGIEA VFQDIEVERA
201 QVFRARNRHF FHGKVEGIR IKITGNAFLQ PPCQHQIGAV DPHHIRLLHG
251 IKNRIEVAQV GKQKQAGIAD TAVAFGYALE DFFGNRQFAV VIGGCRPQAO
301 DVRAELVIHF LRRDDVADGF RHFAFVLIHH ETMGOLFVR RATH*
```

m236/a236 81.0% identity in 258 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

```

g237.seq
1   atgcggggaca aggttgggcgg taatatcgca ctccccgcc cacgaatatt
51  cgatttctaac atcgggaagc tgcggaaaaa ctttaagcat atcttggcgg
101 acaaagctcgg tcatacggcg aggatattgtc ataaattcgt tacccttacc
151 gccgaaaagc agcctgcgct cgcgctgtag gcggtataaa tccaaaatat
201 ggcggttgct gcatactgcc atattgtgtg ggataagccc ttttgtgcgc
251 gcgcccagg gtctcggtggc aataataaag gtgctgacgg caatcgctct
301 gcgttccaaa ggccggaata tcgggttcaa accgacataa gtattgacgg
351 catagaccac atttttacac tgcagctgtc cttcggggct gtaaaccagg
401 caaccgtttt gatacgggtc gatcgcgctc atcggggatt tcgcgaaaat
451 ctgcgcgcgg gcttcggcag cggcgctggc aacacccaac gtgtaattga
501 gcg gatgaag atgcccgga aagggatcga actgtgcgcc ttggtacata
551 tcgctgtcaa gctgctggtt caactcgggt ttatcccaaa gttgataatg
601 atctgcaccg taatgcggtt gggcgtgttc atgccactgc tgcaactctt
651 cccaatgctg cggacggagc gcaaccgtgg cataaccgcy cgtccaactc
701 caatcgatgg catgtttgcg gacgcgttcg tccaccagtt cgaccgcctg
751 caaagactgt tgccaaaacc attgcgcctg ctcaaggcgg acctgttttt
801 caatttcccc cataccgcga gcgtagtcgc tgataaacctg cccgccactc
851 ctgccggacg cgccgaagcc gatacgtgcy gctttccaaa cgagcgcttc
901 atgtcctgtg tcgccagcgg gcaatgcggt acacaaaccg ctcaaacccg
951 cgccgataat gcaggtttcg gctttcagac ggcattggag tttcggataa
1001 acagtatcgg gattaaaccga actaaaataa taagaaggca gatattcttg
1051 aaaatcaggc cgaatcattg tctttgcttt atcgggtata ttttcgggag
1101 gaatgataga gactgtcggg ccatatcgtc caacagaata atccatttga

```

This corresponds to the amino acid sequence <SEQ ID 882; ORF 237.ng>:

g237.pep

1 MRDKVGGNIA LPAPRIFDSN IGKLRKQFKH ILADKLGHTR RIVDKFVILT

51 AEQPAVRAE AVIIQNMAVV AYCHIVADKP FCARAQGGFG NNGKADGNRL

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN
 151 LRAGFGSGAG NTQRVIERMK MPGQGIELCA LVHIAVKLLF QLGFIPLKIM
 201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRIL
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF
 301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRQIFL
 351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq
 1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCGCCGCC CACGAATATT
 51 CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTAAGCAT ATCTGGCGG
 101 ACAAGCTCGG TCATaCGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC
 151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
 201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTGCGCGC
 251 GCCCCAAGG GTTCGGTCGC AATAATAAAG GTGCTGACAG CAATCGCCTT
 301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG
 351 CATAGACCAC ATTTTTCGAC TCGACGCTGC CTTGCGGCGT GTAAACCAGC
 401 CAACCGTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAT
 451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCAAA GTGTAAGTGA
 501 GCGGATGCAG GTGTCCGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA
 551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG
 601 ACTCGCACCG TAATGCCGTT GGGCGTGTTC ATGCCACTGC TGCAACTCTT
 651 CCCAATGCTG CGGACGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
 701 CAATCGACGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
 751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
 801 CAATTTCCCC CATAACCGAG nCGTAATCGC TGATAACCTG CCCGCCACTC
 851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACGTTTC
 901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCAATCCGC
 951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA
 1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
 1051 AAAATCAGGG CGAATCATTG TGTTCGCTT ATCAGGTGTA TTTTCGGACG
 1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAWACAGAAA ATCGGTTGA

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep
 1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT
 51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGGADSNRL
 101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN
 151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIPLKIM
 201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRIL
 251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRAET DTRGFQHNRF
 301 MSLLRQGQCS AQTTQSAADD TGIGFQTALK FRINSMRINR TEIIRRQIFL
 351 KIRANHCVCF IRCIFGRNDT GCRAISSKQK IG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH	TLRIVDKLVILTAEKQSAVRAE				
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH	TRIVDKFVILTAEKQPAVRAE				
	10	20	30	40	50	60
m237.pep	70	80	90	100	110	120
	AVIIQNMAVVAYCHIVTDKPF	FCARPQGFGRNNGGADSNRLAFQRPEYRVQ	TCISIDSIDH			
g237	AVIIQNMAVVAYCHIVADKPF	CARAQGFGGNNGGADGNRLAFQRPEYRVQ	TDISIDGIDH			
	70	80	90	100	110	120
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGT	SDAQSVSERMQVSGXGVELCP				

g237	IFTLDAAFGRVNPQTVLIRFDARHRLLENLRAGFGSGAGNTQQRVIERMKMPGQGIELCA	130	140	150	160	170	180
		190	200	210	220	230	240
m237.pep	LVHIAVKLLFQLGFIPKLI MTRTVMPLGVFMPLLQLFPMLRTDGNRGITALPITIDGMFA						
g237	LVHIAVKLLFQLGFIPKLI MTRTVMPLGVFMPLLQLFPMLRTDGNRGITALPIAIDGMFA						
		190	200	210	220	230	240
		250	260	270	280	290	300
m237.pep	DAFVHQFDRLQRLLPKPLRLRLQADLFFNFPHTAXVIADNLPATPSRRRAETDTRGFQHNRF						
g237	DAFVHQFDRLQRLLPKPLRLRLQADLFFNFPHTAGVVADNLPATPAGRAEADTCGFQNDGF						
		250	260	270	280	290	300
		310	320	330	340	350	360
m237.pep	MSLLRQGCQAQTQSAAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCVF						
g237	MSVFRQRCCGTQTAQTAADNAGFGFQTALEFRINSMRINRTKIIRRQIFLKIRANHCVCVF						
		310	320	330	340	350	360
		370	380				
m237.pep	IRCIFGRNDTGCRAISSXQKIGX						
g237	IGYIFGRNDTDCRAISSXQKIGX						
		370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 885>:

```

a237. seq
1 ATGCGGGACA AGGTTGCGG TAATGTCGCA CTCCCCGCC CACGAATATT
51 CGATTTTGAC ATCGGCAAG TCGGGAAAAA CTTTAAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATACGCGC GGGATTGTGC ATAAACTCGT TATCTTACCC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
201 GACGGTTGTC GCATATGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251 GCGCCCAAGG GTTCTGTGGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGCTCAAAA GGCTTGAATA TCGGATTCAA ACCGGCAFAA GTATTGACGG
351 CGTACACCAG ATTTTTGCAT TCGACGCTGC CTTCGGGGGT GTAAACCAGC
401 CAACCGTTTT GATAAGGTTT AATCGGTATC ATGGGAGAAAT GCTCAAAAT
451 CTTCTGACCA GCTTCGGCAG CGGCGCGGGC GATGCCCAAC GTGTAATTGA
501 GCGGATGGAG AGTCCCGGAC AAGGGATCGA ACTGTGCGCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGCTT CAGTTCAGTG TTATCCAGA GTTGATAATG
601 AGTTGACCGC TAATATTTTT GGGCGTGCTC ATGCCATTGT TGC AATTCTT
651 CCCAATGCTG CGAACGGATG GCAACCGTGG CATAACCTGC CTGCCAATCG
701 CAATCAATGG CATGTTTGCG GACGCGTTCG TCACCAAGT GCACCGCTCG
751 CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCAAACCG ACCTGTTTTT
801 CAATTCCTCT CATACCGCAG GCGTAATCGC TGATAACCTG CCGGCCACTC
851 CGTCCCGAGC GCGGAAACC GATACGCGCG GCTTCCAACA CAACCGCTTC
901 ATGTCCTCTG TCCGCAAGG GCAATGCAGT GCACAAACCA CTC AATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA
1001 ACAGTATGAG GATTAACCGA ATGAAAATAA TAAGAAGGCA GATATCTCTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCGGTTATA TTTTCGGACG
1101 GAATGATACA GGCTGTCGAG CCATATCGTC CAAACAGAAA ATCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 886; ORF 237.a>:

a237.pcp

1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIIQNMVTV	AYCHIVADKP	FCTRAQGFQC	NNKGADSNRL
101	ALQRLEYRIQ	TGISIDGVHQ	IFAFDAAFGG	VNQPTVLIRF	NAYHGRMLKN
151	LRTSPGSGAG	DAQRVIERME	MPGGQIELCA	LHVHAIKLLL	QSFVIPLELM
201	SCTVIFLGLV	MPLLQFFPML	RTDGNRGITA	LPIAINGMFA	DAFVHQDFRL
251	QRLLPKPLRL	LQTDLFFNFL	HTAGVIADNL	PATPSRRAET	DTRGFQHNRF
301	MSLLRQGQCS	AQTTQSAADD	TGIGFOATLK	FRINSMRINR	TEIIRRQIFL
351	KIRANHCVCVF	IGYIFGRNDT	GCAISSSOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
a237	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE					
m237.pep	70	80	90	100	110	120
	AVIIQNMVAVYCHIVTDKPFPCARPQGFGRNNKGADSNRLAFORPEYRVQTCISIDSIDH					
a237	70	80	90	100	110	120
	AVIIQNMVAVYCHIVADKPFCTRAQGFGRNNKGADSNRLALQRLEYRIQTGISIDGVHQ					
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMRFDARHRLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	130	140	150	160	170	180
	IFAFDAAFGGVNQPTVLIREFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
m237.pep	190	200	210	220	230	240
	LVHIAVKLLFQLGFIPKILMTRTVMLGVFMPLQLFPMRLTDGNGRGTALPITIDGMFA					
a237	190	200	210	220	230	240
	LVHIAVKLLQLQFSVIPILMSCTVIFLGVLMPLQLFFPMRLTDGNGRGTALPIAINGMFA					
m237.pep	250	260	270	280	290	300
	DAFVHQFDRLQRLLPKPLRLQADLFFNFPHTAXVIADNLPATPSRRAETDTRGFQHNRF					
a237	250	260	270	280	290	300
	DAFVHQFDRLQRLLPKPLRLQTDLFFNFLTHTAGVIADNLPATPSRRAETDTRGFQHNRF					
m237.pep	310	320	330	340	350	360
	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
a237	310	320	330	340	350	360
	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
m237.pep	370	380				
	IRCIFGRNDTGCRAISSXQKIGX					
a237	370	380				
	IGYIFGRNDTGCRAISSXQKIGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatatc
51  gatgctgcat atccccatta gtcacgcgaa cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctgcgcggcag tgtaaaaaat cgggtttgcy ccgtccaaac
201 atttgatgca actgcggtcg gcccatact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtcggtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttacca cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggc tcaaggcggc
451 gggtatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttccgcaa gccctttttt
551 cagaccgctg gctaaaaaaa aatgccggtg ccgcttccgg ttttctcagc
601 cgtgcggatg aagcaggaaa actgatattg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgtc caagggtcgg
701 ttaatccttt ttaacgggt tttcaagggt tagggattgg ggcaattaca
751 gacagtgcgg taagcccgtt cacagataca gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcaca cttgccgcgg

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851 cgagcctatt acaggacagt gcctttgctg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtagcagagg ccgcagggtac ggtttggcgc ggtaaaaaag
1001 tagaacttaa cccgacccaa tgggattggg ttaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgaggggtgca agacaaacta gtggaggcgg atggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFMM LLAAAISMLH IPISHANGLD ARLRDDMQAK HYPEPGGKYHL
51 FGNARGSVKN RVCVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKTKINTVPQ APFSDRWLKE NAGAAAGFLS
201 RADEAGKLIW ENDPKNWRA NRMDDIRGIV QGAVNPFLTQ FQGVGIGAIT
251 DSAVSPVTDt AAQQTLLQGIN DLGNLSPEAQ LAAASLLQDS AFVAVKDGINS
301 ARQWADAHNP ITATAQTALA VAEAAGTVWR GKKVELNPTK WDWVKNITGYK
351 KPAARHMQTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYt IDSNEKRNKI KNHGLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTGCG CTATTCAAAA ATTCATGATG CTGTTTGCGAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGATG GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CAcTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCATTCTGA
351 TTTGAGCGGC GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTTCATCGAA
401 CAGGTCGCGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACTTCA ACAAAAACAA AGACTAATAT TGTCCCTCAA GCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTCTGAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTTC GGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTAGGAA AATTAAGTCC GGAAGCACA CTGTGTCGG
851 CGAGCCTATT ACAGGACAGT GCTTTGCGG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TAAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAAATTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTACAAC AACAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEPGGKYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```

```

151 DYPPPGGARD IYSYYVKGTS TKTKTNIVPQ APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQOTLQGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS
301 AKQWADAHPN ITATAQTALS AAEAAGTVWR GKKVELNPTK WDVKNTGYK
351 KPAARHMQTL DGEMAGGNKP IKSLPNSAAE KRKQNFKEFN SNWSSASFDS
401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
451 LDSNGNAVKT GNLQKQAKD YLQQQTHIRN LDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

m238.pep	10	20	30	40	50	60
	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAAI SMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHHD SKSTSDFSG					
g238	RVCAVQTFDATAVGPILPITHERTGFEGVIGYETHFSGHGHEVHSPFDNHDSKSTSDFSG					
	70	80	90	100	110	120
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTSTKTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGYEPQGGARDIYSYHIKGTSTKTKINTVPQ					
	130	140	150	160	170	180
m238.pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
m238.pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTD TAAQOTLQGINDLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
g238	FQGVGIGAITDSAVSPVTD TAAQOTLQGINDLGNLSPEAQ LAAASLLQDS AFAVKDGINS					
	250	260	270	280	290	300
m238.pep	310	320	330	340	350	360
	AKQWADAHPNITATAQTALSAAEAAGTVWRGKKVELNPTKWDVKNTGYKKPAARHMQTL					
g238	ARQWADAHPNITATAQTALAVAEAGTVWRGKKVELNPTKWDVKNTGYKKPAARHMQTV					
	310	320	330	340	350	360
m238.pep	370	380	390	400	410	420
	DGEMAGGNKPIKSLPNSAAEKRKQNFKEFNSNWSSASFDSVHKTLPNAPGILSPDKVKT					
g238	DGEMAGGNRPPKSI-TSEGKANAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
m238.pep	430	440	450	460	470	480
	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLD SNGNAVKTGNLQKQAKDYLQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTSGGGWLSRDGTRQYRPPTEKKSQFATTGIQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

a238.seq (partial)

```

1 ATGAATTGCG CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTTCG GCGCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTGA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAGCGGC GCGGTAGACG GTGGTTTTAC CGTTTACCAA CTTATCCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGAGTAATAT TGTTCGCCGA GCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGCAG TAAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAAA TGGGATTGGG TTTAAAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGCCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA

```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

a238.pep (partial)

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGGKYHL
51 FGNARGSVKN RYVAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD AAQQTQGIN HLGNSPEAQ LAAATALQDS AFAVKDGIN
301 ARQWADAHFN ITATAQALA VAEAATTWVG GKKVELNPTK WDVKNTGYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ

```

m238/a238 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPPGGKYHL	FGNARGSVKK
a238	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPPGGKYHL	FGNARGSVKN
	70	80	90	100	110	120
m238.pep	RYVAVQTFDA	TAVSPVLPIT	HERTGFEGII	GYETHFSGHG	HEVHSPFDNH	DSKSTSDFSG
a238	RYVAVQTFDA	TAVGPILPIT	HERTGFEGII	GYETHFSGHG	HEVHSPFDNH	DSKSTSDFSG
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYVKGTS	STKTKNIVPQ
a238	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYVKGTS	STKTKNIVPR
	190	200	210	220	230	240
m238.pep	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDVRGIV	QGAVNPFLMG
a238	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDIRGIV	QGAVNPFLMG
	250	260	270	280	290	300
m238.pep	FQGVGIGAIT	DSAVSPVTD	AAQQTQGIN	DLGKLSPEAQ	LAAASLLQDS	SAFAVKDGIN

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|||||
a238      FQGVGIGAITDSAVSPVTDTAQQTLQGINHLGNLSPEAQLAAATALQDSAFVKGINS
           250      260      270      280      290      300
           310      320      330      340      350      360
m238.pep  AKQWADAHFNITATAQTALSAEEAAGTVWRGKKVELNPTKWDVVKNTGYKKPAARHMQTL
           |||||
a238      ARQWADAHFNITATAQTALAVAEAAATTVWGGKKVELNPTKWDVVKNTGYKTPAVRTMHTL
           310      320      330      340      350      360
           370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRKQNFEEKFNSNWSSASFDSVHKTLTPNAPGILSPDKVK
           |||||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttccacc ataaaggatg tgcccgaaac cggcggatgg aggttttgtt
51  tttctgccgc cgccctgatc gcttcgtgat tcgccaaacg cgcctgttgc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacggt tttctctgtt attattccgg tatcggaccg
301 gcagtcgcgt ccgccacacg caaaactgcg ctccctcgcc tcgggttggc
351 ggcaatttcc gcttcaccgc gctttaatgc cctgccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgccagct cggcaggggc
451 tcgtgttgcg aatatttttt gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaaccgcc gccctcttcc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttaataaag
601 atgctggattg cctggaaggt gcgctcgca ggatcctgcc cccgctcgcg
651 agtacggacg ttttgtgcca cgatctgcgc cagcttgcgg gttgtatcga
701 ttggactttc cgcccgttgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLRRI LLQGDPLFFR
51  LVQSCVEPV LVLLHHNGKS GNAHRKQOKE IRFVHCRSDV FLCYYSIGIP
101 AVRSATRKTAL LALGLAAIS ASPGFNALPT IFRGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSRLLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMTIWRRL
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKGATGG AGGTTTGTGT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTG GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTCGCG
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTCG TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTACCCG GCTTTAATGC CCTGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCACGCG CGGCAGGGG
451 GCGTGTGCG AATATTTTTT GACAACTGC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTTGCAG GTTGTATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CCGGCGGCTA
751 AACCGCTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

m239.pep
 1 MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLR II LLQGDFLFFR
 51 LIQSCEIEPV LVLLHHNGKS GNAHRKQQKE IQFVHCHSDV FLCDCSGIGP
 101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
 201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIRRL
 251 NRSSP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

m239.pep	10	20	30	40	50	60
	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLR I ILLQGDFLFFRLIQSCEIEPV					
g239	MFHHKGIARNRRMEVLFFCRRPDRFVIRQTRLLQPHLR I ILLQGDFLFFRLVQSCEIEPV					
	10	20	30	40	50	60
m239.pep	70	80	90	100	110	120
	LVLLHHNGKSGNAHRKQQKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTA LLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQQKEIRFVHCRSDVFLCYYSIGIPAVRSATRKTA LLALGLAAIS					
	70	80	90	100	110	120
m239.pep	130	140	150	160	170	180
	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
m239.pep	190	200	210	220	230	240
	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
m239.pep	250					
	ATMARAIRRLNRSSPX					
g239	ATMARTIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq

1	ATGCTCCACC	ATAAAGGTAT	TGCCCGAAAC	CGGCGGATGG	AGGTTTTGTT
51	TTTCTGCCGC	CGCCCTGATC	GCTTCGTGGT	TGCCCAAACG	CGCCTGTTGC
101	AGCCTCATTT	GCGCATAATC	CTGCTCCAAG	GCGATTTCTT	GTTTTTTCGC
151	CTTATCCAAA	GCTGTGAAGT	TGAGCCTGTA	CTGGTTTTGC	TGCATCACAA
201	CGGAAAAAGC	GGAAACGCAC	ACCGCAAGCA	GCAGAAGGAA	ATTCAATTG
251	TTCATTGCCA	TTCAGACGTT	TTTCTCTGTG	ATTGTTCCGG	TATCGGACCG
301	GCAGTCCGCT	CGCCACACG	CAAAACCGCA	CTTCTCGCCC	TCGGATTGGC
351	GGCAATTTC	GCCTACCCG	GCTTTAATGC	CCTGCCCGCG	ATTTTCAGGG
401	GCGGCTCGGG	CAAATCCGCT	TCCCTGACCG	CGGCCAGCG	CGGCAGGGG
451	GCGTGTGCG	AATATTTTT	GACAACTGC	TTCACAATGC	GGTCTTCCAA
501	CGAATGAAA	GCAATGACCG	CCAAACGTCC	GCCCTCTTTC	AGACGACACA
551	TGACCTGCGG	CAATACTGCC	CCTACTTCTT	CAAGCTCGCG	GTTAATAAAG
601	ATGCGGATTG	CCTGGAAGGT	GCGCGTCGCA	GGATCCTGCC	CCCGCTCGCG
651	AGTACGGACG	TTTTGTGCCA	CGATCTGCGC	CAGCTTGGCG	GTGTATCGA
701	TTGGACTTTC	CGCCCGTTGC	GCAACAATGG	CGCGCGCAAT	CTGGCGGCTA
751	AACCGCTCTT	CACCATAA			

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
1  MLHHKGIARN  RRMEVLFFCR  RPDRFVVRQT  RLLQPHLRII  LLQGDFLFFR
51  LIQSCEVEPV  LVLLHHNGKS  GNAHRKQOKE  IQFVHCHSDV  FLCDCSGIGP
101 AVRSATRKTA  LLALGLAAIS  ASPGFNALPA  IFRGGSGKSA  SLTAAQRGRG
151 ACCEYFLTNC  FTMRSSNEWK  AMTAKRPPSF  RRHMTCGNTA  PTSSSSRLIK
201 MRIAWKVRVA  GSCPRSRVRT  FCATICASLR  VVSIGLSARC  ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRILLQGDFFLFRLIQSCEIEPV					
a239	MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLRILLQGDFFLFRLIQSCEVEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTTALLALGLAAIS					
a239	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTTALLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
a239	ASPGFNALPAIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
a239	RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIIRLNRSSPX					
a239	ATMARAIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
1  atgatagaag  tcatacat  ttctcgcgcc  gaaacgcgca  gacagtttgc
51  ttgtgccgac  gttggacgat  ttctgcataa  tgccgcgcac  atccaaagag
101 gggtaaacat  gggatcatc  gcgcacggga  gacggtccga  ttttataaag
151 ctgcgtattc  agccggtcgt  tcaaatacgg  ttgcccgcga  tccaatgcct
201 tcgcaatcac  gaacggtttg  attgccgaac  cagggttcgat  catatcggtt
251 acggcacggt  tgcgcgcgtg  ttctgtgtct  gcccgcccg  gtctgttggg
301 atcgtaggag  ggcgtattgg  ccaaggcgag  gatttccccc  gtgcgggcat
351 ccaaaaccac  caccgttccg  gcttttgctt  gatggtattc  gaccgccttg
401 ttcaactctt  cataggccaa  ggtctgaatc  ctctgatcga  gggaaaggat
451 gatgtctttg  ccgttttgcg  gtgctttatt  gcgcggggag  tccaagctgt
501 ccacaatatt  gccctgccgg  tcccgcacaa  caacttccgc  gccgtcttcg
551 ccatacaggc  tgtcttcaag  cgaaagtcc  aaaccttct  gacctttgcc
601 gtcaatatcg  gtaaatccga  tgacgtgtgc  aaacagggtg  cccatcgggt
651 aatggcggtt  taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
1  MIEVIHFFGA  ETRRQFACAD  VGRFLHNAAH  IQRGVNMGII  AHGRRSDFIR
51  LRIQPFVQIG  FARIQCLRNH  ERFDCRTRFD  HIGYGTVAPL  FAVCPAGSVG
101 IVGGRIGQGE  DFPRAGIQNH  HRSGFCLMV  DRLVQLFIGO  GLNPLIEGKD
151 DVFAVLRCFI  ARGVQAVHNI  ALPVPQNNFR  AVFAIQAVFK  RKFQTFLTFA
```

201 VNIGKSDDVC KOVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 901>:

```
m240.beq
1 ATGATAGAAG TCATACATTT CTTCCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCGGATT TATAAGGCTG
151 CGTATTCAGT CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGTTGGATC
301 GTAGGCGGGC GTATTGCGCA AGGCGAGGAT TTCCCCCGTG CCGGCATCCA
351 AaACCACCAT CGTTCGGGCT TTGCGCTGAT GGTATTTCGAC CGCCTTGTTT
401 AACTCTTTCG AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCCTTGGCC TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCACAA CCTTCTGAC CTTTGCGGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGCTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

m240.pep

1	MIEVIHFFGT	ETRRQFACAD	VGRFLHDAAH	IQRGVNMGIA	HGRRSDFIRL
51	RIQPFVQIGF	ARIQCLRNHK	RFCDCRTGFDH	IGYGTVA PLF	<u>AVCPAGPVGI</u>
101	<u>VGGRIGQGG</u>	FPRAGIQXHH	RSFGPLMVFD	RLVQLFIQGG	LNPLIEGKDD
151	VFAVFRGFEXA	RGVQAVHNIA	LPVPQNDFRA	VFAMQAVFKR	KFQTFLTFAV
201	NIGKSDDVCK	OV AHR VM AF			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

m240/q240

		10	20	30	40	50	59
m240.pep		MIEVIHFFGTETRRQFACADVGRFLHDAAH	IQGVNMG	I-AHGR	RSDFIR	LRIQ	PFVQIG
		:		:			
g240		MIEVIHFFGAETRRQFACADVGRFLHNAAH	IQGVNMG	IIAHGR	RSDFIR	LRIQ	PFVQIG
		10	20	30	40	50	60
	60	70	80	90	100	110	119
m240.pep		FARIQCLRNH	KRFDCRTG	FHDHIGY	GTVAPL	FAVCPAG	PVGIVGGRIGQGEDFPRAGIQXH
		:					
g240		FARIQCLRNH	ERFDCR	TRFDHIGY	GTVAPL	FAVCPAG	SVGVIGGRIGQGEDFPRAGIQNH
		70	80	90	100	110	120
	120	130	140	150	160	170	179
m240.pep		HRSGFCLMV	FDRLVQL	FIGQGLN	PLIEGK	DDVFAV	FRGFXARGVQAVHNIALPVPQNDFR
		:		:			
g240		HRSGFCLMV	FDRLVQL	FIGQGLN	PLIEGK	DDVFAV	LRCFIARGVQAVHNIALPVPQNNFR
		130	140	150	160	170	180
	180	190	200	210	220		
m240.pep		AVFAMQAV	FKRKFQ	TFLTF	AVNIGK	SDDVCK	QVAHRVMAFX
		:					
g240		AVFAIQAV	FKRKFQ	TFLTF	AVNIGK	SDDVCK	QVAHRVMAF
		190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 903>:

```

a240.seq
1  ATGATAGAAG  TCATACATTT  CTTCGGCACC  GAAACGCGCA  GACAGTTTGC
51  TTGTGCCGAC  GTTGACGAT  TTCGTCATGA  TGCCGCGCAC  ATCCAAAGAG
101 GGGTAAACAT  GGGTATCGCG  CACGGGAGAC  GGTCCGATT  TATAAGGCTG
151 CGTATTCAGC  CGTTCGTTCA  AATCGACTTT  GCCCGATCC  AATCGCTTCG
201 CAATCAAAA  CGGTTTGATT  GCGCAACCGG  GTTCGATCAT  ATCGGTTACG

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```

251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCCGGCT TTGCTTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTATTGCG CGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
1  MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH	IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF				
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH	IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF				
	10	20	30	40	50	60
m240.pep	ARIQCLRNHKRFD CRTGFDHIGYGTVAPLF	AVCPAGPVGIVGGRIGQGEDFPRAGIQXHH				
a240	ARIQCLRNHKRFD CRTGFDHIGYGTVAPLF	AVCPAGPVGIVGGRIGQGEDFPRAGIQNH				
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFD CRTGFDHIGYGTVAPLF	AVCPAGPVGIVGGRIGQGEDFPRAGIQXHH				
a240	ARIQCLRNHKRFD CRTGFDHIGYGTVAPLF	AVCPAGPVGIVGGRIGQGEDFPRAGIQNH				
	70	80	90	100	110	120
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDD	VFAVFRGFARGVQAVHNIALPVPQNDFRA				
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDD	VFAVFRGFARGVQAVHNIALPVPQNDFRA				
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDD	VFAVFRGFARGVQAVHNIALPVPQNDFRA				
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDD	VFAVFRGFARGVQAVHNIALPVPQNDFRA				
	130	140	150	160	170	180
m240.pep	VFAMQAVFKRKFTFLTFAVNIGKSDDVCK	QVAHRVMAFX				
a240	VFAMQAVFKRKFTFLTFAVNIGKSDDVCK	QVAHRVMAFX				
	190	200	210	220		
m240.pep	VFAMQAVFKRKFTFLTFAVNIGKSDDVCK	QVAHRVMAFX				
a240	VFAMQAVFKRKFTFLTFAVNIGKSDDVCK	QVAHRVMAFX				
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTCA AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCCGGCT TTGCTTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTATGCG CGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHPHE PASSTCAAKS

```

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDL IGCIAHAFNR SPKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGGCG GCCGTGGACA TGACCGTGTG
51  CGATTCCTC ATCGGATGCA TCGCGCACGC TTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTGTG CAAAAGCTGA TTGTTGGCAT CACATCTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGCTCTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVMTVR AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA
51  VGNIGYTIDD NIAGFRIVGF KHADDFDNR EHARIFDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVMTVR	AVDMTVCDL	IGCIAHAFNC
g241	QPTYLLHPSN	KMPSETEQTL	FRRHQIPPSC	RQSVVMTVR	TVDMTVCDL	IGCIAHAFNR
	70	80	90	100	110	120
m241.pep	40	50	60	70	80	90
	SLKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVGF	KHADDFDNR	EHARIFDQ
g241	SFKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVRF	KHHTDLDFNR	ERARIFNTDQ
	130	140	150	160	170	180
m241.pep	100	110	120	130	140	150
	LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV	QKLIVGIIHL
g241	LRIMLTERIV	GRKRHFDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFI	QKLIVGIIHL
	190	200	210	220	230	240
m241.pep	160	170				
	IMQRNHGIFH	DSHICPFRNS	RLITGAFX			
g241	IMQRNHGIFC	NSHICPFRNS	RLITGAFX			
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACCTG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC

```

251	ATCAGATACC	TCCAAGCTGC	CGGCAATCAG	TGGTGGTGAT	GACCGTGCGG
301	ACCGTGGACA	TGACCGTGTG	CGATTTCCTC	ATCGGATGCA	TCGCGCACAC
351	TTTCAACCGT	AGCCTTAAAG	CGATTTTTCA	TGCTGCCAA	AGGATGGTTG
401	CCGTCCACCA	CCGCCTTACC	CTCGGCAACA	TCGGTTACAC	GATAGACGAC
451	AACATCGCGG	GTTTTCAGAT	GTCCGGCTTC	AAACATCATG	CCGACTTCGA
501	CTTCAACAGG	GAACACGCCC	GCATCTTCAA	TACGGACCAA	CTCCGGATCC
551	TGCTCGCCGA	ACGCATCGTC	GGGCGAAAGC	GCCACATCGA	CCGTATCGCC
601	GGCATCCTTA	CCGTGCAACG	CCTCTTCCAC	CAAAGGGA	ATGCCGTCGT
651	AACCGCCGTG	CAGATACGCA	ATCGGTTCTT	CGGTTTTGTC	CAAAGCTGA
701	TTGTGTGGCAT	CATACATCTC	ATAATGCAGC	GAACCACGG	AATTCTTCAC
751	GATAGCCATA	TTTGTCTTTT	CAGGAACAGC	AGATTAAATTA	CAGGCGCATT
801	CTAA				

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```
a241.pep
1  MPTRPTRAAK HTPPTWLQT AYCPRPPYRP PSVQHTHPHE PASSTCAAKS
51  ANRRENFHNA QPTYLHPSN KMPSEMEQTL FRRHQIPpsc RQSVVVMTVR
101 TVDMTVCDLF IGCIAHTFNR SLKADFHACQ RMVAVVHRLT VGNIGYITDD
151 NIAGFIRVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHRIDRIA
201 GILTVQRLFH QRENNAVTVAV QIRNRFFGFEV QKLIVGIHL IMQRNHGILH
251 DSHICPRFNS RLITGAF*
```

m241/a241 96.0% identity in 177 aa overlap

m241.pep				10	20	30	
				RQSVVVM	TVRAVDM	TVCDFLIGCIAHAFNC	
a241	QPTYLLHPSNKMPSEMEQTLFRRHQIP	PPSC	RQSVVVM	TVRTVDM	TVCDFLIGCIAHTFNR		
	70	80	90	100	110	120	
m241.pep		40	50	60	70	80	90
		SLKADFHACQRMVAVHHRLAVGNIGYT	IDDNIAGFR	IVGFKHHAD	FDNFREHAR	IFD	TDQ
a241		SLKADFHACQRMVAVHHRLTVGNIGYT	IDDNIAGFR	IVGFKHHAD	FDNFREHAR	IFD	TDQ
		130	140	150	160	170	180
m241.pep		100	110	120	130	140	150
		LRILLAERIVGRQRHIDRIAGILT	VQRLFHQRENA	VTVAVQIRNR	FFGFVQKL	LIVGI	IHL
a241		LRILLAERIVGRKRHIDRIAGILT	VQRLFHQRENA	VTVAVQIRNR	FFGFVQKL	LIVGI	IHL
		190	200	210	220	230	240
m241.pep		160	170				
		IMQRNHGIFHDSHICPF	RNSRLITGA	FX			
a241		IMQRNHGILHDSHICPF	RNSRLITGA	FX			
		250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 911>:

g241-1.seq

1	ATGATAGAAG	TCATACATT	CTTCGGCACC	GAAACGCGCA	GACAGCTTTGC
51	TTGTGCCGAC	GTTCGACGAT	TTCTGCATGA	GTCCCGCGCA	ATCCAAGAGC
101	GGGTAAACAT	GGGTATCGCG	CACGGGAGAC	TGGCTCGATT	TATAAGGCTG
151	CGTATTACAG	CGTTCGTAT	AATCGGTTT	GCCCGCATCC	AATGCTTCG
201	CAATACAAA	CGTTTGTTA	GCCGAACCGG	GTTCGATCAT	ATCGGTTACG
251	GCACGGTTGC	GCCGCTGTTC	GCTGCTGCCC	GCTCCGGGCC	TGTTGGGATC
301	GTAGGCGGGC	GTATTGGCCA	AGGCGAGGAT	TTCCCCGCTG	CGGGCATCCA
351	AiACCACCA	CGTTCGGCT	TTTGCCTGAT	TGATTCGAC	CGCCTTGTTT
401	AACCTTTCAT	AGGCCAAGGT	CTGAATCCTC	GATCGCAGGG	AAGAGATGAT
451	GTCTTTGCCG	TTTTTTGGGG	CTTTAKTCGC	CGGGGAGTCC	AAGCTGTCCA
501	CAATATTGCC	CTGCGGCTCC	CGCAAAGACA	CTTCGCGCCC	GTCTTCGCCA
551	TGCAAGCTGT	CTTCAAGCGA	AAGTTCCTAA	CCTTCCTGAC	CTTTGCCGTC
601	AATATCCGTA	AATCCGATGA	CGTGTGCAAA	CAGGTTGCCC	ATCGGGTAAT
651	GGCGTTTAA				

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

g241-1.pap

```

1  MPTRPTRAAN PPTETTLWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPS RQSVVMTVR
101 TVDMTVCDFL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCCG GGCAAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCCCT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCGGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTGT
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCG GCATCTTCGA TACGGACCAA CTCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCCTT CAGGAACAGC AGATTAATA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pap

```

1  MPTRPTRAAN PPTPPTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPS RQSVVMTVR
101 AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVGF KHHADDFDNR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pap	MPTRPTRAANPPTPPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPPTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pap	QPTYLLHPSNKMPSETEQLFRRHQIPPSRQSVVMTVRVAVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSETEQLFRRHQIPPSRQSVVMTVRTVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pap	SLKADFHACQRMVAVVHRLAVGNIGYTIDDNIAGFRIVGFKHADDFDNRERARIFDQDQ					
g241	SFKADFHACQRMVAVVHRLAVGNIGYTIDDNIAGFRIVRFKHHTDLDFNRERARIFDQDQ					
	130	140	150	160	170	180
m241-1.pap	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pap	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCCTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1. pep

```

1  MPTRPTRA AK HPTPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRENFHNA OPTYLLHPSN KMPSEMEQTL FRRHQIPPS RQSVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNREFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1. pep	MPTRPTRAANPPTPPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRENSHNA					
a241	MPTRPTRA AKHPTPPTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRENFHNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m241-1. pep	OPTYLLHPSN KMPSETEQTLFRRHQIPPSRQSVVMTVRVDMTVCDFLIGCIAHAFNC					
a241	OPTYLLHPSN KMPSEMEQTLFRRHQIPPSRQSVVMTVRTVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m241-1. pep	SLKADFACQ RMVAVHRLAVGNIGYTIDDNIAGFRIVGFKHHADFDNREHARIFDITDQ					
a241	SLKADFACQ RMVAVHRLTVGNIGYTIDDNIAGFRIVGFKHHADFDNREHARIFNTDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m241-1. pep	LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNREFGFVQKLIVGIIHL					
a241	LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNREFGFVQKLIVGIIHL					
	190	200	210	220	230	240
	250	260				
m241-1. pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	IMQRNHGILHDSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242. seq

```

1  atgatcgggc aacttggtgt tttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaatttgcg gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccc cggtattcgc
201 tttcgtcgcg cagcccgccc aaggccatac ggacatatat ccgccccgtt
251 gctttggcga tggattcgcc caaagaggtt ttgcccacgc ccggagggcc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttggacgg
351 cgaggtattc caaaatccgt tctttgactt ttccaggccg gtagtggctg
401 gcatccagca ccagtcggcg tttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgga gcagggtgtc gatgtagttg cgtacgacgg

```

501 tggattcggc agacatcggc ggcattcatt ttagtttttt cagttcggac
551 aggcattttt cttccgcttc tttggtcata cccgcctttt ttagtgcctgc
601 ctccaaggca tccagtgcgc cgttttcgct ttcttcgccc aattctttgt
651 gtatcgcttt aatctgttcg ttcagataat attcgcggtg ggatttttcc
701 atttggcggt tgacgcgctc gcgtatgcgt ttttcggcct gcataatgtc
751 gagttcggat ccaagctttc ccagcaggaa ttccatccgt ttgccgattt
801 cgggaatctc tccactctgt tggcgttgcg ccagtttcaa ctgcaaatgc
851 gctgcgaccg tatcggttag

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242 . pep

```

1  MIGELVVLVF IEHFKQRAGG IAPKVAAQFV DFVEQEQRVS YACFCHILQN
51  LAGHRADIGT AVPADFAFVA HAAQGHDTIF PPRCFGDGFA QRGFAHARRA
101 DQTQNRFTFEL VHTFLDGEVF QNPFFDFQQA VVVGIQHQSG FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRRHHEFFV QFGQAFFFRF FGHTRLFDAC
201 LQGIQFAVFV FFAQGVYVYRF NLFVQIIIFAL GFFHCLADFAS AYAFFGLHNV
251 EFGFQLCQQE FHPFADFGNL QNLALLRQFO LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242.seq

1	ATGATCGGCA	AAC TTGTTGT	TTT GTTCCGG	ATCGAGCACT	TCGAGCAACG
51	CGCTGGCGGG	ATCGCCTCGG	AAGTCGTTAC	CAAATTTGTC	GATTTCTGTCG
101	AGCAGGAACA	AGGGGTTTTT	CACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
151	CTTACCGGGC	ATAGAGCCGA	TATAGGTGCG	GCGGTGTCCC	CTGATTTCTGC
201	TTTCGTGCG	CACGCCGCC	AAAGCCATGC	GGACATATTT	CCGCCCCGTT
251	GCTTTGCGCA	TGGAATCGCC	CAAGAGGTT	TGTCCCACGC	CCGGAGGGCC
301	GACCAGGCAC	AGAATCGGCG	CTTTGAGTTT	GTCCATACGT	TTTTGGACGG
351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCCAGGCC	GTAGTGGTCG
401	GATCCAGCA	CCAGTCCGGC	TTTGCGCATG	TCCTTGCTGA	CGCGGGATTT
451	TTTCTTCCAC	GGCAGCTCGA	GCAAGATGTC	GATGTAGTTG	CGTACGACGG
501	TGGATTCCGC	AGCACTCGGT	GGCATCATTT	TGAGCTTTTT	CAGTTCGGAG
551	AGGCATTTTT	CTTCGCGTTC	TTTGCTCATA	CCGCCTTTT	TGATATCTGC
601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTCGTC	TTCTTCGCCG	AGGTCTTTGT
651	GTATCGCTTT	AATCTGTTTC	TTCAGATAAT	ATTCCGCGCTG	GGATTTTTTCC
701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATTT
801	CGGGAATTT	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAAATGC
851	CTGCGACCGC	TATCGGTTAG			

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242 . pep

1	MIGKLVVLF	IEHFEQRAGG	IASEVVTQFV	DFVEQEQGVF	HAGFCHILQN
51	LTGHRADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHARRA
101	DQAQNRAFEF	VHTPLDGEVF	QNPFFDFFQA	VVVGIQHQSG	FGDVFADAGF
151	FLPRLQEQSV	DVVAYDGGFR	RHRWHHFEFL	QFGQAFFFFR	FGHTRLFDIC
201	FGQIQEAFVF	FFAQGFVYFR	NLFVQIIFAL	GGFHAFDAS	AYAFFGLHN
251	EPGFQLCQOE	FHPFADFNGF	QNLLARQFO	LMQRCDRIG*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVLVLF	GIHF	EQRAGGI	ASEVVTQ	FVDFVEQE	QGVF
	:	:	:		:	
g242	MIGELVVL	LFVIEH	FKQRAG	GIAPKVA	AQFVDF	VEQEQR
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFA	FVAAHQ	SHADIF	PPRCFG	DGFGA	QRGF
			: :			
g242	AVPADFA	FVAAHQ	GHTDIF	PPRCFG	DGFGA	QRGF
	70	80	90	100	110	120

557

	130	140	150	160	170	180
m242.pep	QNPFDFDFFQAVVVGIIHQSGFGDVADAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					
g242	QNPFDFDFFQAVVVGIIHQSGFGDVADAGFFLPRQSEQGVDDVAYDGGFRRHRWHHFELF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m242.pep	QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS					
g242	QFGQAFFFRFFGHTRLFDACLOGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS					
	190	200	210	220	230	240
	250	260	270	280	290	
m242.pep	AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNQLLALRQFQLQMRCDRIGX					
g242	AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNQLLALRQFQLQMRCDRIGX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 921>:

a242.seq	1	ATGATCGGCG	AACCTGTTGT	TTTGCTCGGG	ATCAAGCACT	TCGAGCAACG
	51	CGCTGGCGGG	ATCGCCCGG	AAGTCGCTAN	CCAATTTGTC	GATTTCGTCG
	101	AGCAGGAACA	ATGGGTTTT	TACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
	151	CTTACCGGGC	ATGGAGCCGA	TATAGGTGCG	GCGGTGTCCC	CGGATTTCCG
	201	TTTCGTGCGC	CACGCCGCC	AAAGCCATGC	GGACATATT	CCGCCCGTT
	251	GCTTTGGCGA	TGGATTCCGC	CAAAGAGGTT	TTGCCACGC	CTGGAGGGCC
	301	GACCAGGCAC	AGAATCGGC	CTTTGAGTTT	GTCCATACGT	TTTTGGACGG
	351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCCAGGCC	GATGTGGTCG
	401	GTATCCAGCA	CCAATCCGC	TTTGCGATG	TCTTGCTGA	CGCGGATTT
	451	TTTCTTCAC	GGCAGTTCGA	GCAGGTGTC	GATGTAGTTG	CGTACGACGG
	501	TGGATTCGCG	AGACATCGC	GGCATCATT	TGAGCTTTT	CAGTCCGAC
	551	AGGCATTTT	CTTCCGCTC	TTTGGTCATA	CCCGCTTTT	TGATATCTGC
	601	TTCCAAGCA	TCCAGTTCG	CGTTTTCGTC	TTCTTCGCCC	AGTTCTTTGT
	651	GTATCGCTT	AATCTGTTG	TTTCTGATA	ATTCGCGCTG	GGATTTTTC
	701	ATTGCGCTT	TGACGCTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
	751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATT
	801	CGGAATTTT	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAAATGC
	851	GCTGCGACCG	TATCGTTAG			

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242.pep	1	MIGELVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
	51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHAWRA
	101	DQAQNRAFEF	VHTFLDGEVF	QNPFDFDFFQ	VVVGIIHQSG	FGDVADAGF
	151	FLPRQFEQGV	DVVAYDGGFG	RHRRHHFELF	QFGQAFFFRF	FGHTRLFDIC
	201	FQGIQFAVFV	FFAQFFVYRF	NLFVQIIFAL	GFFHLAFDAS	AYAFFGLHNV
	251	EFGFQLCQOE	FHPFADFNGF	QNLALRQFQ	LQMRCDRIG*	

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVLLFGIEHFEQRAGGIASEVVTFVDFVEQEQQVFHAGFCHILQNLTGHRADIGA					
a242	MIGELVLLGIIKHFEQRAGGIASEVAXQFVDFVEQEQQVFYAGFCHILQNLTGHRADIGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFAHARRADQAQNRAFEFVHTFLDGEVF					
a242	AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFAHAWRADQAQNRAFEFVHTFLDGEVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m242.pep	QNPFDFDFFQAVVVGIIHQSGFGDVADAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					

```

a242      QNPFFDFFQAVVVGIIHQSGFGDVFADAGFFLPRQFEQGVDDVAYDGGFGRHRRHHFELF
           130      140      150      160      170      180
           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIFALGFFHLAFDAS
           |||
a242      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIFALGFFHLAFDAS
           190      200      210      220      230      240
           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHFPADFGNFQNLALRQFQLQMRCDRIGX
           |||
a242      AYAFFGLHNVEFGFQLCQQEFHFPADFGNFQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcC cgAGTTaccg CCGATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGCGAACA GGTCTTCCTC
201 TTCCTGCAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTGTGTT
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCCACACG GGGCGAaYa GGTCTTCCTC
201 TTCCTGCAA CCCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTGTGTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

```

m243/g243
           10      20      30      40      50      60
m243.pep  MVIVWLPELPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||
g243      MVIVWLPELPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60
           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```


70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATCCAGCGGT TTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTCGCGGA
251 TCACGTCCAC CATTCGTCA ACGGTCACCC TGCCGATGAG CTTTTGTGTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagcccggcc ggcgggttca gacggcattg ccgctttact
51  tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggett cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctactg gccaccgcct gcacgcctg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga tttcggtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatcgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttcac ggcaaaattc tgtccggcga acttgtgcgt
451 atcggcaatt tcctgctggt ggcggcgccg caggttttgc tcgtttgcca
501 aagcgcgag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcgccg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacggtttc caccgcctcc acattttcaa
651 ccgctttctt actgttttgc tgctgtgtct gttcgctcat atcgatatcc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgcgcgc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTONALQEQIN QIIPQTPSGF LPCHRNHSRA
51  QHTVQGQGITL LHHTNHGIGF LLTGHRHLRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRLQILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLAH IVSLKTNWKS KSGYYPKIR
251 TFSRNFQORQ EISHPPPNTL PQPKYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

1	ATGCCGTC	TGG	AAGCCGACA	GGCGGTTCA	GACGGCATTG	CCGCTTTACT
51	TCGATCGGT	TATACGCAA	ACGCGCTTCA	GGAAATAAAT	CAGATTATTC	
101	CCCAGACGCC	TTTACGCTTC	CTTCTGCGCC	ACCGTAACCA	TAGCCGGGCG	
151	CAACACGCGG	TCGGACACGG	TATAACCCCT	CTTCATCACA	CCCACACCGG	
201	TATTCGCTC	CTGTTCGCT	GCCACCGCCT	GCATCGCCTG	ATGGATATTC	
251	GGATCGAGCT	TATCGCCCGC	TTTAGGGTTG	ATTTCCTTGA	TTTGCGTAGC	
301	ATCAAATGCT	TTCTGCAACT	CGTTCAAAGT	CATCTGCACG	CCCATTTTCA	
351	GCGCATCGAA	ATTGCCGCTC	TGATCCAAAA	GCGCCATTTC	CAGATAATCC	
401	TTGACCGGCA	GCATTTCAC	GGCAAACTTC	TGTCGGGCGA	ACTTGTGCGT	
451	ATCCGCAATT	TYTCTGTGGT	GGCGGCGCGC	CAGGTTTTGC	TCGTTTGCCA	
501	AAGCGCGCTG	CTCGTCTTTC	AACTCGCTTT	CCAGCTCGGC	AATCCGCGCC	
551	TGCAAATCCT	CATAAGCCGG	CTCTGCGGCA	GCCTGTTCCT	GCACACCGTC	
601	CGCATTTCT	ACTGTTTCGA	CGGTTTCAC	CGCTCCACA	TTTTCAACCG	
651	CTTCTTCACT	GTTTGTCTGC	TGTGTCTGTT	CGCTCATATC	GTATCCCTTA	
701	AAACAAATTG	GAAATCAAAA	TCCAGTTATT	ACCCGCGCAA	GATAAGGACA	
751	TTTTCAAGAA	ACTTCAAKCA	AAACAGCAGA	ATTTCAAATT	CATTTTCAAA	
801	TCCCCTACCG	AAAAATAAAT	ATAGACGGTA	A		

This corresponds to the amino acid sequence <SEQ ID 932: ORF 244>:

m244 . pep

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTHHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101 IKCFQLQVQS  HLHAHFQRIE  IAALIQKRHF  QIILDRQH FH  GKLLSGELVR
151 IRNFLVAAA  QVLLVCQSA  LVFQLRFQHG  NPRLQILIS  LCGSLFLHTV
201 RISYCFQDGH  RLHIFNRFFT  VLLCLFAHI  VSLKTNWKS  SSSYPKIRT
251 FSRNFXQXGR  ISNSFNSNPL  KKKYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTSPSGFLLRHNRHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTSPSGFLPCRHNHSRAQHTVGQGITT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	: : : : :					
g244	LHHTNHGIGFLTGHRLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m244 . pep	IAALIQRKRFQIILDRQHFHGKLLSGELVRIRNFFLLVAAQAQVLLVCQSAAALLVFQLRFQL					
	:					
g244	ITALIQRKRFQIILDRQHFHGKLLSGELVRIGNFFLLVAAAQVLLVCQSAQLFVFQLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244 . pep	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRFFTULLCLFAHIVSLKTNWKS					
	:					
g244	GNPRLQILISRLGGSLFLYTIVIRISYCLDGFHRLHIFNRFFTULLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244 . pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPPLPKXYRRX					
	: : : :					
g244	KSGYYPSKIRTFSRNFKQEQEISHPPNTLPQPKYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTT CTGTTCTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTCCTTGA TTGCGTAGC
301 ATCAAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAACTTC TGTCCGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCG CAGGTTTGC TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCAATT CCTACTGTCT CGACGGTTTC CACCGCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTGC TGCTGTGTCT GTTCGTCAT ATCGTATCCC
701 TTAAACAAA TTGAAATCA AAATCCAGT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTCAA ATTCATTTTC
801 AAATCCCTA CCGAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEIIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQKRO RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQEIINQIIPQTPSGFLLHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTONALQEIINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	230
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgccgctg aagcccgcc gccgggttca gacggcattg ccgctttact
```

51	tcgatcggtt	tatacgcaaa	acgcgcttca	ggaaataaat	cagattatttc
101	cccagacgcc	ttcaggcttc	cttcctgtccc	accgtaacca	tagccggcgcg
151	caacacacgg	tcggacaggg	tataaccttc	cttcatacaca	ccaacacagg
201	tattggggtc	ctgtctactg	gccaccgcct	gcctcgcttc	attggtatttc
251	ggatcgagct	tatcgcccg	ttaggattg	atttctctga	tttgcgtggc
301	atcaaacgcc	tctgcaact	cattcaaa	catctgcaga	cccatttttc
351	gcgcatcgaa	attaccgtc	tgatccaaaa	ggccatttc	cagataatcc
401	ttgacggca	acatttcaac	ggcaaaactc	tgctcgcgca	acttgtcgct
451	atcggcaatt	tctctgctgt	ggcggcgccg	caggttttgc	tctgtttgcca
501	aagcgcgcag	ttgttcgtt	ttcaactgcg	cttcagcttc	ggcaatccgc
551	gcttcgaaat	cctcataagc	cggctcgccg	gcagccgtgt	cctgtacacc
601	gtccgcattt	ctctactgtc	cgacgggttc	caccgcctcc	acattttcaa
651	ccgctcttcc	actgttttgc	tgtctgtct	gttcgctcat	atcgatatcc
701	tcaaaatcaa	gttgaaatca	aaatccggt	attaccggag	caagataagg
751	acattttcaa	gaaattttcaa	gcaaaaggcag	gaaatttcac	atccgcgcgc
801	gaatacccta	ccgcaaaaac	catataaacg	gtaa	

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pgp

1	MPPEARPAGS	DGIAALLRSV	YTQNALQETN	QIIPQTPSGF	LPCHRNHSRA
51	QHTVQGQGIT	LHHTNHGTFE	LLTGKHLRHL	MDIRELTAR	FRIDPLDLRG
101	IKRLLQLQTS	LHHTHGFQIE	ITALIQKHFH	QIILDRQHFF	GKLLSGELVR
151	<u>IGNELLVAAA</u>	<u>QVLVCSQAQ</u>	LFVFLRFLQL	GNPRLQILIS	RLGGSFLFLYT
201	VRISYCDLGF	HLRHIFNFRF	<u>TVLLLCFLAF</u>	IVSLKTNWKS	KSQGYPSKIR
251	TFSRNFKQRQ	EISHPPNTFL	PQPKYK*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

1	ATGCCGTC	AAGCCGACA	GGCGGGTTCA	GACGGCATTG	CCGCTTTACT
51	TCGATCGGTT	TATACGCAA	ACGCGCTTCA	GGAAATAAAT	CAGATTAATC
101	CCACAGAGCC	TTACGGCTT	CTTCTGCGCC	ACCGTACAAC	TACCCGCGCG
151	CAACACGCGG	TCGGACAGCG	TTAACCCTTT	CTTCATCAAC	CCGACAGGCG
201	TATTCGCGTC	CTGTTGCTT	GCCACGCGCT	GCATCGCCCTG	ATTGATATGC
251	GGATCGAGTG	TATCGCCCGC	TTTAGGGTTG	ATTTCTCTGA	TTTGCGTATC
301	ATCAAAATGCT	TTCTGCAACT	CGTTCAAAGT	CATCTGCACG	CCCATTTTCA
351	GCGCATCGAA	ATTGCCGCTC	TGATCCAAAA	GCGCCATTTC	CAGATAATCC
401	TTGACCGGCA	CGATTTCGAC	GGCAAACCTT	TGTCGCGGCA	ACTTTGCGGT
451	ATTCGCAATT	TyCTGCTGGC	GCGCGCGCGC	CAGGTTTTFG	TCGTTTGCCA
501	AAGCGCGCTG	CTCGTCTTTC	AACTGCGTTT	CCAGCTCGGC	AATCCGCGCC
551	TGCAAAATCT	CATAAGCCGG	CTCTGCGCAC	GCCTGTTCTC	GCACACCGCT
601	CGCATTTCTC	ACTGTTTTCG	CGGTTCCGCA	CGCTCCCAAC	TTTTCACCGC
651	CTTCTTCACT	GTTTGTGTGC	TGTGTCTGTT	CGCTCAIATC	GTATCCCTTA
701	AAACAAATTG	GAAATCAAAA	TCCAGTTATT	ACCGCGCA	GATAAGGACA
751	TTTTCAGAA	ACTTCAAKCA	AAAKCAGAGA	ATTTCAAATT	CATTTCACAA
801	TCCCTTACCG	AAAAATAA			

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pgp

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVQQRILT  LLHHTHGRIE  LFACLRHLRL  MDIRIELTAR  FRVFDLDRS
101 IKCFLQVLQS  HLHHAHQRIE  IAAILQKRHF  QILDRQHFF  GKLLSGELVR
151 IRNFLLVAAA  QVLLVCQSAL  LVFQLRFQLG  NPLRLQILSR  LCGSLFLHTV
201 RISYCFDGFH  RLHI FNRFFT  VLLLCFLFAH  VSLKTNWKSX  SSYYPRKIRT
251 FSNFYXOKOR  ISNSFSNPLP  KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLLRHRNHSRAQH	AVGQRITL			
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLPCHRNHSRAQHT	VGQGITL			
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDF	LDLRSIKCFQLVQSHLHAHFQRIE				
g244-1	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDF	LDLRGIKRLQLIQSHLTHFQRIE				
	70	80	90	100	110	120

	130	140	150	160	170	180
m244-1.pep	IAALIQKRHFQIILDRQHFGKLLSGELVRIRNFFLLVAAQVLLVCQSAALLVVFQLR	QFL				
	:					
g244-1	ITALIQKRHFQIILDRQHFGKLLSGELVRIGNFFLLVAAQVLLVCQSAQLFVVFQLR	QFL				
	:					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFPTVLLLCFAHIVSLKT	NWKS				
g244-1	GNPRLQILISRLGGSFLFYTVRISYCLDGFHRLHIFNRFPTVLLLCFAHIVSLKT	NWKS				
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKX					
	:		: :	: :	: :	
g244-1	KSGYYPSKIRTFSRNFQQRQEISHPPNTLPQKPYKRX					
	:		: :	: :	: :	
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```
1 ATGCCGCTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51 TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCCGACAGCG TATAACCCCT CTTCATACG CCCACACGGG
201 TATTGGGTTT CTGTTCGCTT GCCACGGCT GCATCGCTAG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCCCTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCGCGCT TGATCAAAGA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACTTC TGTCCGCGA ACTTGTGCGT
451 ATCCGCAATT TCTCTGFGTT GCGGGCGCGC CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG TCGCTCGTCT TTCAACTGCG CTTCCAGTC GGCATCCGCG
551 GCCTGCAAA CTCTATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCAATT CTTACTGTCT CGACGTGTCT CACCGCCCTC ACATTTTCAA
651 CCGCTTCTTC ACTGTGTTTG TGCTGTTTTC GTTCGCTTAT ATCGTATCCC
701 TTAACAACAA TTGGAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AATATCCCTCA CCGAAAAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pap

1	MPSEARQAGS	DGIAALLRSV	YTQNALQEIN	QIIPOTPSGF	LLCHRNHSRA
51	QHAVGQRITL	LHHAHHGIGF	LFACHRLHRL	MDIRIELIAR	FRIDFLDLRS
101	IKCFLQLVQS	HLHAHFQRIE	IAALIQKRHF	QILDRQHFH	GKLSGLSELVR
151	IRNFLVAAA	QVLVLCQSAQ	LLVFQLRFQL	GNPRLQILIS	RLCGSLFLHT
201	VRISYCLDGF	HLRHILFNRF	TKVLLCLFAH	IVSLKTNWKS	KSSYYPKIR
251	TFSRNFKRQF	RISNSFNPL	PQL*		

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60	
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLLRHRNHSRAQH	AVGQRITL				
a244-1	MPSEARQAGSDGIAALLRSVYTQNALQEINQII	PQTPSGFLLCHRNHSRAQH	AVGQRITL				
	10	20	30	40	50	60	
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDF	LDLSIKCFQLQVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDF	LDLSIKCFQLQVQSHLHAHFQRIE					
	70	80	90	100	110	120	
m244-1.pep	:						
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDF	LDLSIKCFQLQVQSHLHAHFQRIE					
	70	80	90	100	110	120	
m244-1.pep	IAALIQRKRFQIILDROHFHGKLLSGELVRI	RNFLLVAAQVLLVCQSA-LLVFQLR	FQL				
a244-1	IAALIQRKRFQIILDROHFHGKLLSGELVRI	RNFLLVAAQVLLVCQSAQLLVFQLR	FQL				
	130	140	150	160	170	179	
m244-1.pep	IAALIQRKRFQIILDROHFHGKLLSGELVRI	RNFLLVAAQVLLVCQSA-LLVFQLR	FQL				
a244-1	IAALIQRKRFQIILDROHFHGKLLSGELVRI	RNFLLVAAQVLLVCQSAQLLVFQLR	FQL				
	130	140	150	160	170	180	
m244-1.pep	GNPRLQILISRLCGSLFLHTVRI	SYCFDGFHRLHIFNRFFT	VLLLC	FAHIVSLKTNWKS			
a244-1	GNPRLQILISRLCGSLFLHTVRI	SYCLDGFHRLHIFNRFFT	VLLLC	FAHIVSLKTNWKS			
	180	190	200	210	220	230	239
m244-1.pep	GNPRLQILISRLCGSLFLHTVRI	SYCFDGFHRLHIFNRFFT	VLLLC	FAHIVSLKTNWKS			
a244-1	GNPRLQILISRLCGSLFLHTVRI	SYCLDGFHRLHIFNRFFT	VLLLC	FAHIVSLKTNWKS			
	190	200	210	220	230	240	

240 250 260 270
 m244-1.pep KSSYYPRKIRTFSRNFXQQRISNFSNPLPKKX
 |||||
 a244-1 KSSYYPRKIRTFSRNFKQQRISNFSNPLPKKX
 250 260 270

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 941>:

```
g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgcc tctgttttcga
51  ccagacacag cgtgcccggt tcggcaacag cgaagtttac gccgctcaag
101 ccgacatcgg cagtgtctga aatatcgcg agggctttgc gggcgaatcc
151 ggtcagttgg tccacgtctg ctgtaagcgg tgtgcgcagg ttttggtgga
201 acagttcgct gacctgttct ttggttttat ggattgcggg catcacgata
251 tgggtcgggt ttctgcctgc catttggacg ataaactcgc ccaagtcgct
301 ttcaccgcgc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 ctctcgctgac catggatttg cctttgacca tcagcttgcc gtttttggt
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgccca
451 gtgtactttc acgcccact tagtcagggt ttcttccaac tgctccagca
501 gcqcqqqtaa
```

This corresponds to the amino acid sequence <SEQ ID 942; ORF 246.ng>:

g246 .pep

1	MYGRNGSTQA	AVAFVFDQTQ	RARFGNGEVY	AAQADIGSAV	NIAQGFAGES
51	GQLVHVVCKR	CAEVLVEQFA	DLFFFGMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDFDAD	HGFAFDHQLA	VFGCDDVVDN	LAGFGRGRFP
151	VFYHQAOLSOV	FFOLLOOGR*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 943>:

m246.seq (partial)

```
1 ATGCACGGGC GGTACGGTGG TACTCAAGCG ACCGTTgCTT CGTTTTCCAC
51 CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCACGAAAC
101 CGACATCGGC AGTgCTGTAA ATATCGCGCA GTGCTTTACG GGCAGAACCG
151 GTcAGTTGGT TcATACGCTC TGTcACGGCG GTACCGAGGT TTTGGTGGAA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTTGTG GATAGCAGGC ATCACCATAT
251 GGGTCGGTTT TTGCcCTGCC ATTTGGACGA TGAACTCGCC CAAGTCGCTT
301 TCTACCGCTT TAATGcYttT TGCTTCAAGA TAATGtTTCA GCTCGATTTC
351 CTCGCTGACC ATCGATTTCG CTTTGACCAT CAGCTTGGCCG TTTTGGGCTG
401 TGATGATGTC GTGGATAATT TGGCAGGCTT CGGTcGGGGT TTTCTGCCG...
```

This corresponds to the amino acid sequence <SEQ ID 944; ORF 246>:

m246.pep (partial)

1	MHGRYGGTQA	TVAFVFHQTC	RTCFNSGKVY	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYIVCQR	RTEVLVEQFA	NLFFGFVDSR	HHDMGRFFAC	HLDDLEAQVA
101	FYRFNAFCFK	IMXQLDFLAD	HRFAFDHOLA	VFGCDVVDN	LAGEGRGECP

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

m246/g246

[illegible]

565

	70	80	90	100	110	120
m246 . pep	130	140	150			
	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246 . seq (partial)

```

1  ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTTGCCT TCGTTTTCCA
51  CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAAA
101 CCGACATCGG CAGTGTCTGTA AATATCGCGC AGTGCTTTAC GGGCGAAGCC
151 GGTCAGTTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTGGTGGGA
201 ACAGTTCGCT AACCTGTTCT TTGGTTTTAT GGATTGCGGG CATCACGATA
251 TGGGTCGGTT TTTCACCTGC CATTGGACG ATGAACGCG CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATT
351 CCTCGCTGAC CATCGATTG CCTTTGACCA TCAGCTTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGCAGGCT TCGCCCGGTG TTCCCGCCA
451 GTGTACTTTT ACGCCCAACT TGCTCAGGTT TTCTTCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246 . pep (partial)

```

1  MHGRNGGTQA TVAFVFHQQT RTCFSNGEVH ATQTDIGSAV NIAQCFTGEA
51  GQLVYVVR+R CAEVLVEQFA NLFFGFMDCG HHDMGRFFTC HLDDELAQVA
101 FHRFNAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVDD FAGFGRCFRP
151 VYFYAQLGQV FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQQTQRTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQQTQRTCFNSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
m246 . pep	70	80	90	100	110	120
	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFACHLDELAQVAFHRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
m246 . pep	130	140	150			
	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
a246	HRFAFDHQLAVFGCDDVDDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247 . seq

```

1  atgaaacgta aaatgctaaa cgtaccaaag ggcgggttatg atggtatgaa
51  ggggttttacc attggtgaat ttctggttgc ggccttgctc agtataattg
101 tcctgatagc ggtcgatcgc agttacttta catcccgga attaaatgat
151 gtggcaaacg agcgtcttgc cattcaacag gatttgcgga atgcggcaac
201 attaatgtgc cgcgatgcaa gaatggcggg gagcttcggt tgtttcaata
251 tgtccgagca tactaaagac gatattgttg attcaagtaa tcaaactcaa
301 tctaacccttg caaaaccggg tgccaaacaa gaaaatcccc ttttttcctt
351 aaaaaggagc ggcattggata aacaactgat tcccgttgct gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggttttccaa
451 tacggtatcg atgatcttga tgcgagtgc gagactgttg tagtcagcag
501 ctggttccaa atagcaaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatatc

```

```

601 accgcgcaga aacatgtggt caatgcctat gcggtcggca ggtttggcaa
651 taatgaggaa agtttggtcc gcttccaatt ggatgataag ggcaagtggg
701 gtaatcctca gttgctcgtg aaaaaggtta aacgtatgga tgtgcggtat
751 atttatgttt ccggttgctc tgaagatgaa gatgccggca aagaggaaaa
801 attcagatat acgaataaat tcgacaaatc caaaaatgct gttacgcctg
851 ccggggtgga ggttttattg tgatgcggcc ttaatgccaa gatgcccgtt
901 tcttcagaca atagtattta gtctaccgt atcaatgcga caatacgcgg
951 gggaaattgta tgcgcacaaca qaacactttg a

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

g247.pcp

1	MKRKMLNVPK	GGYDGMKGFT	IVEPLVAGLL	SIIVLIAVVS	SYFSTRKLND
51	VANERLAIQQ	DLRNAATLIV	RDARMQSPGF	CFNNSHHTQ	DIVDSSNQTV
101	SNLAKPGAKR	ENPLFSLKRS	GMDKQLIPVA	ESIDIKYPGF	IQRNLNATQF
151	YGIDDLASA	ETVVSSCSK	IAPKPKKIST	LQEAKSALQI	TNDNKKQNGNI
201	TRQKHVVNAY	AVGRFGNNEE	SLFRFQLDDK	GKWNQPQLLV	KKVKRMDVRY
251	IYVSGCPDE	DAGKEKFRY	TNFKPDKSKNA	VTPAGVEVLL	DSGLNAKIAA
301	SSDNSIYAYR	INATTRGGNV	CANRTI.*		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 949>:

m247.seq (partial)

1	ATsAGACGTA	AAATGCTAAA	CGTwsyArAA	GGCAGTTATG	ATGGTATGAA
51	AGGTTTTTACC	ATTATGAAT	TTTTGGTTGC	GGGCCTGCTC	AGTATGATTG
101	TCCTGATGGC	GGTCGGATGC	AGTTACTTCA	CATCCCGGAA	ATTAAATGAT
151	GCGGCAACG	AGCGTCTTGC	CGCGCAACAG	GATTTGCGGA	ATGCGGCAAC
201	ATTGATTGTC	CGCGATGCGA	GGTACGACG	CGGCTTCGGT	GTGTTCAATA
251	TGTCCGAGCA	TCCTGCAACT	GATGTTATTC	CCGATACGAC	GCAACAAAAT
301	TCTCCTTTTT	CCTTAAAAAG	GAACGGTATA	GATAAACCTA	TTCCCATAGC
351	GGAACTCTTA	AATATCAATT	ATCAGAATTT	TTTCCAGGTT	GGTAGCCGAT
401	TGATTTTTC	ATACGGAATC	GATGATGTTA	ATGCAAGCAC	CGCGACTACC
451	GTCGTGAGCA	GCTGTGCCGC	AATATCGAAA	CCGGGCAAGC	AAATCCCTAC
501	TTTAGAAGAT	GCAAAAAAAG	AATTGAAGAT	TCCGGATCAG	GATAAGGAGC
551	AAAATGGCAA	TATAGCGCGT	CAAAGGCAATG	TGGTCAATGC	CTATGCGGTC
601	GGCAGGATTG	CCGATGAGGA	AAAGTTGTTC	CGCTTCCAAT	TGGATGATAA
651	GGGCAAGTGG	GGTAATCTCT	AGTTGC		

This corresponds to the amino acid sequence <SEO ID 950; ORF 247>:

m247.pep (partial)

1	XRRKMLNVXX	GSYDGMKGFT	IIEFLVAGLL	SMIVLMVGS	SYFTSRKLDN
51	AANERLAAQQ	DLRNRATLIV	RDARMAGGFG	CFNMSEHPAT	DVIPDTTQQN
101	SPVFSKLRNG	DKLPIAESS	NINYQNFFQV	GSALIFQYGI	DDVNASTATT
151	VSSCAAISIK	PGKIPTLED	AKKELKIPDQ	DKEQNGNIAR	QRHVVNAYAV
201	GRIADEESLF	RFQLDDKGKW	GNPOL....		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/q247

```

      10      20      30      40      50      60
m247.pep  XRRKMLNVXGSDGMKGFTIIIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAANERLAAQQ
           :| ||| | :| ||| ||| | :| ||| ||| | :| ||| ||| | :| ||| ||| |
g247      MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIAVVSSTSRKLNVDVANERLAIQQ
           10      20      30      40      50      60

      70      80      90      100
m247.pep  DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFLSKRN
           ||| ||| ||| ||| ||| ||| ||| :| :| :| :| :| :| :| :| :| :| :| :|
g247      DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAQKAKQENPLFSLKRS
           70      80      90      100      110      120

      110      120      130      140      150      160
m247.pep  GIDK-LIPIAESSNINYQNFFQVGSALIFQYGIDVDNASTATTVVSSCAAISKPGKQIPT
           |:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

```


567

```

g247      GMDKQLIPVAESIDIKYPGFIQRLNALVFPQYGIDDLASAETVVVSSCSKIAKPGKKIST
           130          140          150          160          170          180

m247.pep  170          180          190          200          210          220
LEDAKKELKIPDQDK EQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKWGNPQL
|::||: |:| ::|| ||||:|:|||||||::: ||||| | | | | | | | | | | | | | |
g247      LQEAKSALQITNDDK-QNGNITRQKHVVNAYAVGRFGNGNEESLFRFQLDDKGKWGNPQLL
           190          200          210          220          230

g247      VKVKVRMDEVRYIYVSGCPEDEDAGKEEFKRYTNKFDSKNAVTPAGVEVLDDLSDGLNAKIA
           240          250          260          270          280          290

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 951>:

```

a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCCT  AGTATGATTG
101 TCCTGATGGC  GGTCCGATCG  AGTTACTCTA  CATCCCGGAA  ATTAATATGA
151 CGGGCAAAACG  AGCGTCTTTC  CGGCAACACG  GATTTCGCGA  ATGCGCGAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTTCAATA
251 TGTCCGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAAC
301 CAACATGTCC  CTGTAAAACC  CGGTGCCAAA  CAGAAAAATC  CCTTTTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCTTATTCG  TGAATCCACA  GATATTAAT  ATCCGGGTTT  TGCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAGAGAGT  CATTACAGAT  TACTAATGAT
601 GATAACAAAA  ATGGAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TCGCGTCCGG  AGGATTGCCG  GTGAGGAAGG  TTTGTTCCGC  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCGTGAA  AAGATATAGA
751 CATATGAAAG  TGCGGTATAT  CTATGTTTCC  GACTGTCCTG  AAGATGACGA
801 TGCCGGCCAA  GAGGAAAAAT  TCAAATATAC  GGGTACATTG  GACAGCTCCA
851 CAAATGCTGT  TACGCCCCGC  GGGGTGGAGG  TTTTATTGAG  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAAT  CATTTATTATG  CTTACCGTAT
951 CGATCGGACA  ATACGCGGGG  GAAATGTATG  CGCAACACGA  ACACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 952; ORF 247.a>:

a247. pep

1	MRRKMLNVPK	GNYDGMKGFT	IIIEFLVAGML	SMIVLMAVGS	SYFTRSKLND
51	AANERLSAQQ	DLRNAATLIV	RDRMAGGFG	CFNMSEHTKN	DIIVDPSKQT
101	QHVPVKPGAK	QENPLFSLEW	ANTNTNTNNT	AKLIPIAEST	DIKYPGFAQA
151	RPALIFQYGI	DDLDAEATV	VVSSCSKIAK	PGKKISTLQE	AKSALQITND
201	DKQNGNITRQ	RHVVNAYAVG	RIAGEEGLFR	FQLDDKGKWG	NPQLLVKKIR
251	HKMKVRYIVS	DCPEDDDAGK	EEKFYKTGTF	DSSTNAVTPA	GVEVLLSXGT
301	DTKIAASSDN	HIYAYRIDAT	IRGNVNCARN	TL*	

m247/a247 70.9% identity in 244 aa overlap

	10	20	30	40	50	60
m247.pep	XXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
a247	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	-----	PDTTQ	XXXXXXXXXX
a247	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	-----	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
a247	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
	130	140	150	160	170	180

568

```

                170      180      190      200      210      220
m247.pep      PGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIADEESLFRFQLDDKGKW
                |||:| ||::||: ||: ||:| |||||:|||||:|||||:|||||:|||||:|||||
a247          PGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVNAYAVGRIAGEEGLFRFQLDDKGKW
                190      200      210      220      230

                240      250      260      270      280      290
m247.pep      GNPQL
                |||||
a247          GNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKYTGTFDSSTNAVTPAGVEVLLSXG

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

```

g247-1.seq (partial) ..
1   CCCGGTGCCA AACAAAGAAA TCCCCTTTT TCCTTAAAAA GGAGCGGCAT
51  GGATAAACAA CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTTGTAGTC AGCAGCTGTT CCAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTGC
401 TCGTGAAAAA GGTAAACGT ATGGATGTGC GGTATATTTA TGTTCCGGT
451 TGTCCTGAAG ATGAAGATGC CGGCAAGAG GAAAAATTCA GATATACGAA
501 TAAATTCGAC AAATCCAAAA ATGCTGTTAC GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TGCACAAATA CGCGGGGAA ATGTATGCGC
651 AACAGAACAA CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

```

g247-1.pep (partial) ..
1   PGAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYGIDD
51  LDASAEVTVV SSCSKIAPG KKISTLQEAK SALQITNDDK QNGNITRQKH
101 VVNAYAVGRF GNNEESLFRF QLDDKGKWN PQLLVKKVKR MDVRYIYVSG
151 CPEDEDAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDSSLN AKIAASSDNS
201 IYAYRINATI RGGNVCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

```

m247-1.seq
1   ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51  AGGTTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTGCGATCG AGTTACTTCA CATCCCGGAA ATTAATGAT
151 GCGGCAACAG AGCGTCTTGC CGCGCAACAG GATTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTTCAATA
251 TGTCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAAT
301 TCTCCTTTT CTTAAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTCCAGGTT GGTAGCGCAT
401 TGATTTTTC ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTGTTC CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAAATCCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCGGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAGAGGAA CAATCAATA TACGATAAAA TTCGACAGCG CCCAAATGC
801 TGTTACGCCC GCCGGGTGG AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTCAGAC AATCATATT ATGCTTACCG TATCGATGCG
901 ACAATACGCG GGGGAAATGT ATGCGCAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

```

m247-1.pep
1   MRRKMLNVFK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51  AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPTTTQON
101 SPFSLKRNGI DKLIPIAESS NINYQNFFQV GSALIFQYGI DDVNASTATT
151 VVSSCAAIK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEEGLF RFQLDDKGKW GNPQLLVKKV RHMVRVYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TDTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*

```

m247-1 / g247-1 72.1% identity in 222 aa overlap

	70	80	90	100	110	120
m247-1.pep	NAATLIVRDARMAGGFGCFNMSEHPATDVI	PD	TTQQNSP	FLSKRNGIDK-LIPIAESSNI		
			: :	: :	: :	
g247-1				PGAKQENPLFSLKRS	MDKQLIPVAESIDI	
				10	20	30
	130	140	150	160	170	180
m247-1.pep	NYQNFFQVGSALIFQY	GIDDVNASTATT	TVSSCAAISKPGKQIPT	LEDAKKELKIPDQDK		
	: : :	: : : :	: : : : :	: : : : :	: : : : :	
g247-1	KYPGFIQRLNALV	FQYGI	DDLDA	SAETVVVSSCSKI	AKPGKISTLQ	EAKSALQITNDDK
	40	50	60	70	80	90
	190	200	210	220	230	240
m247-1.pep	EQNGNIARQRHV	VNAYAVGRIAD-EEGL	FRFQLDDK	GKGNPQLLV	KKVRHMKVRIYYVS	
	: : :	: : : : :	: :	:	:	
g247-1	-QNGNITRQKH	VNAYAVGRFGNNEESL	FRFQLDDK	GKGNPQLLV	KKVKRMDVRIYYVS	
	100	110	120	130	140	
	250	260	270	280	290	300
m247-1.pep	GCPEDDDAGKEET	FKYTDKFD	SAQNAVTPAG	VEVLLSSG	TDTKIAASSDNH	IYAYRIDAT
	: : :	: : : : : :	:	: : :	:	
g247-1	GCPED	EAGKEEF	FRYTNKFD	SKNAVTPAG	VEVLLSGL	NAKIAASSDNSIYAYRINAT
	150	160	170	180	190	200
	310					
m247-1.pep	IRGGNV	CANRTLX				
g247-1	IRGGNV	CANRTLX				
	210	220				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

1	AATAATACAG	CTAAATTGAT	TCCTATTGCT	GAATCCACAG	ATATTAAATA
51	TCCGGGTTTT	GCCCAAGGCT	GTCGCGCATT	GATTTTCCAA	TACGGCATCG
101	TACGACTTTGA	TGCGAGTGCT	GAGACTGTGT	TAGTCACAGC	CTGTGTCAAA
151	ATAGCAAAAC	CGGGTAAGAA	AATATCTACC	TTGCAAGAAG	CAAAAGAGTCG
201	ATTACAGACT	ACTAATGATG	ATAAACAAAA	TGGAAATATC	ACCCGTCAAA
251	GGCATGTGGT	CAATGCCATG	CGGGTCGGCA	GGATTGCCCG	TGAGGAAGGT
301	TTGTTCCGCT	TCCAATTGGA	TGATAAGGCG	AAGTGGGGTA	ATCTCCAGTT
351	GCTCGTGAAA	AAGATTAGAC	ATATGAAAGT	GCGGTATATC	TATGTTCCGG
401	ACTGTGCTGA	AGATGACGAT	CGCGGCAAG	AGGAAAATTC	CAAAATATCG
451	GGTACATTGC	ACAGCTCCAC	AAATGCTGTT	ACGCCCGCGC	GGGTGGAGGT
501	TTTATTGAGT	AGCGGTACTG	ATACCAAGAT	TGCCGCTTCT	TCAGACAATC
551	ATATTTATCG	TTACCGTATC	GATGCGACAA	TACGCGGGGG	AAATGTATGC
601	GCAAAACAGAA	CACTTTGA			

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

a247-1.pap (partial) ..

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLDSA ETVVVSSCSK
51  IAKPGKKIST LQEAKSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEKFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIIYARI DATIRGGNVC
201 ANTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

[illegible]

570

```

m247-1      YAVGRIADEEGLFRFQLDDKGKWNQPQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            | |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgccagc tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggttttgcc
201 ggagggcgaa tttcaggttt tggatttggg atatgctgcg gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaaggtc tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgagg caggcgctcg caaatgcccg cgctatatta tcgaatatatt
501 aggcgtgaag aacggacaaa atgtttatcg ggttactgcc aaggcctggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLVVTAAG SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNGSEEA FGNIVVQKPK AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIIYLGVK NGQNVYRVTA KAWGKNANTV VVLQSYVGN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTGAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWT
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGTCTT TGGCCGAGkC GkCTwTGCGG
151 GAAGGCGAAC TTCAGGTTTT GGATTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAACTGTG GAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTT ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GGwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXR
51  EGELQVLDLE YDTSKVTFS ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGKEYKKG TRSVTKMPRY IIEYLGvXNG
151 ENVYRVTAKA WGKNANTVVV LQSYVSNND *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep      10      20      30      40
              GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
              | ||: |||| | |||| | |||| | |||| | |||| | |||| |

```

571

```

g248      MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFVLTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| ||| :|||||: :||| |||||
g248      LAEALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP
           70      80      90      100      110      120

           110      120      130      140      150
m248.pep  TVEAVKRSCPA---NSTDLCKKXKEYKKGTRSVTKMPRIYIEYLVGXNGENVYRVTA
           :||||||| |||||:| |||:| :|:||||||| ||:|||||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRIYIEYLVGXNGQNVYRVTA
           130      140      150      160      170      180

           160      170      180
m248.pep  KAWGKNANTVVVLQSYVSNINDEX
           |||||:||||
g248      KAWGKNANTVVVLQSYVGNDEQX
           190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVLTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCA KSTGLCIDNK GMEYKKGTQS
151 VSKMPRIYIE YLVGXNGENV YRVTAWGWK NANTVVVLQS YVSNND*

```

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep      GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
               |||:||||| ||||| ||||| ||||| ||||| ||||| |||||
a248          MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLTAAQSYNTEQRISANESDRKLALS
               10      20      30      40      50      60

               50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           |||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      LAEALREGEFQVLDLEYDTSKVTFSENCGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           70      80      90      100      110      120

               110      120      130      140      150      160
m248.pep  VEAVKRSCPANSTDLCIDKKXKEYKKGTRSVTKMPRIYIEYLVGXNGENVYRVTAWGWK
           ||||| |||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
a248      VEAVKRSCAKSTGLCIDNKGMEYKKGTQSVSKMPRIYIEYLVGXNGENVYRVTAWGWK
           130      140      150      160      170      180

               170      180
m248.pep  NANTVVVLQSYVSNINDEX

```

a248

|||||
NANTVVVLQSYVSNINDEX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```
1 ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51 GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAGGTC TGTGTCCCG AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTT GACAATATCG TGGTCAAGG
351 CAAGCCACC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTCAATCT TATGTAAGCA ATAATGATGA GTAA
```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```
1 MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVLVTTAAQ SYNTEQRISA
51 NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCPA NSTDLCIDKK GMEYKKGTRS
151 VSKMPRYIIE YLGVKNGENV YRVTAKEWK NANTVVVLQS YVSNDE*
```

m248-1/g248 89.1% identity in 202 aa overlap

```
10 20 30 40 50 60
m248-1.pep MRKQNTLTGIPTSDGQRFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS
g248 MRKQNTLTGIPTSDGQRFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS
10 20 30 40 50 60

70 80 90 100 110 119
m248-1.pep LAEALREGELQVLDLEYDTDSKVTFSKGLCAAVNVRTNND-NEEAFDNIVVQKPT
g248 LAEALREGELQVLDLEYADSKVTFSKGLCTAVNVRTNNGSEAFGNIVVQKPT
70 80 90 100 110 120

120 130 140 150 160 170
m248-1.pep TVEAVKRSCPA----NSTDLCIDKKGMEYKKGTRSVSKMPRYIIEYLGKNGENVYRVTA
g248 AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYIIEYLGKNGQNVYRVTA
130 140 150 160 170 180

180 190
m248-1.pep KAWGKNANTVVVLQSYVSNINDEX
g248 KAWGKNANTVVVLQSYVGNNDQX
190 200
```

m248-1/a248 97.0% identity in 197 aa overlap

```
10 20 30 40 50 60
m248-1.pep MRKQNTLTGIPTSDGQRFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS
a248 MRKQNTLTGIPTSDGQRFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS
10 20 30 40 50 60

70 80 90 100 110 120
m248-1.pep LAEALREGELQVLDLEYDTDSKVTFSKGLCAAVNVRTNNDNEEAFDNIVVQKPT
a248 LAEALREGELQVLDLEYDTDSKVTFSKGLCTAVNVRTNNDNEEAFDNIVVQKPT
70 80 90 100 110 120

130 140 150 160 170 180
m248-1.pep VEAVKRSCPANSTDLCIDKKGMEYKKGTRSVSKMPRYIIEYLGKNGENVYRVTAKEWK
a248 VEAVKRSCPAKSTGLCIDNKGMEYKKGTRSVSKMPRYIIEYLGKNGENVYRVTAKEWK
130 140 150 160 170 180
```

```

              190
m248-1.pep  NANTVVVLQSYVSNNDEX
              |||||
a248        NANTVVVLQSYVSNNDEX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249.seq
1   atgaagaata atgattgctt gcgcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtattttgg
101 cattgctgtc cgtacagttg cggacagtcg cttccgtcag ggaggcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatggt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcggtgct
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249.pep
1   MKNNDCRLRK NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDLDSNKK N YSLYMGKQTL SAVDGEFMLD
101 AEKSKAQLAE EQLKRFSHEL KNALPDAVAI HYAVCKDSSG DAPTLSDSGA
151 FSSNCDNKAN GDTLIKVLWV NDSAGDSDIS RTNLEVSGDN IVITYQARVG
201 GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATTT TCGGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTTCGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTTCGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249.pep
1   MKNNDCFRLLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVXXXXXXXX
51  XXXXXXXXXXXX XLMGMLMNP TIDSDSNKK N YNLYMGNHTL SAVDGDFAID
101 AMKTKGQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLSGNAF
151 SSNCDNKANG DTLIKVLWVN DSAGDSDISR TNLEVSGDNI VITYQARVGG
201 RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

```

              10      20      30      40      50      60
m249.pep  MKNNDCFRLLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
           |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     120
m249.pep  XLMEGMLMNPITIDSDSNKKNYNLYMGNHTLSAVDGDFAIDAMKTGQLAEALKRFSYEL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      NLMEGMLMNPITIDSDSNKKNYSLYMGKQTL SAVDGEFMLDAEKSQAQLAEELKRFSHEL
           70      80      90      100     110     120

           130     140     150     160     170     179
m249.pep  KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND SAGSDSDIS
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      KNALPDAAAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVND SAGSDSDIS
           130     140     150     160     170     180

           180     190     200
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51 GCTGATAGAA GTCTTGGTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCAGTTG CGGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCAGCAGAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AAAC TAAGAC GCAGTTGGCA GAGGCACAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TGCGGCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTCGTCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1  MKNNDCFRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  QTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLSAGS
151 TFSSNCDGSA NGDTLIKVLW VND SAGSDSI ARTNLETNGN NIVYTYQARV
201 GRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

           10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     119
m249.pep  XLMEGMLMNPITIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEALKRFSYE
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      NLMEGMLMNPITIDSDSNKKNYNLYMGNHHALSVVDGDFQVDAIKTKTQLAEALKRFSYE
           70      80      90      100     110     120

           120     130     140     150     160     170
m249.pep  LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVND SAGSDSI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVND SAGSDSI
           130     140     150     160     170     180

```


575

```

          180      190      200
m249.pep  SRTNLEVSGDNIVYTYQARVGGREX
          :|||||:|:|||||:|||||
a249      ARTNLETNGNNIVYTYQARVGGREX
          190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 973>:

m249-1.seq

```

1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCG CTCCCGTCAG GGAGGCGGAG
151 ACACAAACCA TCGTCAGCCA AATCACGCAA AACCTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATT TCGGATGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTTCGGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCGGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 974; ORF 249-1>:

m249-1.pep

```

1  MKNNDICRLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGLMNP TIDSDSNKKN YNLYMGNHTL SAVDGDFAID
101 AMKTKQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLSGNAF
151 SSNCNDKANG DTLIKVLWVN DSAGSDISR TNLEVSGDNI VYTYQARVGG
201 RE*

```

m249-1/g249 90.1% identity in 203 aa overlap

```

          10      20      30      40      50      60
m249-1.pep MKNNDICRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
          |||||:|:|: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249       MKNNDICRLKPNQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
          10      20      30      40      50      60

          70      80      90     100     110     120
m249-1.pep NLMEGLMNP TIDSDSNKKN YNLYMGNHTL SAVDGDFAIDAMKTKQLAE AQLKRFSYEL
          |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||
g249       NLMEGLMNP TIDSDSNKKN YNLYMGKQTL SAVDGEFMDAEKSKAQLAE AQLKRFSHEL
          70      80      90     100     110     120

          130     140     150     160     170     179
m249-1.pep KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCNDKANGDTLIKVLWVND SAGSDIS
          |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||
g249       KNALPDAAAIHYAVCKDSSGDAPTLSDSGAFSSNCNDKANGDTLIKVLWVND SAGSDIS
          130     140     150     160     170     180

          180     190     200
m249-1.pep RTNLEVSGDNIVYTYQARVGGREX
          |||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||
g249       RTNLEVSGDNIVYTYQARVGGREX
          190     200

```

a249/ L36117

gi|643582 (L36117) prepilin leader sequence requires cleavage to be active [Pseudomonas aeruginosa]
 >gi|1161222 (L48934) involved in type 4 fimbrial biogenesis; contains pre-pilin like leader sequence [Pseudomonas aeruginosa]
 >gi|1246299 (L76605) reference L36117, L48934 [Pseudomonas aeruginosa] Length = 185
 Score = 50.4 bits (118), Expect = 9e-06
 Identities = 45/183 (24%), Positives = 84/183 (45%), Gaps = 26/183 (14%)

Query: 13 QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITONLMEGLMNP TI 72
 QSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + + + NL+E M +P
 Sbjct: 12 QSGFSMIEVLVALLISIGVLGMIA MQGKTIQYTADSVERNKAAMLGSNLLSMRASP KA 71
 Query: 73 DSDSNKKNYNLYMGNNHLSVVDGDFQVDAIKTKTQLAEA---QLKRFSYELKNALPDAA 129

576

D + M G A + T L + A + L ++ ++KN LP A
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAGSAFPTAPSSCTPLPDAIKDRLGCWAEQVKNELPGAG 126
 Query: 130 AI---HYAVCKDSSGVAPTLASSTFSSNCDGSANGDTL-IKVLWVNDASGDSIARTNL 185
 + Y + C + S + CDG G L I + + W + A ++
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLIIRLAWRGKQGACVNAADSSA 172
 Query: 186 ETN 188
 + T +
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ				
a249	MKNND	CFRLKDPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ				
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLMEGMLMNP	TIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEALKRFSYE				
a249	NLMEGMLMNP	TIDSDSNKKNYNLYMGNHHSVVDGDFQVDAIKTKTQLAEALKRFSYE				
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKNALPDAAAIHYAVCKDSSGNAP	TLGNAFSSNCDNKANGDTLIKVLWVNDASGDSI				
a249	LKNALPDAAAIHYAVCKDSSGVAP	TLASSTFSSNCDGSANGDTLIKVLWVNDASGDSI				
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRTNLEVSGDNIVYTYQARVGG	GREX				
a249	ARTNLETNGNIVYTYQARVGG	GREX				
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1  atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51  aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggta
101 tgcagggcgg gcaaaaaggt atgggcccggc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatgccac cataaccttt atgattaatt
251 cgcggcataat cctgatgggg ggccggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1  MHTASPRDE FIRIKESP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1  ATGCACACCT TCCCCGATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51  CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTGCCAC GGTC AACCTG TGGGCGAAGC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1  MHTPSPHNEF IRGIKESPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51  MNFAGGSEFA TVNLWAEPL ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

m250/g250

```

      10       20       30       40       50       59
m250.pep    MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGSWLEMLLMTSMNFAGGSEF
             |||::||| | | | | | | | | | | | | | | | : | | | | : | | | | |
g250         MTHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMRLEMLLMTGMNFAGGSEF
             10       20       30       40       50       60

      60       70       80       90      100      110
m250.pep    ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAERNTAEKSARRTVFYVX
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
g250         ATVNLWAEPLPILLIATITFMINSRHILMGGGACHAHERNTAEKSARAVFYV
             70       80       90      100      110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 979>:

a250.seq

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGGCGG	CTCCGAGTTT	GCCACGGTCA	ACCTGTGGGC
201	GGAACTCTTG	CCGATACTCG	TTATCGCCAC	CGTAACTTT	ATGATTAATT
251	CTCGGCATAT	CCTGATGGGG	G.CGGCACTT	GCCCGCACC	TGAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

This corresponds to the amino acid sequence <SEQ ID 980; ORF 250.a>:

a250 . pep

1 MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MSWLEMLLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTCPAPER
101 TAEKSRRATV FYV*

m250/a250 94.6% identity in 111 aa overlap

```

10          20          30          40          50
59
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGSWLEMLLMTSMNFAGGSEF
|
||:|||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGSWLEMLLMTGMNFAGGSEF
10          20          30          40          50
60

60          70          80          90          100         110
m250.pep
ATVNLWAEPLPILLIATVTFMINSRHIILMGGGACPAAPERNTAEKSRRARTVFYVX
|||||||||||||||||||||||||||||||||:|||||||||
a250
ATVNLWAEPLPILLIATVTFMINSRHIILMGXGTCPAAPERNTAEKSRRARTVFYVX
70          80          90          100         110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 981>:

g251.seq

```

1  atgcctgacc caatagggat tcttttcgct gccgtcgggg ttgatttttt
51  tgccgttggt ttgagggggc gttttcaacg aataggcgcg gtggcatgt
101 tgataataat aatcctgatg gcggaggtcg gaacccaaac gtcgtaacc

```

151	gagggttgacg	ctcaggttgt	ggcggatttt	ggcggtatcg	aaggattttt
201	tgaatgccgc	ctgcaagagc	ctgtggcttt	ccccgtaa	cacgcggtcg
251	gatttgtagt	aggaagacgg	cttgtcggca	ctcgggcggc	aatatttgtc
301	cgaaccgtcg	gcggaacagt	gcgtctgctg	aaaatgattg	tccaaaccga
351	tgcctcgcgc	gtcgtaagag	aggcgggcac	aatccgccca	agtgtcttta
401	tcggcatctg	tatagacata	ttccaaacgc	tacggcgttt	tggtgtgcgt
451	ctcgtcgtaa	aacacgcgcc	taccgtattc	cgcgcccaac	tcgcgacgct
501	tttcaccggt	ggtaatcagc	ccgctgtatt	tcgggcgcgc	cgcgtatttg
551	ccgtagccct	ttatcgatcc	gtatttttta	tttccatcaa	aaaccgcctt
601	ggtcaggaat	gcgggaacgc	tcatatcgcg	cgtgtcga	gtttgcgtcg
651	tccgtctcgag	ctcgcgcgcg	atagtgtgcc	gtttgttttc	aaaacgaaaa
701	ccggggcgga	acaqccacqa	ccqgccttcq	tatga	

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pcp

1	MPDPGIGILFA	AVGVDFFAV	LRGRFORIGA	VGMLIIIIILM	AEVGTKTVVT
51	EVDAQVVA	GGIEGFE	LQEPVAF	HAVGFVVG	LVGTRAAIF
101	RTVGGTV	KMIVQTD	VVREAGI	SVFIGIG	QFTVAAF
151	LVVVKH	RAHLTR	GNQPAV	RFFAVAS	YVFIFIK
201	QGEQRNR	RVESLL	YAADVV	KTKT	RAEOP

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 983>:

m251.seq

1	ATGCGTGCTG	CGGTAGTCGT	AGCGCAAGCC	CGCGCCGACA	TCCGCCCAACC
51	TGCCCAAACG	GACATTGTCC	CGAACTGCCG	CGTAATAGCT	TTTACCGTTG
101	ATGCTGCGCG	GCGTGCAGTC	CGTATAAGTA	TTGTTGCCCA	AGCGGCAGAT
151	TTGCCCCGTA	ACGCAATTC	CCCTGCCTAT	GGTGACCCAA	TAGGGGCTGG
201	TTTCACTGCC	TTGGGGCTG	ATTTTGTTC	CGTTGTTTTG	AGGGGGCGTG
251	TTTCGACAA	AGTGGCGGTT	GGCATTTTGA	TAATAAATCT	CCTGATGGCG
301	GAGATTAGAG	CCAAAGCGGT	CAAACCCGAG	ATTACAAGCT	AGGTGTTGGC
351	GGATTTTGGC	GGTATCGAAG	GATTTTTTGA	ATGCCGCTG	CAAGAGCCTG
401	TGGCTTCC	CGTAAATCAC	GCGATCGGAT	TTGTAATAGG	AAAACGGCTT
451	GTCGGCACTC	GGGCGGCAAT	ATTTGTCCGA	ACCGTCGGCA	GAACAGTGGC
501	TCTGCTGAAA	ATGATTATCC	AAACCGATGC	CCTGCGGTC	GTAAGAGAGG
551	CGGCACATA	CCGCCCAAGT	GCTTTATCG	GCATTGGTAT	AGACATATTC
601	CAAACCGTAG	CGGCTTTTGG	TGTGCGCTCT	TCGTGAAAC	ACGCCCGTAC
651	CGTATTCCGC	GCCCACCAGC	GCACCGTTTT	CGCCGTTGGT	AAACAGTCCG
701	CCGTATTTGT	GTTTGCCCGC	GTAATTGCCG	TTACCGGGCA	AAGAACCCGC
751	CTGTTTTTTA	TTTGATCAAA	AAACCGCCTT	GGTCAGGAAT	GCCGGAACCG
801	TCATATCGCG	GCTTTCGAAA	GTTTGTTCG	TGTGTTGAG	TATGCCGCCG
851	ATGTAGTGCC	CGTTATTCTC	AAAACGAAAA	CCCGGGCGGA	ACAGCCACGA
901	CCGGCTTTTC	TATGA			

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

1	MRAAVVVAQA	RADIRPPAQT	DIVPNCRVIA	FTVDAARRAV	RISIVAQAAD
51	LPRNDISPAY	GDPIQAGFTA	VGADFFFAVL	RGVRRRIGAV	GMLIIILIMA
101	EIRAKAVKPE	IHAQGVADFG	GIEGFFECVL	QEPVAFPVNH	AIGFVIGKRL
151	VGTRAAIFVR	TVGRTVRLLK	MIQTDLAPV	VREAGIIRPS	VFIGIGIDIF
201	<u>QTVAAGFVRL</u>	VVKHARTVFR	AHORTVFAVG	KQSAVFVVAR	VFAVTGQQTR
251	LFFFCIKNRL	GQECRNRIIA	RVESLLRVFE	YAADVVPILIL	KTKTREAQPR
301	PAFV*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

40 50 60 70 80 90
 m251.pep TVDAARRAVRISIVAQAADLPRNDISPAYGDPFIGAGFTAVGADFFAVVLRGRVRRIGAVG
 ||||| :|||:||||| ||| :|||
 g251 MPDPFIGILFAAVGVDFFAVVLRGRFQRIGAVG
 10 10 20 30

579

	100	110	120	130	140	150
m251.pep	MLIIIIILMAEIRAKAVKPEIHAQVVADFGGIEGFFECRLQEPVAFPVNHAIGFVIGKRLV					
g251	MLIIIIILMAEIVGKTQVTEVDAQVVADFGGIEGFFECRLQEPVAFPVNHAIGFVIGKRLV					
	40	50	60	70	80	90
	160	170	180	190	200	210
m251.pep	GTRAAIFVRTVGRVRLKMIQTDALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
g251	GTRAAIFVRTVGGTVRLKMIQTDALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
	100	110	120	130	140	150
	220	230	240	250	260	270
m251.pep	VKHARTVFRAHQRTVFAVGKQSAVFVVARVFAVTGQRTLFFICIKNRLGQECRNRIAR					
g251	VKHARTVFRAHLRTVFTVGNQPAVFAAARVFAVASYSR-VFFIFIKNRLGQECRNRIAR					
	160	170	180	190	200	210
	280	290	300			
m251.pep	VESLLRVFEYAADVPLILKTKTRAEQPRPAFVX					
g251	VESLLRAFEYAADVVPFVKTKTRAEQPRPAFVX					
	220	230	240			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 985>:

```

a251.seq
1  ATGCGTGCTG CGGTAGTCGT AGCGCAACCC CGCGCCGACA TCCGCCACAC
51  TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTGCCGTTG
101 ATGTGCGCGC GCGTGCAGTC CGTATAAGTA TTGTGCCCCA AGCGGCAGAT
151 TTGCCCCGTA ACCACATTTC CCCTGCCTAT GCTGACCCAA TAGGGTTGGT
201 CCTTGCCGCC GTTGGGGTTG GCGGTTTTAG GGGGCGTTTT CGACGAATAG
251 GCGCGGTTGG CATGTTGATA ATAATAATCC TGATGGCGGA GATTAGAGTC
301 AAAGCGGTCA AAACCGAGAT TCACGCTCAG GTTGTGGCGG ATTTTGGCGG
351 TATCGAAGGA TTTTTTGAAT GCCGCTGCA AGAGCCTGTG GCTTTCCCCG
401 TAAATCACGC GGTGGGATTT GTAGTAGGAA AACGGCTTGT CGGCACTCGG
451 GCGGCAATAT TTGTCCGAAC CGTCGGCAGA ACAGTGCCTC TGCTGAAAT
501 GATTGTCCAA ACCGATGCCC TGCCGGTCGT AAGAGAGCGC GGCATAATCC
551 ACCCAAGTGT CTTTATCGGC ATTGGTATAG ACATATTCCA AACCGTAGCG
601 GCTTTTGGTG TCGCTCTCGT CGTAAACAC GCCCGTACCG TATTCGCGC
651 CCACCAGCGC ACCGTTTTCG CCGTTGGTAA ACAGACCGCC GTATTGTGG
701 TCGCCCGCGT ATTTGCCGTT GCCTCTTATC GGTCCGTATT TTCTATTTTC
751 ATCAAAAACC GCCTTGGTCA GGAATGCCGG AACCGTCATA TCGCGCGTGT
801 CGAAAGTTTG TTGCGTGTGT TCGAGTATGC CGCCGATGTA GTGCCGTTTG
851 TTTTCAAAAC GAAAACCCGG GCGGAACAGC CACGATCGGC TTTCGTATGA

```

This corresponds to the amino acid sequence <SEQ ID 986; ORF 251.a>:

```

a251.pep
1  MRAAVVVAQP RADIRPPAQT DIVPNCRVIA FAVDAARRAV RISIVAQAAD
51  LPRNHISPAY ADPIGLVLAA VGVGGFRGRF RRIGAVGMLI IIILMAEIRV
101 KAVKTEIHAQ VVADFGGIEG FFECRLQEPV AFPVNHAVGF VVGKRLVGTR
151 AAIFVRTVGR TVRLKMIQV TDALPVVREA GIIHPSVFIG IGIDIFQTVA
201 AFGVRLVVKH ARTVFRAHQ RTVFAVGKQTA VFVVARVFAV ASYRSVFSIF
251 IKNRLGQECR NRHIAVESL LRVFEYAADV VPFVKTKTR AEQPRSAFV*

```

m251/a251 88.5% identity in 304 aa overlap

	10	20	30	40	50	60
m251.pep	MRAAVVVAQARADIRPPAQTDIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY					
a251	MRAAVVVAQPRADIRPPAQTDIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m251.pep	GDFIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIILMAEIRAKAVKPEIHAQVVADFG					
	: : : :					

580

```

a251      ADPIGLVLAAVGVGGF----RGRFRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVVADFG
              70          80          90          100          110

              130          140          150          160          170          180
m251.pep  GIEGFFECRLQEPVAFPNVHAIGFVIGKRLVGTRAAIFVRTVGRVRLMKMIQTDLAPV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECRLQEPVAFPNVHAVGVVVGKRLVGTRAAIFVRTVGRVRLMKMIVQTDALPV
              120          130          140          150          160          170

              190          200          210          220          230          240
m251.pep  VREAGIIRPSVFIGIGIDIFQTVAAFVGVRLVVKHARTVFRHQRTVFAVGKQSAVFVVAR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIRPSVFIGIGIDIFQTVAAFVGVRLVVKHARTVFRHQRTVFAVGKQSAVFVVAR
              180          190          200          210          220          230

              250          260          270          280          290          300
m251.pep  VFAVTGQRTLRFFICIKNRLGQECNRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR
              ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a251      VFAVASYSR-VFSIFIKNRLGQECNRNRIARVESLLRVFEYAADVVPFVKTKTRAEQPR
              240          250          260          270          280          290

m251.pep  PAFVX
              |||
a251      SAFVX
              300

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 987>:

g253.seq

```

1  atgatcgaca gggaccgtat gttgcgggac acgttggaac gtgtgcgtgc
51  ggggtcgctt tggttatggg tgggtggtggc atcgatgatg tttaccgccg
101 gattttcagg cacttatctt ctgatggaca atcaggggct gaatttcttt
151 ttagttttgg cgggagtggt gggcatgaat acgctgatgc tggcagtatg
201 gttggcaacg ttgttcctgc gcgtgaaagt gggacgggtt ttcagcagtc
251 cggcgacgtg gtttcggggc aaaggccctg taaatcaggc ggtgttgctg
301 ctgtatgcgg accagtggcg gcaaccttcg gtacgatgga aaataggcgc
351 aacggcgcac agcttctggc tctgcacgct gctcggaatg ctggtgtcgg
401 tattgctgct gcttttggtg cggcaatata cgttcaactg ggaaagcacg
451 ctggtgagca atgccgcttc ggtacgcgcg gtggaaatgt tggcatggct
501 gccgtcgaaa ctcggtttcc ctgtcccga tgcgcggcg gtcatcgaa
551 gtcgtctgaa cggcaatatt gccgatgcgc gggcttggtc ggggctgctg
601 gtcggcagta tcgtctgcta cggcatcctg ccgcgcctct tggcttgggt
651 agtgtgtaaa atccttttga aaacaagcga aaacggattg gatttgaaa
701 aaacctatta tcaggcggtc atccgccgct ggcagaacaa aatcaccgat
751 gcggatacgc gtcgggaaac cgtgtccgcc gtttcgccga aaatcgtctt
801 gaacgatgcg ccgaaatggg cgtcatgct ggagaccgag tggcaggacg
851 gccaatggtt cgagggcagg ctggcgagg aatggctgga taaggcgctt
901 gccgccaatc gggaaacagg tgccgcgctg gagacagagc tgaagcagaa
951 accggcgcaa ctgcttatcg gcgtacgcgc ccaaactgtg ccggaccggg
1001 gcgtgctgcg gcagattgtg cggctttcgg aagcggcgca gggcggcgcg
1051 gtggtgcagc ttttgccgga acaggggctt tcagacgacc tttcgaaaaa
1101 gctggaacat tggcgtaacg cgctgaccga atgcgcgcg gcgtggtctg
1151 agcctgacag ggtggcgag gaaggccgtt tgaaagacca ataa

```

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

g253.pep

```

1  MIDRDRMLRD TLERVRAGSF WLWVVASMM FTAGFSGYTL LMDNQGILNFF
51  LVLAGVLGMN TLMLAVLAT LFLRVKVGFR FSSPATWFRG KGPVNQAVLR
101 LYADQWRQPS VRWKIGATAH SLWLCTLLGM LVSLLLLLV RQYTFNWEST
151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRLNGNI ADARAWGSL
201 VGSIVCYGIL PRLLAVVCK ILLKTSENGL DLEKTYQAV IRRWQNKITD
251 ADTRRETVSA VSPKIVLNDK PKWALMLETE WQDQWFEGR LAQEWLDKGV

```

301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRLQIV RLSEAAQGGG
351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRVAO EGRLKDO*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 989>:

```
m253 .seq
1  ATGATTGACA  GGAACCGTAT  GCTGCGGGAG  ACGTTGGAAC  GTGTGCGTGC
51  GGGGTCGTTT  TCGTTTGTGG  TGGTGGCGGC  GACGTTTGCA  TTTTACCCTG
101 GTTTTTAGT   CACTTATCTT  CTAATTGGACA  ATCAGGGTCT  GAATTTCTTT
151 TTGGTTTGG   CGGGCGGTGT  GGGCATGAAT   ACGCTGATGC  TTGCAGTATG
201 GTTGGAATG   TTGTTCTCTG  GTGTGAAAGT   GGGGCGTTTT  TTCAGCAGTC
251 CGGCGACGTG  GTTTCGGGGC  AAAGACCCTG   TAAATCAGGC  GGTGTTGCGG
301 CTGTATGCGG  ACGAGTGGCG  GCAACCTTCG   GTACGTTGGA  AAATAGGCGC
351 AACGTCGCAC  AGCCTGTGGC  TCTGCACGCT   GCTCGGAATG  CTGGTGTCGG
401 TATTGTTGCT  GCTTTTGGTG  CGGCAATATA   CGTTCAACTG  GGAAGACACG
451 CTGTTGAGCA  ATGCCGCTTC  GGTACGCGCG   GTGGAAATGT  TGGCATGGCT
501 GCCGTCGAAA  CTCGTTTCC   CTGTCCCGA    TGCGCGGGCG  GTCATCGAAG
551 GCCGTCGAA   CGGCAATATT  GCCGATGCGC   GGGCTTTGGT  GGGGCTCGTG
601 GTCGGCAGTA  TCGCCTGCTA  CGGCATCCCTG  CGCGCCTGCG  TGGCTTGGGT
651 AGTGTGTAATA  ATCCTTTTGA  AAACAAGCTA   AAACGGATTG  GATTGGAATA
701 AGCCCTATTA  TCAGGCGGTC  ATCCGCGCGT   GGCAGAACAA  AATCACCGAT
751 GCGGATACGC  GTCGGGAAAC  CGTGTCCGCC   GTTTCACCGA  AAATCATCTT
801 GAACGATGCG  CCGAAATGGG  CGGTTCATGCT  GGAGACCGAG  TGCAGGACG
851 GCGAATGGTT  CGAGGGCAGG  CTGGCGCAGG   AATGGCTGGA  TAAGGCGGTT
901 GCCACCAATC  GGGAACAGGT  TGCCGCGCTG   GAGACAGAGC  TGAAGCAGAA
951 ACCGGCGCAA  CTGCTTATCG  GCGTGCGCGC   CCAAAGTGTG  CCGGACCGCG
1001 GCGTGTTCG   GCAGATTGTC  CGACTCTCGG   AAGCGGCGCA  GGGCGGCGCG
1051 GTGGTGACAG  TTTTGGCGGA  ACAGGGGCTT   TCACAGCGAC  TTTCGGAAAA
1101 GTCGGAACAT  TTGCGTAACG  CGCTGGCCGA   ATGCGGCGCG  CGGTGCGTTG
1151 AGCCTGCAG   GGGCGCGCAG  GAAGGGCGTT   TGAAGACCA   ATAA
```

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253.pep

1	MIDRNRMLRE	TLERVAGSF	WLWVVAATFA	FFTGFSVTYL	LMDNOGLNFF
51	<u>LVL</u> <u>AGV</u> <u>LGM</u>	<u>TLML</u> <u>AVWL</u> <u>AM</u>	<u>LFLRV</u> <u>KVGR</u> <u>F</u>	<u>FSSPAT</u> <u>WFRG</u>	<u>KDPVNQ</u> <u>AVLR</u>
101	LYADEWRQPS	VRWKIGATSH	<u>SLWL</u> <u>CTL</u> <u>LGM</u>	<u>LVS</u> <u>VLLLL</u> <u>LV</u>	<u>RQYTFN</u> <u>WEST</u>
151	LLSNAASVRA	VEMLAWLPSP	LGFPVPDARA	VIEGRNLNGNI	ADARAWSGLL
201	<u>VGS</u> <u>IAC</u> <u>YGIL</u>	<u>PRLL</u> <u>AWV</u> <u>VCK</u>	<u>ILLK</u> <u>TS</u> <u>ENGL</u>	<u>DLEK</u> <u>PYYQ</u> <u>AV</u>	<u>IRR</u> <u>WQNK</u> <u>ITD</u>
251	ADTRRETVSA	VSPKIIINDA	PKWAVMLETE	WQDGEWFEGR	LAQEWLADKVG
301	ATNREQVAAL	ETELQKQPAQ	LIGIVRAQTV	PDRGVLRQIV	RLSEAAQGGGA
351	VVQLAEQGL	SDDLSEKLEH	WRNALAECCA	AWLEPDRAAO	EGRLKDO*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/g253

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFVLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	: :					
g253	MIDRDRMLRDTLERVRAGSFVLWVVASMMFTAGFSGTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFRLVKVGRFSSPATWFRGKDPVNQAVLRLRYADEWRQPSVRWKIGATSH					
g253	TLMLAVWLATLFLRVKVGRFSSPATWFRGKGPNQAVLRLRYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
g253	SLWLCTLLGMLVSVLLLLLRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
	130	140	150	160	170	180

582

	190	200	210	220	230	240
m253 . pep	VIEGR	LNGNIADAR	WSGLLVG	SIACYGIL	PRLLAWV	CKILLKTS
g253	VIEGR	LNGNIADAR	WSGLLVG	SIVCYGIL	PRLLAWV	CKILLKTS
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 . pep	IRRWQ	NKITDAD	TRRET	VS	SAVSPKI	ILNDAPK
g253	IRRWQ	NKITDAD	TRRET	VS	SAVSPKI	VLNDAPK
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 . pep	ATNRE	QVAAL	ETELK	QKPAQ	LLIGV	RAQTV
g253	AANRE	QVAAL	ETELK	QKPAQ	LLIGV	RAQTV
	310	320	330	340	350	360
	370	380	390			
m253 . pep	SDDL	SEKLE	HWRNAL	AECGA	AWLEP	DRAAQ
g253	SDDL	SEKLE	HWRNAL	TECGA	AWLEP	DRVAQ
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a253 . seq
1  ATGATCGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51  GGGGTCGTTC TGGTTGTGGG TGGCGGCGGC GACGTTTGCG TTTTTCACCG
101 GTTTTTCAGT TACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
151 TTGGTTTGG CGGGCGTGT GGGCATGAAT ACGCTGATGC TGGCAGTATG
201 GTTGGCAATG TTGTTCTGCG CCGTGAAAGT GGGGCGTTTT TTCAGCAGTC
251 CGGCGACGTG GTTTCGGGGC AAAGACCTTG TCAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTGGA AAATAGGCGC
351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTGCG
401 TATTGTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCACG
451 CTGTTGGGCG ATTCTCTTTC GGTACGGCTG GTGGAATGT TGGCATGGCT
501 GCCTGCGAAA CTGGGTTTTC CCGTGCCTGA TGC GCGGGCGG GTCATCGAAG
551 GTCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGGTC GGGGCTGCTG
601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTCT TGGCTTGGGC
651 GGTATGCAAA ATCCTTTTGA AAACAAGCGA AAACGGCTTG GATTTGGAAA
701 AGCCCTATTA TCAGGCGGTC ATCCGCCGCT GGCAGAACAA AATCACCAGT
751 GCGGATACGC GTCGGGAAAC CGTGTCCGCC GTTTCGCCGA AAATCGTCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAA TGGCAGGACG
851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGCGCTT
901 GCCGCCAATC GGGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGCGCAAA CTGCTTATCG GCGTGC GCGC CCAAAGTGTG CCCGACCGCG
1001 GCGTGTGCG GCAGATCGTC CGACTTTCGG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGCAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTCGGAAAA
1101 GCTGGAACAT TGGCGTAACG CGCTGACCGA ATGCGGCGCG GCGTGGCTGG
1151 AACCCGACAG AGCGGCGCAG GAAGGCCGTC TGA AAACCAA CGACCGCACT
1201 TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a253 . pep
1  MIDRNRMLRE TLERVRAGSF WLWVAAATFA FFTGFSVTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVWLAM LFLRVKVGFR FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLV RQYTFNWEST
151 LLGDSSSVRL VEMLAWLPAK LGFFVPDARA VIEGR LNGNI ADARAWSGLL
201 VSGIACYGIL PRLLAWAVCK ILLKTS ENGL DLEKPYQAV IRRWQNKITD
251 ADTRRET VSA VSPKIVL NDA PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGA
351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRAAQ EGRLKTNDR
401 *

```


m253/a253 97.2% identity in 395 aa overlap

m253.pep	10	20	30	40	50	60
	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
a253	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
m253.pep	70	80	90	100	110	120
	TLMLAVWLAMLFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMLFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
m253.pep	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLGDSSSVRLVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	190	200	210	220	230	240
	VIEGRNLNGNIADARAWSGLLVGSIAACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIAACYGILPRLAWAVCKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
m253.pep	250	260	270	280	290	300
	IRRWQNKITDADTRRETVSASPKIILNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWQNKITDADTRRETVSASPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
m253.pep	310	320	330	340	350	360
	ATNREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
m253.pep	370	380	390			
	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcgcg gcaggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccggtt gcaactggtt ctttgagaaa cgggcccggc
301 tggacggtat ttctactgtc ctggctgctg gcggctgcag gaatcgacac
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggtcttgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcgagc gcggtatgct
501 gtacagcgtc ggcatctact ggtttgtaa cgatgaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aacccaat
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMY VLIAGSYTPF ALVSLRNGPG
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYVMGW MVLAVMKSIL
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
 201 VSVYGYVI*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT
 51 GTACCACGGA ATTGCAGCCG GAAACTGAA AAGCATTTTG AAAAAACCG
 101 ACCACTGCAT GATTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
 201 GCTGCTGGCG GCTGCAGGAA TCGACAAGA ACTCACCATC GGACGGAATA
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG
 301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
 351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTCCGC ATTTACTGGT
 401 TTGTAAACGA TGAATAATC CGACACGGGC ACGGAATCTG GCATCTGTTT
 451 GTATTGGGCG GCAGCATCAC CCAATTTGTC AGCGTGACG GTTACGTAAT
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI KKTDHCMYV LIAGSYTPFA
 51 LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IVIYVMGMW
 101 VLAVMKSILTA SLPSAGLAWL AAGGMLYSV GIYWFVNDEK IRHGHGIWHLF
 151 VLGGSITQFV SVYGYVI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254.pep				10	20	30
				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HLSGLILAAAGLMLLLKTIGHGDGYRIFSVSVYGISLLL					
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KKTDHCMYV	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAAGIAQELT
g254		KKTDHCMYV	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAAGIAQELT
	80	90	100	110	120	130
m254.pep		100	110	120	130	140
		IVIYVMGMW	MVLAVMKSIL	TASLPSAGLAW	LAAGGMLYSV	GIYWFVNDEK
g254		IAIYIVMGW	MVLAVMKSIL	TASLPPAGLAW	LAAGGMLYSV	GIYWFVNDEK
	140	150	160	170	180	190
m254.pep		160				
		VLGGSITQFV	SVYGYVIX			
g254		VLGGSITQFV	SVYGYVIX			
		200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTGGA GCGGTTTGAT
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
 151 CTGCTCTATT TGAGTTCTTC GCTGTACCAC GGAATTGCAG CCGGAAAACG
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTAT GTGCTGATTG
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CCGGCCGGGG

a254 . pep

```

1  MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIATYIVMGW MVLAVMKSLL
151 ASLPAGPAGL LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

m254/a254 97.6% identity in 167 aa overlap

		10		20		
30	m254.pep	VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL				
a254	HLSGLILAAAGLALMLLKTIHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL					
		20	30	40	50	60
70						
		40	50	60	70	80
90	m254.pep	KKTDHCMIYVLIAGSYTPFALVSLRNPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS				
a254	KKTDHCMIYVLIAGSYTPFALVSLRNPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS					
		80	90	100	110	120
130						
		100	110	120	130	140
150	m254.pep	IIVIYVMGWMVLAVMKSLTASLPAGLAWLAAAGMGLYSVGIIYWFWNDEKIRHHGGHWHLF	: : :			
a254	IAIYIVMGWMVLAVMKSLTASLPAGLAWLAAAGMGLYSVGIIYWFWNDEKIRHHGGHWHLF					
		140	150	160	170	180
190						
		160				
m254.pep	VLGGSITQFVS VYG YVI X					
a254						
	VLGGSITQFVS VYG YVI X					
	200					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

q255 . pep

1 MVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVE
51 NGFAQTDGDV GGFDMQFRAD GIQGFaHTVH IVQFGDLAL VGGKKRILGN
101 VFAAFKPDDF FADLGNVGGD FRAEFFFPQF FGNSSGNAG CGFAGGTPAA
151 APVVARTVFV PIGIVGVSGA EGGGDVAVVE AALVGVAD*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1001>:

m255.seq

1	GTGGTTGGAC	AGGAAGCCTT	GCGGGGTCAG	TTCGTCGCCG	TGTTTCGCTGC
51	CGCGTTTCGT	TACGCTGTCA	AAACCTGCGC	CGATTTCAC	GCCTTTGACG
101	GCGTTGATGC	CCATCATCGC	GTAGGCGATT	TCGGCATCGA	GCGCGTCAAA
151	AACAGGTTTCG	CCCAAGCCGA	CAGGGACATT	GGCTGCTTCG	ATATGTTTCT
201	TACGCTCGAC	GGAAATCCAAG	GATTTGCGCA	CGCTGTCCAT	ATAGTATTTCC
251	AGCTCCGCAA	TTTGGCTATG	GTTTGGCGCA	AAAAAAGAT	TTTGGGAAAT
301	GTGTTTCGAG	CCTTCAAACC	GGATTTCCTT	TTCGCCGACT	TGGGTAACGT
351	AGGCGGTGAT	TTCCGTGCCG	AATTTTCTTT	TCAACCATTT	TTTGGCAACG
401	GCTCCGGCAG	CAACGCGGGC	GCGGTTTCA	CGGGCGGAGC	TCCTGCCGCC
451	GCCCGGGTAG	GCGCCGCTGC	CGTATTTGTG	CCAATAGGTA	TAGTCGCGGT
501	GCGCCGGGCG	TGAAGCTGGT	GCGATGTTGC	CGTAGTCTTT	GCTGCGCTGG
551	TCGGTATTGC	GGATTAA			

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

m255 . pep

1 VVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVK
51 NRFAQADRDI GCFDMQLRAD GIQGFABAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNNGSGNAG GGFTGGAPAA
151 AAVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/q255

[illegible]

	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```
a255.seq
1  GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTCGCTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GCGGTCGAA
151 TACGGGTTCG CCAAGCCGA CGGGACGTT GCGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTTC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTTCGCAG CCTTCAAACC GGATTTCCTT TCGCCGACT TGGGTAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATT TTTGGCAACG
401 GCTCCGGCGG CAACGCGGGC GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTT GCTGCGCTGC
551 TCGGTATTGC GGATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```
a255.pep
1  VVGQEALRGE FVAVFAAALR YAVKTCADFH AFDGVDAAHHG VGDFGIEAVE
51  YGFAQADGDV GGFMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDFF FADLGNVGGD FRAEFFQPF FNGSGGNAG GGFAGGTPAA
151 APVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*
```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVVGDFGIEAVKNRFAQADRD					
	:					
a255	VVGQEALRGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVVGDFGIEAVEYGFAGQADGDV					
	10	20	30	40	50	60
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	:					
a255	GGFMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	:					
a255	GGFMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	FRAEFFQPFNGSGSNAGGGFTGGAPAAAVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	:					
a255	FRAEFFQPFNGSGSNAGGGFAGGTPAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
m255.pep	FRAEFFQPFNGSGSNAGGGFTGGAPAAAVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	:					
a255	FRAEFFQPFNGSGSNAGGGFAGGTPAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```
g256.seq
1  atgctcgcgg tacgcaatcg gggttggcac ggcgcagtcg tccatttcgg
51  cagctcgggc ggcgtagcga acaccgcccc ggtgttctac cacttgggtg
101 ataccgccga aatcgctttt gctttggaca cgctaccgcg gcgttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttgggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgccgtat
251 ccgccccgtg tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301 acgcggctgc tctacacgcg ctacttcctc cgcacactga taccctaaag
```

```

351 acgttcgctc caaggttttc agacggcatt tgccgcaggg tgcaaaacac
401 tgggcgagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451 cggcacgact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501 tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgccgc
551 ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601 caacctgcac acggcgggca cgccggcttt gtcagcagca ccggcggcag
651 gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttgacagct
701 tccgcacaaa caggcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

g256.pep

```

1 MLAVNRGWH GAVVHFRSCG GVANTAPVIFY HLGDTAEIAF ALDTLTARYR
51 EIYAVGVSLG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNANDP FLPPEALPRA DEASEAVTLF
201 QPAHGGHAGF VSSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

m256.seq

```

1 ATGCTTGCGG TACGCGATCG GGGTTGGCAC GCGTAGTCG TCCATTTCCG
51 CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101 ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCCGC GCGTTACCGT
151 GAAAtATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTATCT
251 CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTCGA CAGCGGCATC
301 ACGCGGCTGC TCTACACGCG CTACTTCCTC CGCACCTGA TACCCAAAGC
351 AAAATCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451 CGGCACGACT ACTACGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCCCT GCCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCCTGTTT
601 CAGCCGCGAT ATGGTGGTCA TGTCGGCTTT GTCAGCAGCA CCGGCGGCAG
651 GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCTAT TCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

m256.pep

```

1 MLAVDRGWH GVVVHFRSCG GIANTAPVIFY XLGDTAEIAF TLDTFARYR
51 EIYAVGVSLG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRRFDSGI
101 TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNANDP FLPPEALPRA DEVSEAVTLF
201 QPAYGGHGVF VSSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

m256/g256

	10	20	30	40	50	60
m256.pep	MLAVDRGWHGVVHFRSCGGIANTAPVIFYHLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
g256	MLAVNRGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAFALDTLTARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGKKALPQAAVISAPVDAEAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: :					
g256	GNAPAKYLGEQGKKALPHASAAVSAPVDAEAGSRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	:					
g256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNANDP					

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEVSEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

a256.seq

```

1   ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGTAGTCG TCCATTTCGG
51  CAGCTGCGGC GCGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACGCGCGA AATTGCCTTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTC AGACGGCATT TGCCCGAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCGA GACGAAGTGT CCGAAGCCGT TACCTGTGTC
601 CAGCCGACAC ACGTGGTGTC TGTGCGCTTT GTCGGCAGCA CCGCGCGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

a256.pep

```

1   MLAVRDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIYAVGVSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVFYXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
m256.pep	70	80	90	100	110	120
	GNALAKYLGEQKKALPQAAVISAPVDAEAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
m256.pep	130	140	150	160	170	180
	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNAVNDP					
	130	140	150	160	170	180
m256.pep	190	200	210	220	230	240
	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

g256-1.seq

```

1   ATGATTTTGA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACA CCGCGACCC GCATACCGCC

```

```

101 GCGAGATGCT TCCCACAGC ACGGGTAAAA CAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTCGCC CGATGCGCCG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTGGAACGT ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GGCAGTCG TCCATTTCG CAGCTGCGGC
301 GCGTAGCGA ACACGCCGCC GGTGTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACC GCCTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGCAAAA AGGCATTGCC GCACGCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAAACAGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCCTGCCGC CCGAAGCCCT
801 GCGCCGTGCA GACGAAGCGT CCGAAGCCGT TACCTGTTC CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCTAT TTTGACAGT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVNRGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EIYAVGVS LG NAPAKYLGE
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFA DHDYRQTSK PLLKHVAKP
251 LLLNAANDP FLPEALPRA DEASEAVTLF QPAHGHHAGF VSSTGGRHL
301 QWLQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCC GCGCCC GCATACCGCC
101 GAGAGCTGCT TCCCACAGC ACGGGTAAAA CCAAGTCGCT CTACGACTTT
151 TCAGACGGCA TTTGCCCCGA TGCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGACGCC ATTACGCGGT CGAAGTATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCCGCGC CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCGC
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 GGCAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAG CGGCTGCTCT
551 ACACGCGCTA CTCCTCCGC ACCCTGATAC CCAAAGCAA ATCGCTCCAA
601 GGTTTTCAGA CGGCATTGCG CGCAGGCTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGC CACGACTACT
701 ACCGCCAACC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCTGTCTCA ATGCCGTCAA CGACCCCTTC CTGCGGCGCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CCTGTTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCGC AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPDTPF FLRNGNADTI AAKFLQHPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVDRGWHG VVVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYR EIYAVGVS LG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFA DR HDYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHGVFV SSTGGRHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

          10      20      30      40      50      59
m256-1.pep MILTPDTPFFLRNGNADTIAAKFLQHPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
          |||||:|||||:|||||:|||||:|||||:|||||
g256-1      MILTPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
          10      20      30      40      50      60

          60      70      80      90     100     110     119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVDRGWHG VVVHFRSCGGIANTAPVYFHLGDTAEIAF

```


591

```

|||||
g256-1  LVVLFHGLEGSSRSHYAVELMLAVRNRGWVGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
          70      80      90      100     110     120
m256-1.pep 120      130      140      150      160      170      179
          TLDTFAARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAGRFRDSCI
          :|||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1  ALDTLTARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVAPVDAEAAGSRFRDSCI
          130      140      150      160      170      180
m256-1.pep 180      190      200      210      220      230      239
          TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFAPLHGFADRHDIYRQTSC
          |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1  TRLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFAPLHGFADRHDIYRQTSC
          190      200      210      220      230      240
m256-1.pep 240      250      260      270      280      290      299
          KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHGVFVSSTGGRRLHL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1  KPLLKHVAKPLLLNNAANDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRRLHL
          250      260      270      280      290      300
m256-1.pep 300      310      319
          QWLPQTVLSYFDSFRTNRRX
          |||||
g256-1  QWLPQTVLSYFDSFRTNRRX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA  CACCGCCGGA  CACACCCTTT  TTCTCCGCA  ACGGCAATGC
51  CGACACGATT  GCCGCCAAAT  TCCTGCAACG  CTCGCACCT  GCATACCGCC
101 GCGAGCTGCT  TCCCGACAGC  ACGGGTAAAA  CCAAAACCGC  CTACGACTTT
151 TCAGACGGCA  TTTCGCCCGA  TGCGCCGCTG  GTCGTGCTGT  TTCACGGTTT
201 GGAGGCGGCG  AGTGGCAGCC  ATTACGCGGT  CGAACTGATG  CTCGCGGTAC
251 GCGATCGGGG  TTGGAACGGC  GTAGTCGTCC  ATTTCGCAG  CTGCGGCGGC
301 GTAGCGAACA  CCGCCCCGGT  GTTCTACCAC  TTGGGCGATA  CCGCCGAAAT
351 TGCCTTTACT  TTGGACACGC  TCGCCGCGCG  TTACCGTGAA  ATATACGCCG
401 TCGGCGTATC  GCTGGGCGGC  AACGCGCTGG  CAAAATATT  GGGCGAACAG
451 GCGGAAAACG  CGCTGCCGCA  AGCCGCCGCC  GTCATCTCCG  CACCCGTCGA
501 TGCAGAGGCG  GCAGGCAACC  GCTTCGACAG  CGGCATCACA  CGGCTGCTCT
551 ACACGCGCTA  CTTCTCCGCG  AACTGATAC  CCAAAGCAG  GTCGCTCCAA
601 GGTTCAGAG  CGGCATTGCG  CGCAGGGTGC  AAAACACTGG  GCGAGTTTGA
651 CGACCGTTTC  ACCGCACCGC  TGCACGGCTT  TGCCGATCGG  CACGACTACT
701 ACCGCCAAAC  TTCCTGCAAA  CCGCTGCTCA  AAGACGTTGC  CAAACCGCTG
751 CTCCTGCTCA  ATGCCGTCAA  CGACCCCTTC  CTGCCGCCCG  AAGCGCTGCC
801 CCGCGCAGAC  GAAGTGTCGG  AAGCCGTTAC  CCTGTTCCAG  CCGACACACG
851 GTGGTCATGT  CGGCTTTGTC  GGCAGACCCG  GCGGCAGGCT  GCACCTGCAA
901 TGGTTGCCGC  AGACCGTCCT  GTCCTATTC  GACAGCTTCC  GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.pep
1  MILTPPDTPF  FLRNGNADTI  AAKFLQRSAP  AYRRELLPDS  TGKTKTAYDF
51  SDGISPDAPL  VVLFHGLEGG  SGSHYAVELM  LAVRDRGWNG  VVHFRSCGG
101 VANTAPVFYH  LGDTAEIAFT  LDTLAARYRE  IYAVGVSLGG  NALAKYLGEQ
151 GENALPQAAA  VISAPVDAEA  AGNRFDSGIT  RLLYTRYFLR  TLIPKARSLQ
201 GFQTAFAAGC  KTLGEFDDRF  TAPLHGFADR  HDYRQTSCCK  PLLKHVAKPL
251 LLLNAVNDPF  LPPEALPRAD  EVSEAVTLFQ  PTHGGHGVFV  GSTGGRHLHQ
301 WLPQTVLSYF  DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

          10      20      30      40      50      60
a256-1.pep MILTPPDTPF  FLRNGNADTI  AAKFLQRSAP  AYRRELLPDS  TGKTKTAYDF  SDGISPDAPL
          |||||:|||||:|||||:|||||:|||||:|||||
m256-1  MILTPPDTPF  FLRNGNADTI  AAKFLQRSAP  AYRRELLPDS  TGKTKVAYDF  SDGISPDAPL
          10      20      30      40      50      60
          70      80      90      100     110     120
a256-1.pep VVLFHGLEGG  SGSHYAVELM  LAVRDRGWNG  VVHFRSCGG  VANTAPVFYH  LGDTAEIAFT
          |||||:|||||:|||||:|||||:|||||:|||||
m256-1  VVLFHGLEGG  SSRSHYAVELM  LAVRDRGWNG  VVHFRSCGG  IANTAPVFYH  LGDTAEIAFT

```

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVS LGGNALAKYLGEQGENALPQAAAVISAPVDAEAAAGNRFD SGIT					
m256-1	LDTFAARYREIYAVGVS LGGNALAKYLGEQGGKALPQAAAVISAPVDAEAAAGRRFDSGIT					
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFAADRHYYRQTSCK					
m256-1	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFAADRHYYRQTSCK					
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVG FVSTGGRLHLQ					
m256-1	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVG FVSSGGRLHLQ					
	250	260	270	280	290	300
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	WLPQTVLSYFDSFRTNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

g257.seq

```

1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcgggcggtt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaaggtgtcg cgctgggttc cggcgcgagg ctgcgctgtg tcggcggtga
201 cgacagacag gcggcggtt tggtaataa ggttttggcg gaagtggcgc
251 gtttggaata aatgttcagc cttaccgtg aagacagcct gatcagccgt
301 ctgaacgcgc acggttatct gacttcgcct ccggcggtt ttttggaaat
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

g257.pep

```

1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMF5 LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIFTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

m257.seq

```

1  ATGGGCAGGC ATTTCGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GCGGGGGA C. GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAATGT GTTTTCTGG
151 AAAGGTGTG CACTGGGTTC CGGTGCGGA. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATTGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTATCT GACTTCGCGG TCGGCGGATT TTTTGGAACT
351 GkTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

m257.pep

```

1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNDD EKRNENVFFW
51  KGVALGSGAX LRLFGVDDRR AADLVNKLVA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLXLXSL AAIFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10

20

30

40

50

60

593

```

m257.pep  MGRHFGRQRFLTVAAVAAGTAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAD
          |||||:||||:||||: ||||| ||||| |||||:||||:|||||:|||||:
g257      MGRHFGRRRRFLTAAAVAVAGA AVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:||||:||||: ||||| ||||| |||||:||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKKVLAEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC ATTTCGGGCG CAGGCGTTTT TTGACAGTTG CCGCCGTTGC
51  GCGGCGCGGC GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAATAAAGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151 AAAGGTGTCT CACTGGGTTC CGGTGCGGAG CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGAAAAA AATGTTTCTG CTTTACCGTG AAGACAGCCT GATCAGCCGT
301 CTGAACCGTG ACGGTTATTT GACTTCGCCG CCGGCGGATT TTTTGGAACT
351 GTTGAGCCTG GCCGTGATAT TCACGCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF LTVAAVAAG AAVSFLPNPF AADDEKRNKD EKRNNVFFW
51  KGVALGSGAE LRLFGVDDRR AADLVNKKVLA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAX
          ||||| :|||||: |||||
|||||
a257      MGRHFGRRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:||||:||||: ||||| ||||| |||||:||||:|||||:|||||:
||
a257      LRLFGVDDRRRAADLVNKKVLAEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |||||
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

g258.seq

```

1 atgcgcccgt tcctaccgat cgcagccata tgcgcccgtc tcctgctgta
51 cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtggt gtccgcccgtt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcggtgtt
201 cggttcgcag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttcctg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccggcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccca
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccga caagaacattt ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaa agcataggcg gcgtattgta
651 cgcgcaggga tggttgtcgg caggtacgca caacggcgcg gattacgcgc
701 tgttcttccg ccagccgatt cccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcggcgcaa atatgccgaa ttgagttaca gaaaaaagg
801 tttgcagacc tttttctg taacctgtct gattgcctcg ctgctgtcga
851 tttttcttgc gctggtaatg gcaactgtatt ttgcccgcg tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag gcggtggcg aggggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagttcggg cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcg ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctentacccc ctctcttgtt
1151 gccgtaccgc ggtgttttcc acttgctcatt cctccccctt ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

g258.pep

```

1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51 LARYVILLK DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVFPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKRGLQT FFLVTLIAS LLSIFLALVM ALYFARFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLDG LTTGVVVSYP LSCCRAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

m258.seq

```

1 ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTGTGA
51 CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTCTT
101 GGTGGATTGT TGCCTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTCGCAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTTG AGCAAGTCCG CATTGAATTT GGCGGCAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGCTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCTT
701 TGTTTTTCCG TCAGCGGTT CCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCCGCCG TTTCTGCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA

```

```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACsTT CAACAAAGCG GCGGAACAGA TTYTGGGGAT GCCGCTTACC
1201 CCCcTGtGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAA GAAGCCGCGT
1451 GGGGCGAAgt GGCGaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCCGCCGA ACgGsTGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAAA TCCTGACGCG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCCG CAATTATGCG
1651 CGTTCCCTT CGTCAAATT GGAATCAG GATTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGTTT GCGGCGGACT
1751 TGCCGGCGAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

m258.pep

```

1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51 LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSQAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAVPO IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDfsQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAAQSL AEFVFAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGGKLDEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/g258

m258.pep	10	20	30	40	50	60
	MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVAFSAML VLSAVLARYVILLK					
g258	MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVSFSAM L VLSAVLARYVILLK					
	10	20	30	40	50	60
m258.pep	70	80	90	100	110	120
	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
g258	DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSLNL					
	70	80	90	100	110	120
m258.pep	130	140	150	160	170	180
	SKSALNLAADNALGNAVPOIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK					
g258	SKSALDLAADNAVSNAPVQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK					
	130	140	150	160	170	180
m258.pep	190	200	210	220	230	240
	SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV					
g258	SINPHQFDQPLDKEHWEIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI					
	190	200	210	220	230	240

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	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
	:::			:		
g258	PENVAQDAVLIEKARAKYAELSSYSKKGLQTFVLVTLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDIFSQTRPVLNRNDEFGRLTKLFNHMTEQLSIAKEADERNRRREEAA					
	:					
g258	PILSLAEGAKAVAQGDIFSQTRPVLNRNDEFGRLTKLFNHMTEQLSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDEQGCLKTFNKAAEQILGMPLTPLWGSSRRHGWHGVSAAQSSL					
	:		:	:		
g258	RHYLECVLDGLTTGVVVSYPPLSCCRTAVFSTCHSSPLSYFX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1027>:

```

a258.seq
1 ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51 CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTC
101 GGTGGATTGT TGCCTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCGGTT
151 TTGGCAGCTT ATGTCTATATT GCTGTTGAAA ACAGAGCCGC AGCGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCCGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTTCTG TTCGCGGTTT CCGCACAGTT TATCAACGGC
301 ACGATTAAAT CGTGGTTCGG CAACGATAAC CACGAGGCGC TTGAACGCAG
351 CCTCAATTGT AGCAAGTCCG CATGAATCT GCGCGCAGAC AACGCCCTTG
401 GCAACGCCAT CCCCGTGCAG ATAGACCTCA TCGCGCGCGC TTCCTCGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACAGCGCG GTTCGGTCAG GGATTTGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGCG TGGCTGTCGG CAGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCGGGT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGCGCAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTTCTGG ACACCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGCT ACTGGTCATG GCACTGTATT TCGCCGCGCG TTTCTGCGAA
901 CCCGTCTAT CGCTTGCCGA GGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCACAACGA CGATTCGGA CGCTTGACCA
1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCGCGT AGACATTATC TCGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACCTT CAACAAAGCG GCGGAACAGA TTTTGGGGAT GCCGCTTACC
1201 CCCCCTGGG CGACGAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTCCGCCCAT CGCGCGCGCG CGAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGC AACGGCAACG GCGTGGTAA
1401 GGTGATTGAC GACATCACC TTGGATACA CGCGCAAAA GAAGCCCGCT
1451 GGGGCGAAGT GGCAAAACGG CTTGCACACG AATTCGCAA TCCGCTCAGC
1501 CCCATCCAGC TTTCTGCCGA ACGGCTGGCG TGGAATTTGG GCGGGAAGCT
1551 GGACGAGCAG GACGCGCAAA TCCTGACACG TTCGACCGAC ACCATCATCA
1601 AACAAGTTGC GGCATTAATA GAAATGGTCG AGGCATTCCG CAATTACGCG
1651 CGTTCGCCCT CGTCAAATT GAAAAATCAG GATTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTACG AAGCTGGTCC GTCCGGGTTT CCGCGCGAAG
1751 TTGCCGCGA ACCGCTGATG ATGGCGGCGG ATACGACCGC CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATGCCGCC GAAGCGGCGG AAGAAGCCGA
1851 TGTGCCCGAA GTCAGGGTAA AATCGGAAGC GGGGCGAGGAC GGACGGATTG
1901 TCCTGACAGT TTGCGACAA AGCAAGGGGT TCGCGAGGGA AATGCTGCAC
1951 AATGCCTTCG AGCCGTATGT AACGGACAAA CCGGCTGGAA CGGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGCG CGCATCAGCC
2051 TGAGCAATCA GGATGCGGGC GCGCGGTGTG TCAGAATCAT CTTGCCAAAA
2101 ACGGTAGAAA CTTATTGCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```

a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLOT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLNRNDEF RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLEDE DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIIEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*

```

m258/a258 99.0% identity in 584 aa overlap

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLA	DYFWWIVAFS	AMLLLVLSAV	LARYVILLK		
a258	MRRFLPIAAICAVVLLYGLTAATGSTSSLA	DYFWWIVAFS	AMLLLVLSAV	LARYVILLK		
	70	80	90	100	110	120
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFL	FGVSAQFING	TINSWFGNDT	HEALERSLNL		
a258	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFL	FGVSAQFING	TINSWFGNDT	HEALERSLNL		
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNAPVQIDLIGAASLP	GDMGRVLEHY	AGSGFAQLAL	YNAASGKIEK		
a258	SKSALNLAADNALGNAPVQIDLIGAASLP	GDMGRVLEHY	AGSGFAQLAL	YNAASGKIEK		
	190	200	210	220	230	240
m258.pep	SINPHKLDQPFPGKARWEKI	QAGSVRDLES	SIGGVLYAQQ	WLSAGTHNGR	DYALFFRQPV	
a258	SINPHKLDQPFPGKARWEKI	QAGSVRDLES	SIGGVLYAQQ	WLSAGTHNGR	DYALFFRQPV	
	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAE	LSYSKKGLOT	FFLATLLIAS	LLSIFLALVM	ALYFARRFVE	
a258	PKGVAEDAVLIEKARAKYAE	LSYSKKGLOT	FFLATLLIAS	LLSIFLALVM	ALYFARRFVE	
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQ	TRPVLNRNDEF	GRLT	TKLFNHMT	EQLSIAKEAD	ERNRRREEAA
a258	PVLSLAEGAKAVAQGDFSQ	TRPVLNRNDEF	GRLT	TKLFNHMT	EQLSIAKEAD	ERNRRREEAA
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDE	QGCLKTFNKA	AEQILGMPLT	PLWGSSRHGW	HGVSAQQSLL	
a258	RHYLECVLEGLTTGVVVFDE	QGCLKTFNKA	AEQILGMPLT	PLWGSSRHGW	HGVSAQQSLL	
	430	440	450	460	470	480
m258.pep	AEVFAAIGAAAGTDKPVHVK	YAAPDDAKIL	LGKATVLPED	NGNGVVMVID	DITVLIHAQK	
a258	AEVFAAIGAAAGTDKPVHVK	YAAPDDAKIL	LGKATVLPED	NGNGVVMVID	DITVLIHAQK	

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLEQDAQILTRSTDITVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLEQDAQILTRSTDITIKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIKFNAEEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

```

g259.seq
1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaatctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgcgcgatt gtccgcgctc
151 gcgctggtgt ggctggcggtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgctc
301 gccctgctgg tcaaaaacca cggcaaaagg atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgcacg attgccgccc
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgcctcg
451 ggcgaaacct atggcgcgct gttcgccgat attttcgagt tgcggcgccg
501 tttggaaagg cgcgcgttca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggttg gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

```

g259.pep
1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

```

m259.seq (partial)
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAACTCTG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTCCGCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGmGGC
501 TTTGGAAGGG CGCGCGTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGGmGATGC CTGCCGTTCG GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

```

m259.pep (partial)
1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```


599

151 GETYGRVPAD IFELSALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG
 201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVPADIFELSALEGRAFKGLMLKT					
g259	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVPADIFELSAALERRAFKGLILKT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRCCLPFGNGVGVGRQSGVAGDFKNIR					
g259	AEYKXHLRRCCLPFGNGVGFGRQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1 ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
 51 TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAATCTGG TCAATCAGA
 101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
 151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGCGCGTT CAAAGGCTAA
 201 GCGCGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACACC
 251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
 301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
 351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
 401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTCCGCTCG
 451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCCGCCGC
 501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
 551 AAAA.CATCT TCGGCGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
 601 CGCGCTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCG GAAAAGTCCA
 651 A

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1 MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
 51 ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
 101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDASV
 151 GETYGRVPAD IFELSALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG
 201 RAQSGVAGDF KNIGKVQ

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					

600

	10	20	30	40	50	60
m259.pep	70	80	90	100	110	120
a259	70	80	90	100	110	120
m259.pep	130	140	150	160	170	180
a259	130	140	150	160	170	180
m259.pep	190	200	210			
a259	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GGCCTTCGTG TCGGTCGCTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGCA CGCTTCTTGG CAACACTTGG AACACAAGCC GCAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCAGAACTT ATGGCGCGGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GGCCTTCGTG TCGGCGCCTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGCA CGCTTCTTGG CAACACTTGG AACACAAGCC GCAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCAGAACTT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTTCG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGLMLLT AEYKNIFGDA CRSETALELG
201 ALNQLAQEIS KTSEKSKRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALS AVLVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALS AVLVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
m259-1	SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALE					
m259-1	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALEGRAFGMLKLT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC  ACGCTTCTGT  CCAAAGCCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTTGCCGGTT  TTTTGACCGC  GCAATCTGG  TTCAATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CCTCGCTTC  TGTCCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GCGTTCGTG  TCGGCGCGTT  CAAAGGCTAA
201 GCGGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATACACC
251 CCGTCCTGCA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAATGCTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAAGGG  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCG  ACGACGAAGA  CGCGCGCACG  ATTGCCGCCG
401 AGTTGGCAAA  AATGGATATG  TTTGCATTGG  GGACGGACGC  GGTGCGCTCG
451 GCGGAAACCT  ATGGACGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTGCGCGGC
501 TTTGGAAGGG  CGCGCGTTCA  AAGGAATGTT  GAAACTGACG  CGCGAATATA
551 AAAACATCTT  CGCGGATGCC  TGCCGTTGCG  AAACGGCGTT  GGAGTTGGGC
601 GCGCTCAATC  AGGCGTTGCA  GGAGATTTC  AAAACATCGG  AAAAGTCCAA
651 ACGGATATTT  TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQKAYTEEL  PPLLSALS AV
51  ALVWLAWAFV  SARSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQML
101 ALLVKNHKGK  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTD AVAS
151 GETYGRVFAD  IFELSAALEG  RAFKGLMLLT  AEYKNIFGDA  CRSETALELG
201 ALNQLQEIS  KTSEKSKRIF  Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALS AVLVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALS AVLVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
m259-1	SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALEGRAFGMLKLT					
m259-1	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALEGRAFGMLKLT					
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELGALNQLQEISK TSEKSKRIFYX					
m259-1	AEYKNIFGDACRSETALELGALNQLQEISK TSEKSKRIFYX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq



1	atgggtgcgg	gtgtagtatt	cgttgtcttt	cagccgttct	tcagcctgtt
51	tcgagcggtg	ttcgagggcg	gagtcggtat	agtcgagggg	gcgcacgatg
101	ccgctgaatg	cgacttcttg	tccgaggaat	ttaccctgat	ccggatcggg
151	gatgttttta	ttgattcggg	aggtcagata	acggcccggg	tctttcaggc
201	ctttgggtga	aacctctggc	cctttgggtg	acagcagcct	gccttcctggg
251	cccgagagca	ggcgcgcgcg	ggcagcggtt	tctttgcggg	aaacgatttg
301	cgggtctgcg	ataaagacgc	ggtagaagtt	gacatcgatg	gcgggaatac
351	cgtatccgga	cacttcctta	tccggactga	ttttgacgac	ggggatgccg
401	tctgtctgtt	ccaagccgag	gcgcggttcg	ccgccaacgt	agcgcaacac
451	caataccttg	cccggtataa	tcaggtcggg	atttgggatt	tgatcccggt
501	tcgcgcceca	cagggggggg	catttgccac	gggctgtaca	ggtatttggc
551	cgaataaccg	cacagqqtgt	cgcctctttt	ga	

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

q260.pep

1 MGAGVVFVVF QPFFSLFRAL FEGGVGIVEG AHDAECDL SEEFTRIRIG
51 DVFIDSVGQI TARFFQAFVG NPGAQGVQPP AFRAREQARR GSGFFAGNDL
101 RVLHKDAVEV DIDGGNTVSG HFLIRTDFFD GDAVCLFQAE ARFAANVAQH
151 QYLARINOVG IVDLIPVRAP OGGTIATGCT GICPKYPTGC RPV*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1043>:

m260.seq

1	ATGGGTGCGG	GTATGGTATT	CGTGTCTTT	CGGCCGTCT	CCAGCCTGTT
51	TCGAGCGTTG	TTCGAGGACA	GAGTCGGTAT	AGTCGAGGGA	GCGCACGATG
101	CCGCTGAATT	CGACTTCCTG	CCCAGGAAT	TTACCCGTAT	CCGGATCGGT
151	GATGTTTSTA	TTGATTCCGT	AGGTCAGGTA	GCGGCCCGGC	TCTTTCACGC
201	CTTTGGTGTA	AACCTCGTGT	CGTTTGGTGT	ACAGCAGCCT	GCCTTCCGGG
251	CCCGAGwra	sGCGCGGyGC	GGCAGCGGTT	TCTTTGCGGA	AAACGATTTG
301	CGGATGCCGC	ATAAAGATGC	GGTAGAAGTT	GACATCGATG	GCGGGAATAC
351	CGTATCCGGA	CAC'TTCCTTA	TCCGGACTCA	TTTGTACGAC	GGGGATGCCG
401	TCTGTCTGTT	CCAAGCCGAG	GCGCGGTTTC	CCGTCAACGT	GCGCGAACAC
451	CAATACCTGG	TCCGGATAAA	TCAGGTCGGG	ATTGTGGATT	TGATCCCGGT
501	TCGCGTyCCA	CAG			

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260 . pep

1 MGAGMVFVVVF RPFSSLFRAL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51 DVFIDSVGQV AARLFQAFGV NPGAFGVQQP AFRARXXARX GSGFFAGNDL
101 RMPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVRINQVG IVDLIPVRVP Q

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/q260

	10	20	30	40	50	60
m260.pep	MGAGMVFVFRPFSSSLFRALFEDRVGIVEGAHDAECDLPEEFTRIRIGDVFIDSVGQV					
	: :					
g260	MGAGVVFVVFQPFSSSLFRALFEGGVGIVEGAHDAECDLSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFAFGVQQPAFRARXXARXSGGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
	: :					
g260	TARFFQAFGVNPGAFAFGVQQPAFRAREQARRSGGFFAGNDLRVLHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQLVRINQVGIVDLIPVRVPQ					
g260	HFLIRTDFFDDGDAVCLFQAEARFAANVAQHQLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

```
a260.seq
1   ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GGCGCGGCGC GGCAGCGGTT TCTTTCGCGG AAACGATTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GGCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTGGCC
551 CGAAATGCCC CACAGGTGTG CGCCTGTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

```
a260.pep
1   MGAGMVVFVF RPFSSLFRL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51  DVFIDSVGVQ AARLFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*
```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRLFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGVQV					
a260	MGAGMVVFVFRPFSSLFRLFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGVQV					
	10	20	30	40	50	60
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVLRINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPPQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

```
g261.seq
1   atggagcttg ggcataatcgt attccttctg ctttgcgcgc gttcagacgg
51  cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctccggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctgttcgcgg atgtagtcga acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtac atcagcggcg tgtggatttg aaaaatcgtag
251 tccatcgcca gattaagggt aacgttcgat gatttgacga acacgccgcg
301 gcagtcggga tagcccgaaa aatcggtttc gcacacgccc gcgatgatgt
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc
451 gatggcggcg gtttcgatgg cggcggtttc gtccatcagg gcgttgtgcg
501 taatctgcgc catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttcacgc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgcccgtag gtttgattg
```

701 qcttttttqgt ttqa

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1	MELGHIVFLV	LCARSDGLFT	FQTFRQPAFA	QDARAFAAA	ADDTLVAGVG
51	LFADVQHAH	FVRQRPRLRL	GQVHQRRVDL	KIVVHRQIKG	NVHGDFDEHAA
101	AVGIARKIGF	AHARDDVPDT	LPFGKNGGVK	QEKRVTPVHK	GIGNAVVGGF
151	DGGGFDGGG	VHQGVVRNLP	HQAQIEYGLT	DTQILRDPLC	AFQLDGMALP
201	VSEGDGLDVF	APVGLDCLNQ	AGGRILTARE	DDOGFLV*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1	ATGGAGCTTG	GGCATATCGT	ATTCCTTATG	GTTTGCGCGT	GTTCAGACGG
51	CCTTTTACT	TTCCAGATAT	TCCGCCAGCC	cGgGTTCCGC	CAAGATACAG
101	CTCGGGCAT	CCGGcGACCC	GCCAGCAGAT	CCGTTATAGC	AGGTGTGGGT
151	TTTGCGCGG	ATATAGTCCA	GACGCGCAT	TTCGTCCGCG	AACGCCACG
201	TTTGCGCCTT	GGTCAGATAC	ATCAGCGGCG	TGTGGATTTG	AAAATCATAG
251	TCCATCGCCA	AATTAGGGT	AACGTTTCATC	GATTTGACAA	ACACGTCGCG
301	GCAGTCGGGA	TAGCCGGAGA	AGTCGGTTTC	GCACACGCCC	GCGATGATGT
351	GCCGTTATCC	CTGCCCTTTG	GCGTAATTCG	CGGCATAGAG	CAGGAAAAGC
401	gCGTTGCGCG	CGTCTACAAA	GGTATTCGGA	ACGCCGTTTT	CGGCAGTTTC
451	GATGGCGGCG	GTGTCGTCCA	TCAGGGCATT	GTGCGTAATC	TGCCGCATCA
501	GgCTcAAGTC	GAGTACGGTT	TGTTTGACGC	CCAAATCCTG	CGCAATCCAG
551	CGGGCAGCTT	CCAGCTCGAC	GGCATGGCCT	TGCCCGCTAT	GGAAAGTAAT
601	GGCTTGACAG	TTTTCGCGCC	CGTAGGTTTG	GATTGCCTAG	ATCAGGACGG
651	TGGTCGAATC	CTGACCGCCC	GAAAAGATGA	CCAGGCTTTG	TTGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1	MELGHIVFLM	VCACSDGLFT	FOIFRQPAFA	QDTARAFAAA	ADDAVIAGVG
51	LLADTVQHAH	FVRQRPRRL	GQIHQRRVDL	KIIVHRQIKG	NVHRFDKHVA
101	AVGIAGEVGF	AHARDLVPYV	LPFGVNRGIE	QEKRVAAVYK	GIRNAVFGSF
151	DGGGVVHQGI	VRNLPHQAQV	EYGLFDAQIL	RNPAGTFQLD	GMALPVLSEN
201	GLDVFAPVGL	DCLNQAGGRI	LTARKDDOGL	LV*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/q261

		10	20	30	40	50	60
m261.pep		MELGHIVFLMVCACSDGLFTFQIFRQPAFAQD	TARAF	AAAADD	AVIAGVGLLADIVQHAH		
		: : : : : :					
g261		MELGHIVFLVLCARSDGLFTFQTFRQPAFAQD	TARAF	AAAADD	TLVAGVGLFADVVQHAH		
		10	20	30	40	50	60
		70	80	90	100	110	120
m261.pep		FVRQRPRRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA	AVGIAGEVGF	AHARD	DDVPYP		
		:					
g261		FVRQRPRRLRLGQVHQRRVDLKIIVHRQIKGNVHGFDEHAA	AVGIARKIGF	AHARD	DDVPDT		
		70	80	90	100	110	120
		130	140	150	160	170	
m261.pep		LPFGVNRGIEQEKRVA	AVYKGIRNA	VFGSFDGGGV	-----VHQGI	VRNRLPHQAQVEYGLF	
		: : : :					
g261		LPFGKNGGVKQEKRV	TPVHKGIGNA	VVGFFDGGGFDGGGF	VHVQGV	VRNRLPHQAQIEYGLT	
		130	140	150	160	170	180
		180	190	200	210	220	230
m261.pep		DAQILRN	PAGTFQLDGMAL	PVLES	NGLDV	FAPVGLDCLNQAGGR	ILTARKDDQGLLVX
		: : :					
g261		DTQILR	DPLCAFQLDGMAL	PVSEGDGLD	VFAPVGLDCLNQAGGR	ILTAREDDQGLLVX	
		190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGCT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTCAATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTGT GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTT CCGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTTCGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHGFDKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHOGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQRAH					
	10	20	30	40	50	60
m261.pep	70	80	90	100	110	120
a261	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAVGIAGEVGFHARDDVPYP					
	70	80	90	100	110	120
m261.pep	130	140	150	160	170	180
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHOGIVRNLPHQAVVEYGLFDAQIL					
	130	140	150	160	170	180
m261.pep	190	200	210	220	230	
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgcaa
51  accgcgcta gaggcggtac ccaaaaacaa cggctttatc cccaacctca
101 tcggcggtatt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgcccgaac cagcctgacc gccggcgaag tcgaagtgat
201 ccggtatcat gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccgc ctttgccggc aggtaaatct gacgatgcc aactcgcgcc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

451 gtcgaagtcg taatgggcgt agccttggca actttgtgca actacgccaa
501 caacctcgcc caaacccgaaa tcaaccccaa attgcaggca tacgcctaa

This corresponds to the amino acid sequence <SEQ ID 1054; ORF 263.ng>:

g263 . pep

1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIGVLANA PEALAFYQEV
51 GKLNAANSLT AGEVEVIRII AVR TNQCSFC VAGHTKLATL KKL LSEQSLN
101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDDELNAF LEAGYNRQQA
151 VEVVMGVALA TLCNYANNLA QTEINPKLQA YA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1055>:

m263.seq (partial)

```

1      ..GCAGCAGGCG AATTTGACGA TGCCAAACTC GGC GCGCTCG CCGCCTTCAC
51     CCAAGCCGTA ATGCGCAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101    CATTTTTCGA TGCGGGGTCA ATCCAGCAGC AGGCAAGTCGA AGTCGTGATG
151    GGCCT .AsyC TgGCAACCTC TGCAACTAC GTCAACAACC TCGGACAAAC
201    CGAATCAAC CCCGAATTGC AGGCTTACGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1056; ORF 263>:

m263.pep (partial)

```

1      ..GCAGCAGGCGC AATTTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51     CCAAGCCGTA ATGCGCAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101    CATTTTTCGA TGCGGGGTCA AACCAGACAG AGGCAGTCGA AGTCGTGATG
151    GGCGT.AsyC TgGCAACCTC GTCAACTAGC GTCAACAACC TCGGACAAAC
201    CGAAATCAAC CCCCGAATTGC AGGCTTACGC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/g263

```

                                     10      20      30
m263.pep                          AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
                                   |||:|||||||:|||||:|||||:|||:
g263    QCSFCVAGHTKLATLKKLLSEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSDD
          80      90      100     110     120     130

               40      50      60      70
m263.pep      ELKAFFDAGYNQQQAVEVMGVXLATLCNYVNNLGQTINPELQAYAX
              |:|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
g263    ELNLFLEAGYNRQQAVEVMGVALATLCNYANNLAQTEINPKLOAYAX
          140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1057>:

a263.seq

1	ATGGCACGTT	TAACCGTACA	CACCTCGAA	ACGCCCCCG	AAGCCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAACAA	CGCTTTATC	CCCAACCTTA
101	TCGGCGTATT	ATCAAACGCC	CCCCAAGCT	TGGCGTTTTA	CCAAGAAGTC
151	GGCAAGCTCA	ACCGCGCCAA	CAGCTGACC	GCCGGCGAAG	TCGAAGTAAT
201	CCAGATTATT	GCGGCCCGCA	CCAACCAATG	CGGCTTCTGC	GTGGCAGGGC
251	ACACCAAAC	CGCAACCTG	AAAAAATCC	TTCCGAACA	ATCCGTCAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GCTCGCCGCT	TTTACCCAAG	CCGTAATGGC	AAAAAAAGGC	GCGGTATCCG
401	ACGGAAGACT	CAAAGCATTT	TTTGTATGCG	GCTACAACCA	GCAGCAGGCA
451	GTCTGAATCG	TGATGGGCGT	AGCATTGGCA	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCAACCCGGA	ATTGCAGGCT	TACGCCTGA

This corresponds to the amino acid sequence <SEQ ID 1058; ORF 263.a>:

a263.pep

1 MARLTVHTLE TAPEAAKARV EAVLQNNGFI PNLIGVLSNA PEALAFYQEV
51 GKLNAANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KLLSEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA
151 VEVVMGVALA TLCNYVNNLG QTEINPELOA YA*

m263/a263 97.4% identity in 77 aa overlap

```

                                10      20      30
m263.pep                      AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
                                |||||
a263      QCGFCVAGHTKLATLKKLLSEQSVKAARALAAGEFDDAKLGALAAFTQAVMAKKGAVSDE
              80      90      100      110      120      130

              40      50      60      70
m263.pep      ELKAFFDAGYNQQQAVEVVMGXLLATLCNYVNNLGQTEINPELQAYAX
              |||||
a263      ELKAFFDAGYNQQQAVEVVMGVALATLCNYVNNLGQTEINPELQAYAX
              140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

```
g264.seq
1   ttgactttaa cccgaaaaac ccttttcttc ctcaccgcgc cggttcggcâc
51  acatcccttc cagacggcat cgcgcgacgc agtgggtcaag ccggaaaaaac
101 tgcacgcctc cgccaaccgc agctacaaag tcgcggaatt cacgcgaâac
151 ggcaacgcct cgtgggtacgc cggcagggtt caccggcgca aaacttcâgg
201 cggagaccgc tacgatatga acgcctttac cgccgcccac aaaaccctgc
251 ccatccccag ccatgtgctc gtaaccaaca ccaaaaacgc caaaagcgtc
301 atcgtccgcg tcaacgcacc cggccctttc caccgcgaac gcatcatcga
351 cgatccaaa gctcgcgcgc aaaaaattggg cttgttcagc caagggcâgg
401 cacacgtcaa aatcgaacaa atcgtccgcg gccaatccgc accggttgcc
451 gaaaacaaag acatctttat cgacttgaaa tctttcggta cggaaacâga
501 agcacaagcc tatctgaacc aagccgccca aaatttcgcc gtttcgtcat
551 caagcccgaa cctctcggtt gaaaaacgcc gttacgaata cgttgtcâaa
601 atgggccgtt ttgcttcgca ggaacgcgcc cgcgaagccg aagcgcaggc
651 acgcggtatg gttcgggcga tactgacctc cgggttga
```

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

1	<u>LTLTRKTLFL</u>	<u>LTAAGFTHSL</u>	<u>QTASADAVVK</u>	PEKLHASANR	SYKVAEFTQT
51	GNASWYGGRF	HGRKTSGGDR	YDMNAFTA AH	KTLPIPSHVR	VTNTKNGKSV
101	IVRVNDRGPF	HGNRIIDVSK	AAQKLG FVS	QGTAVHKIEQ	IVPGQSAPVA
151	ENKDI FIDLK	SFGTEHEAQA	YLNQAQNF A	ASSSSPNLSV	EKRREYEVVK
201	MGP FASQERA	AEAEAQARGM	VRAVLTSG*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

```
m264.seq
1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACCGCCG CATTCGGCAC
51  ACACTCCCTT CAGACGGCAT CGCGCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC GCCTAACCGC AGCTACAAG TCGCCGGAAC ACGCTACACG
151 CGGAAAAACC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CTCGTGTGTA
201 CGGCGGCAGG TTTCACGGGC GCAAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCGGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAAAT GGGCTTTGTC AACCAGGGA CGGCACAGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCGGTT GCCGAAAAAC AAGACATCTT
501 TATCGACTTG AAATCTTTCG GTACGGAAAC CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CCAAAACTTC GCCGTTCGT CATCGGGTAC GAACCTCTCG
601 GTTGA AAAAC GCGGTTACGA ATACGTCTGC AAAATGGGAC CGTTTACCTC
651 CGAGGAACGC GCCGCCGAAG CCGAAGCTCA GGC GCGCGGT ATGGTTCGGG
701 CGGTATTGAC CGCCGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264 . pep

1	<u>LTLTRKTLFL</u>	<u>LTAAFGTHSL</u>	QTASADAVVK	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGG	FHGRKTSGE	RYDMNAFTAA	HKTLPIPSYV
101	RVNTNKGKGS	VIVRVNDRGP	LFGNRIIDVS	KAAAQKLGFV	NQGTAVHKIE
151	QIVPGQSAPV	AENKIDIFDL	KSFGEHEAQ	AYLNQAAQNF	AVSSSGTNLS
201	VEKRRYEYVV	KMGPTTSQER	AAEAEAAQAR	MVRVALTAG*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTAHHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTSGGDRYDMNAFTAHHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGTAAHV KIEQIVPGQSAPVAENK DIFID LKSF GTEHEAQ					
g264	FHGNRIIDVSKAAQKLG FVSQGTAAHV KIEQIVPGQSAPVAENK DIFID LKSF GTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFQSERAAEAQAQGMVRAVLTAGX					
g264	AYLNQAAQNFAASSSPNLSVEKRRYEYVVKMGPFASQERAAEAQAQGMVRAVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCGAAAAAC	CCTTTTCCTC	CTCACCGCCG	CATTCCGGCAT
51	ACATTCTTTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAAC
101	TGCACGCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAA	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTACGCAG	ACCGGCAACG	CCTCGTGGTA
201	CGGCGGCAGG	TTTACGGGCG	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCGGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	GCGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCGG
401	CGCAAAAATT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAAATCGTCC	CGGGCCAATC	CGCACCGGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCCG	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTAAGFIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTSGGE	RYDMNAFTAA	HKTLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAQKLG FV	NQGTAAHV KIE
151	QIVPGQSAPV	AENKDIFIDL	KSFGTEHEAQ	AYLNQAAQNL	ASSASNP NLS
201	VEKRRYEYVV	KMGPFASQER	AAEAQAQARG	MVRAVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEVVVKMGPF TSQERAAEAEQA RGMVRAVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEVVVKMGPF TSQERAAEAEQA RGMVRAVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```
m265 . seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTGGGCTTG
51  GCGCGGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGCGCGAA
151 ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTTGATGTT
201 CATAT.TTT GCCTTTGTAA ATCGTGGGTT GGAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTGCGCTTC GCGGCGCGCT TCCTGCGAGG TAAACGGTCC
351 CATTTTGACG ACGTATTCGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```
m265 . pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGA EMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGA EMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNRGLENV DINKVSNNRQ PAVNTARTIP RAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNNRQPEVSTARTIP RACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

```

a265.seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGC GCGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCATCA GTGCGGTTGC GCGGCGGTG AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... . . . .GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCTCTCGG GCGCGTTTC TGCGAGGCAA ACGTCCCAT
351 TTTGACGACG TATTCTGTAA

```

a265.pep

1	MSVILPPTRA	NAAFSAWARL	MILSCLLCWC	AACPWSSSPC	PSWWASAGAE
51	MPISAVAAAV	KRRRLKFIFA	PAKYLX..XC	LKDVKAGHQP	AVNTARTIPR
101	A*ASASAARS	CEANGPILTT	YS*		

```

      10      20      30      40      50      60
m265.pep  MSVILPPTRANAAFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSSAVAAEV
          |||||
a265      MSVILPPTRANAAFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMPISAVAAAV
          |||||
      10      20      30      40      50      60

      70      80      90     100     110     120
m265.pep  KRRCLMFIXFQFVNRGLENVVDINKVSNNRQPAVNTARTIPRAXASASAARSCEVNGPILT
          ||| | || : : : : |||||
a265      KRRRLKFI---FAPAKYLXXCLKDVKAGHQPAVNTARTIPRAXASASAARSCEANGPILT
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      70      80      90     100     110

m265.pep  TYSX
          ||||
a265      TYSX
          120

```

```
g266.seq
1 agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccatcatg
51 accgcaccca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tgttcggcgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgatc gagctggcgg cagggttcgc gctgaccgcc
201 tctcttgctc acatcctega atcccgtagc ggagcggtag acaatcaggc
251 ttgggagttt tacgccaccg tcgtctgcct gtacctatt ttgcgcttc
301 cgtgttcgt gcggcgggat ttttggcaca cgcgcaacaa qqaataa
```

g266.pap

1 MQFRRHRRRQ CPNRKPIMTA SMYILLVLAL IFANAPFLT TRLFVGAALKR
51 KHFGHHLIEL AAGFALTASL AYILESRAGA VHNQGWE¹FYA TVVCLYLIFA
101 FPCEVRRYFW HTRNRE*

```
m266.beq
1  ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCGCCGAC AACGCCTAAA
51  CAAAGGCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAAAGCCGCC TTCCTCACCA CAGAGCTGTT CGGCGTGCCG
151 rCACTCAAGC GCAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAGGAT
251 CGGTACACGA CTAGGGTTGG GAGTTTtATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTTG CGTTTCCATG TTTTGTGTGG CGGTATTTTT GGCACACCGG
351 CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
  51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
 101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAAALKRKHFGHH
          10      20      30      40      50

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVR RYFWHTRNREX
          60      70      80      90     100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAA
  51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTG CTGCTTGCTT
 101  TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
 151  CCGCTCAAGC GCAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
 201  TTTCCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
 251  CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
 301  CTGATTTTTC CGTTTCCCTG TTTCTGTGG CGGTATTTT GGCACACGCG
 351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
  51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
 101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTKLFGIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90     100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:
g267.seq

1	atgcaagtcg	ccttttttct	cgccgtggtg	ttcaaaaata	tgggtttcca
51	caatcgcatc	ggtcgggcag	gcctcttcgc	agaaaccgca	gaagatgcac
101	ttggtcaggt	cgatgtcgta	acgcttgggt	cggcgggtgc	cgtcttcgcg
151	ttcttccgat	tcgatgttga	tcgccattgc	cggacacacc	gcctcgcaca
201	atttacacgc	gatgcagcgt	tcctctccgt	tcggaaaacg	gcgttcgcgcg
251	tgcagaccgc	ggaacgcgac	ggattcggcc	gtttttctct	cgggaaaaata
301	aattgtgtct	ttgcggggcaa	aaaagtgttt	gagcgtttacg	cccatgcctt
351	tgaccagttc	gccaa gcaga	aagggtttta	ctaa	

This corresponds to the amino acid sequence <SEQ ID 1076; ORF 267.ng>:

g267.pcp

1 MQVAFFLAV FKNMGFHNRI GRAGLFAETA EDALGQVDVV TLGAAGAVFA
51 FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLFGKI
101 NCVFAGKKVF ERYAHAFDQF AKQKGFY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1077>:

m267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCGTGGA	TTCAAAATA	TGGGTTTCCA
51	CAATCGCATC	AGTCGGGCAT	GCCTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTAC	CGTCTTCACG
151	TTCTTCCGAT	TCGATGTTAA	TCGCCATTGC	CGGACACACT	GCCTCACACA
201	ACTTACACGC	GATACACCGC	TCTTCGCCGT	TCGGATACCG	CcGCTGCGCG
251	TGCAGACCGC	GGAAACGCAC	GGATGCGGCG	GTTTCTCTTT	CGGGGAAATA
301	AATTGTGTCT	TTGCGGGCGA	AAAGTTTTTT	GAGCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTT	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1078; ORF 267>:

m267 . pep

1 VQVAFFLAVV FKNMGFHNRI SRACLFAETA EDALGQVDVV TLGAARTVFT
51 FFRFDVNRHC RTHCLTQLTR DTPLFAVRIP PLRVQTAETH GLRRFLFGEI
101 NCVFAGEKVF ERYAHTFYQF AKQKGFY*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 267 shows 82.7% identity over a 127 aa overlap with a predicted ORF (ORF 267.ng) from *N. gonorrhoeae*:

m267/g267

		10	20	30	40	50	60
m267.pep		VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVVTLGAARTVFTFFRFDVNRHC				
		:					
g267		MQVAFFLAVVFKNMGFHNRI	IGRAGLFAETAEDALGQVDVVTLGAAGAVFAFFRFDVDRHC				
		10	20	30	40	50	60
		70	80	90	100	110	120
m267.pep		RTHCLTQLTRDTPLEFAVRIPPLRVQTAETHGLRRFLFGEINCVFAGEKVFERYAHTFYQF					
g267		RTHRLAQFTRDAAFLSVRKLTALRVQTAETHGLRRFLFGKINCVFAGKKVFERYAHAFDQF					
		70	80	90	100	110	120
m267.pep	AKQKGFYX						
g267	AKQKGFYX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1079>:

a267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCGTGGA	TTCAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGCGAG	GCTTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TGTGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGCGCGCTGC	CGTCTTCGCG
151	TTCTTCCGAT	TCGATGTTGA	TCCGCAATGC	GGGGACAGCG	GCTTCCACAA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	CGGTTGCGCG
251	TGCAGACCCG	GGAAACGCAC	GGATTGCGCG	GTTTCTCTT	CGGGAAAATA
301	AATCGTGCTT	TTGCGGGCAA	AAAAGTTTTT	GAGCGTTACG	CCCATACTTT
351	TTACCAATTG	CCCAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNM	GFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVFTFF	FRFDVNRHC	
a267	VQVAFFLAVVFKNM	GFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFF	FRFDVDRHC	
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTP	FAVRIPPLRVQTAETH	GLRRFLFGEIN	CVFAGEKVFERY	AHTFYQF	
a267	GANGFTQFTRDAA	FLAVWITALRVQTAETH	GLRRFLFGKIN	RVFAGKKVFERY	AHTFYQF	
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101 cctgcggaag cgaagagact aaagagattt tggcctaaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251 gtttgggcat aaccgtcgat gaagtcgcaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgcaga
351 tgtgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgat
451 tatgtcaaaa ctattttctta cagcgctccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctgggtgc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgaggga
651 ggcagaagaa gcggcggcgc aggaggcatt gggtcgggag caggaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctcgcagaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggtc ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGINPFSG KEISCGSEET KEILVKLVDR
51  NVEGETVKTF DDAFKDQAF ADIGISHIRR MVERLGITVD EVRTEKTD
101 SSKLKCEAAL KLDVPDDVD YAVANQSIG NSHKKTPDFF EPYYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSLVSMAL IKEPLDKAKQ
201 RNEKLEAEEA TAQEAREEEE AAQAEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASQK TWKSGMDKIC ANNAKAEET PNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDENVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGACAAA GTGAAACAAA GGAACGAAGA
```

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```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCTGCGC
151  AG.CAGTTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCG TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCTAGC
301  GAACTGGCAT GCAAAACGGC GAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   ..MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAAARVS EWEERYKLSR
51  XQFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEAAE-----
                                |||:|||:|||:|||:|||:|||:|||:|||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  --EAAAQEALGREQEAAARVSEWEERYKLSRSQFEQFWKGLPQTQVQNKLP SQKTWKSMD
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      AEEAAAQEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTQVQNKLP SQKTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      KICANNAKAEGKTPNGIKVSELACKTAEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCTGCGC
151 AGCGAGTTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCTAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEEAAAQEALGREQEAAARVSEWEERYKLSRXQFEQFWKGL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAAEEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```


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	10	20	30	40	50	60
	70	80	90	100	110	120
m268.pep	PQTVQNKLPQSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
a268	PQTVQNKLPQSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAEARLEELHNRK					
	70	80	90	100	110	120
	130	140				
m268.pep	KALIDEMXREADKKELSKRLX					
	:					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHK FKHCSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLPQASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

		10	20	30	
m268-1.pep		VQSRDGLHKFKHCSAAMALIKEPLDKVKQRNE			
		: : ::			
g268	KEGAYYVKTISYSVQPTDDKSKIFAELSQAHDIIHPLSELVS--MALIKEPLDKAKQRNE				
	150	160	170	180	190 200
	40	50	60	70	80
m268-1.pep	ELEAAE-----EAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	:				
g268	KLEAAEATAQEAREEEAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	210	220	230	240	250 260
	90	100	110	120	130 140
m268-1.pep	KLQASQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE				
g268	KLQASQKTWKSMDKICANNAKAEGKTPNGIKVSELACKTAEARLEELHNRKKALIDE				
	270	280	290	300	310 320
	150	159			
m268-1.pep	MAREADKKELSKRLX				
	:				
g268	MVREEDKKELPKRLX				
	330				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHCSAAMA LIKEPLDKAK QNNEELEAAE EAAAEALGR
51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKQASQ KTWKSGMDKI
101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLEDEMAREAD
151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHCSAAMALIKEPLDKAKQ	NEELEAAE	EAAAEALGR	EQEVDVSEW		
m268-1	VQSRDGLHKFKHCSAAMALIKEPLDKVQ	NEELEAAE	EAAAEALGR	EQEVDVSEW		
	10	20	30	40	50	60
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKQASQ	KTWKSMDKI	CANNAKAEGE	TPNGIKFSEL		
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKQASQ	KTWKSMDKI	CANNAKAEGE	TPNGIKFSEL		
	70	80	90	100	110	120
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKA	LLEDEMAREAD	KKELPKRLX			
m268-1	ACKTAETEARLEELHNRKKA	LLEDEMAREAD	KKELSKRLX			
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggtttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgtc
51 cagcccttgg atttgggagg tgggtggtgt gtggtcgagg tcggcttttt
101 cctgcaaacc ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttggcg
151 gtttcgccgt gggactttat ccggaacacg gcttcgcccc aggtgtcggc
201 ggctttgatg cacagtttta aaaccaggcg tttggggcgg ttttctgcgc
251 cgcccggtgc cattttgctg tccaatcgcg gggttaaaaa accgttgctg
301 ttaagtgcgc cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc
351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MVWRVNCAAT AALIFSSSPW IWAUVVWWSR SAFSCKPCAS LDASSAPALA
51 VSPWDFIRNT ASPKVSAAIM HSFKTRALGR FSAPPVAILL SNRGVKKPLS
101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTGT
101 CTTGCAAACC TTGCGCCACG TGCCCGCGTC CAGCGCTGTC GTTGATGGTT
151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTGCGCGGC
201 TTTGATGCAC AGTTTAAAAA CCAGGGCTTT GGGGCGGTTT TCGTCCGCGC
251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCGTTT
301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGTCTCTCT GCCTTTCGTT
351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MVWRVNCAAT AVLIFSSSPW IWAUVVWWSR SALSCKPCAT CPRPAPALMV
51 SPWDFIQNTA SPKVSAAIMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
101 KFSSVQVDT SALLCLSLRS *

Computer analysis of this amino acid sequence gave the following results:

m269.pep	MVVRVNC AATAVLIFSSSPWIWA AVVWWSRSALSC KPCATCP-RPAPALMVSPWDFIQNT	59
g269	MVVRVNC AATAALIFSSSPWIWAVVWWSRSAPFCKPCASLDASSAPALAVSPWDFIRNT	60
m269.pep	ASPKVSAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSPKFSVQVDT SALLCLSLRS	119
g269	ASPKVSAALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSPKSPSVQVDT SALLCLSLRS	120
m269.pep	SX 121	
	II	
q269	SX 122	

a269.seq

```
1 ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCGCGT CCAGCGCGCC GCGTGTGACG
151 GTTCGCGCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTTA AAACCAGGGC TTTGGGCGCG TTTTCGTGCG
251 CGCCTGTCGC CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTGTGCG
301 TTAAAAATTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA
```

a269.pep

1	MVWRVNCAAT	AVLIFSSSPW	IWAAVWVWAR	SALSWRFCAS	VPASSAPALT
51	VSPWDFIQNT	ASPKVSAALM	HSFKTRALGR	FSSPPVAILL	SGRGVKKPLS
101	EKSSVOVDLT	SALLCLSLWS	S*		

		10	20	30	40	50	59				
m269.pep		MVWRVNC	AATAVLIFSSSP	PWIWA	AVVWSRS	ALSCKPCATCP	-RPAPALMVSPWDF	IQNT			
					:	:					
a269		MVWRVNC	AATAVLIFSSSP	PWIWA	AVVWSRS	LSWRFCASV	PASSAPALT	VSPWDF	IQNT		
		10	20	30	40	50	60				
	60	70	80	90	100	110	119				
m269.pep		ASPKVSA	AALMHSFK	TRALGR	FSSPPV	AILLSER	GVKKPL	SFKFSS	VQVDT	SALLCL	SLRS
a269		ASPKVSA	AALMHSFK	TRALGR	FSSPPV	AILLSER	GVKKPL	SFKFSS	VQVDT	SALLCL	SLWS
		70	80	90	100	110	120				
	120										
m269.pep		SX									
a269		SX									

```
g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gactgctgc tgactgcctt
51  tgccgccttc aagctcgttt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg agggctgcac gctgcggcac
151 ggaagccgtg tccgcgcgcg cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccc cgggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcatc cgctgcccg tctgtgtcga
351 aggcaggcgc gattttacgc cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgcqaa taa
```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

g270.pep

```

1  MNKNRLLLLL ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca. CAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTT
401 AGACGGCATT TACCGCCGAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep

```

1  MNKNRLLLLL ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRLLLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRLLLLLAALLLTAFAAF KLVLLQWWQA QQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARIRLPVCVEGRR					
	70	80	90	100	110	120
	70	80	90	100	110	120
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTT
401 AGACGGCATT TACCGCCGAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep

```

1  MNKNRLLLLL ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
```

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALLIAFAAVKL	VLLQWQAXQPQAVAAQCDL	TEGCTLPDGS	SRVRAAAVS	
a270	MNKNRKL	LLAALLIAFAAVKL	VLLQWQAXQPQAVAAQCDL	TEGCTLPDGS	SRVRAAAVS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFS	MKNMDMGFNRYMFERQPSGTWQAVRI	RLPICVEGRR			
a270	TKKPFDIYIEHAPAGTEQVSISFS	MKNMDMGFNRYMFERQPSGTWQAVRI	RLPICVEGRR			
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAE					
a270	DFTADITIGSRTFQTAFTAE					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

1	atgttcagtt	cgcggtatggc	gaggatttgg	gcgacggggg	taacggtgtg
51	tatggtcagt	ccgtgtccgg	cggtgacgac	caagcccaaa	tcgccggcga
101	aatgcgcgcc	gttttggatg	cgctcgaaact	gcctgatttg	ttcggcgctgg
151	ctttgtgctg	cgccatattgc	gccggtgtgc	agctcgacaa	cgggcgcgcc
201	gacatcacgg	gcggcttggg	tttgccgtgc	gtcggcatcg	ataaacaagg
251	acacgcgtat	gcccgcgtcg	gtcaggattt	tggcgaattc	ggcgattttt
301	tcctgttgcg	ccaatacgtc	caaaccgcct	tcggtcgtga	tttcctgcgc
351	tttttcaggc	acgatgcaca	cgtcttccgg	catcacttta	agcgcgtttt
401	cgagcatttc	ttccgtcaac	gccatttcaa	ggttcaggcg	cgtgcggatg
451	gcgtttttga	cggcaaatca	atccgcgtct	ttgatgtggc	ggcgggtcttc
501	gcgcaggtgc	atggtaataca	ggtctgcacc	gtgcgttttc	gcaaccagtg
551	ccgcctccac	ggggctggga	taa		

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

1	MFSSRMARIW	ATGVTL	CMVS	PCPAL	TKPK	SPAKCAP	FWM	RSNCLIC	SAW
51	LCASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTRMP	PAS	VRILANS	AI
101	SCCANTSKPP	SVVISCRF	SG	TMHTSS	GITL	SAFSSISS	VN	AISRFR	VRM
151	AFLTANTSAS	LMWRRSS	RRC	MVIRSA	PCVS	ATSAAST	GLG	*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

1	AwGTTcagtt	CGCGGatggc	GAGGATTtgg	GCGATGGggg	TAACGTTgtg
51	TATGTCAGT	CCGTGTCCGG	CGTTGACGAC	CAAGCCCAAA	TCGCCGGCGA
101	AATGCGCGCC	GTTTTGGATG	CGCTCGAACT	GCCTGATTG	TTCGGCGTGG
151	CTGCGCGCGT	CGGCATACGC	GCCTGTGTGC	AGCTCGACAA	CGGGCGCGCC
201	GACATCACGG	GCGGCTTGA	TTTGCCTGTC	GTCCGCATCG	ATAAACAAAG
251	ACACGCGTAT	GCCTGCGTCG	GTCAGGATTT	TGGTGAACCC	GGCGATTTTT
301	TCCTGTTGCG	CCAATACGTC	CAAACCGCCT	TCGGTCGTGA	TTTCCTGACG
351	TTTTTCAGGC	ACGATGCACA	CGTCTTCCGG	CATCACTTTC	AAAGCGTTTT
401	CCAACATTTT	TTCCGTCAAC	GCCATTTC	AA	
451	GCGTTTTTGA	CGGCAACAC	GTCCGCGTCT	TTGATGTGGC	GGCGGTCTTC
501	GCGCAGGTGC	ATGGTAATCA	AATCCGCACC	GTGCGTTTCG	GCAACCAGTG
551	CCGCCTCCAC	GGGGCTGGGA	TAA		

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

1	XFSSRMARIW	AMGVTL	CMVS	PCPAL	TKPK	SPAKCAP	FWM	RSNCLIC	SAW
51	LRASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTRMP	PAS	VRILVNP	AI
101	SCCANTSKPP	SVVISXRF	SG	TMHTSS	GITF	KAFSNISS	VN	AISRFR	VRM
151	AFLTANTSAS	LMWRRSS	RRC	MVIKSA	PCVS	ATSAAST	GLG	*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC					
	10	20	30	40	50	60
m271.pep	70	80	90	100	110	120
	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTSKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSALFSCCANTSKPPSVVISCRFSG					
	70	80	90	100	110	120
m271.pep	130	140	150	160	170	180
	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVKSAPCVS					
g271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAPCVS					
	130	140	150	160	170	180
m271.pep	190					
	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

```

1  ATGTTTCAGTT CGCGGATGGC GAGGATTTGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT  CCGTGTCCGG CGTTGACGAC CAAGCCCAA TCGCTGGCAA
101 AATGCGCGCC  GTTTTGGATG CGCTCGAACT GCCTGATTTG TTCGCGGTGG
151 CTGCGCGCGT  CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG  GCGGCTTGGA TTGCCTGTC GTCGGCATCG ATAAACAAGG
251 ACACGCGTAT  GCGCGCGTCG GTCAGGATTT TGGTGAATTC GGCAATTTTG
301 TCTTGTTCGC  CCAATACGTC CAAGCCGCCT TCGGTCGTGA TTCCTGACG
351 TTTTCCGGC  ACGATGCACA CGTCTCCGG CATCACTTTA AGCGCGTTTT
401 CGAGCATTTT  TTCCGTCAAC GCCATTTCAA GGTTCAGGCG CGTGC GGATG
451 GCGTTTTTGA  CAGCAAACAC GTCCGCGTCT TTGATGTGGC GCGGCTCTT
501 GCGCAGGTGC  ATGGTAATCA GGTCGGCACC GTGCGTTTCG GCAACCAGTG
551 CCGCCTCCAC  GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

```

1  MFSSRMARIW AMGVTLCMVS PCPALTTKPK SLAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNSAIL
101 SCCANTSKPP SVVIS*RFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
m271.pep	70	80	90	100	110	120
	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTSKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTSKPPSVVISXRFSG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVKSAPCVS					
a271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1   atgactgcaa aggaagaact gttcgcatgg ctgcgccata tgaacaaaaa
51  caaagggtcc gacctgtttg tgacgaccca tttcccgccc gctatgaagc
101 tggacggcaa aatcaccgcg atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcctcgacc aacgagtgcg atttcgcat cagcctgccc gacaccagcc
251 gcttccgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttgcgc tgaaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctccggcaaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgct gcgtcaggcg
601 ccggatgtga tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc ttgcccgaag cggggcattt gtgtatggcg acgtgcacg
701 ccaacagcac caatcaggcg ctcgaccgca tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgtcaacc ttcaggcggt
801 tatttcgcaa cgcctcgttc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga ttccggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcgt
1051 ttggcggtag agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1   MTAKEELFAW LRHMNKNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESINLPPALK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSGFHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDLELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1   ATGACCGCAA AGGAAGAAGT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTTC TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCTG ATCAGGACG AACCCTGAC GGCgGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGGCGG

```

```

551 TGGATACGGA AAACCTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACCAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCtGA TTTCGGAGTT GATTCAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAAATGCC ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CaaAGTTyCA GCCCCGATT
1101 GGnACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272 . pep

```

1  MTAKEELFAW LRHMxQNKGs DLFVtTHFPp AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IORGATALVF
101 RTITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLcMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLyQLYE KGDISLQeAL KNADSAHDLR
351 LAVQLRSRRA QsXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272 . pep	10	20	30	40	50	60
	MTAKEELFAWLRHMxQNKGsDLFVtTHFPpAMKLDGKITRITDEPLTAEKcMEIAFSIMS					
g272	MTAKEELFAWLRHMKNKGsDLFVtTHFPpAMKLDGKITRITDEPLTAEKcMEIAFSIMS					
	10	20	30	40	50	60
m272 . pep	70	80	90	100	110	120
	AKQAEFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRTITSKIPKFESLNLPPVVK					
g272	AKQAEFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRAITSKIPKFESLNLPPALK					
	70	80	90	100	110	120
m272 . pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIIITQR					
g272	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIIITQR					
	130	140	150	160	170	180
m272 . pep	190	200	210	220	230	240
	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLcMATLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLcMATLHANSTNQA					
	190	200	210	220	230	240
m272 . pep	250	260	270	280	290	300
	LDRIINFFPEERREQLLTDLsSLNLQAFISQRLVPRDGGKGRVAAVEVLNLSPLISELIHN					
g272	LDRIINFFPEERREQLLTDLsSLNLQAFISQRLVPRDGGKGRVAAVEVLNLSPLISELIHN					
	250	260	270	280	290	300
m272 . pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYEKGDISLQeALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYEKGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360


```

          370
m272.pep  QXSXSPDLXLLX
          || :||| |||
g272      QSSDPDLELLX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTTCG TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGTCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTTCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AACTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCATT
801 TATTTGCAA CGCTCGTTC GCGGAGACGG CGGCAAGGCG AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCCTTGCA GGATGCCTTG AAAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATTT
1101 GGAAGTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPPVLK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMMT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272.pep  MTAKEELFAWLRHMNKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
          ||||| :|||||
a272      MTAKEELFAWLRHMNKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
          10      20      30      40      50      60

          70      80      90      100     110     120
m272.pep  AKQAEFFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRTITSKIPKFESLNLPPVLK
          ||||| :|||||
a272      AKQAEFFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRITSKIPKFESLNLPPVLK
          70      80      90      100     110     120

          130     140     150     160     170     180
m272.pep  DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
          ||||| :|||||
a272      DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
          130     140     150     160     170     180

```

	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFFPEERREQLLDLSLNQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLLDLSLNQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
	370					
m272.pep	Q S X S P D L X L L X					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

g273.seq

```

1  atgagtccttc aggcgggtatt tatataccccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcacccg ttttctctgcc gtttcttgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcgcca gccgcgcccg acattggcat tgtgttcatt
251 gttgttcctt aacgggtataa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggcgc gtgccgctga aatcaaggcg
351 gtttgagaag tgtttccnac gcgcccgcgc tatgtgccga aatattattt
401 gtcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgccctg ctttttgctt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

g273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPFLV AFEIKDDAGK QRGSRARHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

m273.seq

```

1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCTCCG TTTCTCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGCAAG CAGCGCGCA GCGCGCCCG ACATTAGCAT TGTGTTTATT
251 GTTGTTCCTT AATGCTTAAA AACCCGCCTG TCCGTGCAAC CGTTTTAAGG
301 CGGCAAATTG CAAAATTGT TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG GTTTCCTGAC GCGCCGCCCT GTGTGCCGGA GTTATTTGTC
401 GCTCACCTGC AAAATCGCCA AGAACCGCCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTTGKTWTC AAGCAGTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

m273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFPVFLPLL V AFEIKDDAGK QRGSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGQSGKHADRCQDIGVFKAGTFFPVFLPLL					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGQSGKHTDRRQDIGVFEAGTFFTVFLPFLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQGRSRRHXHCVHCCSLMLKNPPVRATVLRQIAKFVCGRVPLKSGRFEG					
g273	AFEIKDDAGKQGRSRRHWHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSRREFK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSSRA-ALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVLPFVXQAVFSYAX					
g273	CFXRARPMCRNIIICRSPAKSPRTRFAEFPRCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

```

1  ATGAGTCTTC AGGCGGTATT TGTATACCCC CCAAGCCGTA CCGCACAAATA
51  CAACGAAAT CAGGAAAACG GCGGTAAAGC TCATAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCCGT CAGGATATAG GCGTATTCCA GACCGGAAC
151 CCATTACCG TTTTCCTGCC GCTTTTGTG GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT AATGTTTATT
251 GTTGTTCCTT AACGTTAAA AACCGCCCG TCCGTGCAAC CGTTTTTAAG
301 AGGCGGTAAA TCACAAAGTT TGTGGCGGA CGTGCTCTCT TACAATCAGG
351 GCGGTTTAA GGGCATGATG CACTGCCCGG TGTGCCGGAT ATTATTTGTC
401 GCTCACCTGC AAAATTGCCA AGAACGCGCT TTGCGGGATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTGCCTGCTT TTTGTTTTTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1  MSLQAVFVYP PSRTAQYNEN QENGGAHKQ GQSGKHADRR QDIGVFQGTG
51  PFTVFLPLFV AFEIKDDAGK QGRSRRH*H NVHCCSLTVK NPPVRATVFK
101 RR*ITKFVGG RALLQSGRFK GHDALPRVPD IICRSPAKLP RTRFAGFPHC
151 PLVSYGVCLL FVFQAVFSYA *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGQSGKHADRCQDIGVFKAGTFFPVFLPLL					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGGQSGKHADRRQDIGVFQGTGTPFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRRHXHCVHCCSLMLKNPPVRATVLRQIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRRHXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVLPFVXQAVFSYAX					
a273	GHDALPRV-PDIIICRSPAKLPRTTRFAGFPHCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGCG  CGATTTTGT  CGTCatCGCC  AgcgTCGCTA  TGTTTTTTGT
51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAGGATG
101 GCAAGCATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151 CATATCGGGG  TGCAGGTCCT  CATTTCTCCC  GATATGAATG  CGGCAAAAGT
201 GTTTGTTCGG  ggCgagtTTG  ACGGCAACA  GCCTTTGAAC  CTGCTGCTGA
251 TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301 GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTgt  tcaaAACCT
351 TCCGCCGGCC  AACCACTGGT  ATGTGCGCGT  GGAggacgCG  GCAGGCGTGT
401 GGCAGCGTCG  GAACAAATGG  ATTACCAGCC  AGGGCAATGC  GGTGCGATTG
451 ACCCCGATGG  ACAAACTTTT  CAATAATGCA  GGAAGCAAAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDDY  YKDGKHIDIQ  LHRDEEAVRR
51  HIGVQVLISP  DMNAAKVFVG  GEFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101 GSAQNGRAEY  EAVFKTLPPA  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151 TPMDKLFNNA  GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGCG  CGATTTTGT  CGTCATCGCC  AGCGTCGCTA  TGTTTTTTGT
51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAAGACG
101 GCAAACATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151 CATATCGGGG  TGCAGGTTCT  CATTTCCCCC  GATATGAATG  CGGCAAAAGT
201 GTTTGTTCGG  GGCAGGTTTG  ACGGCAACA  GCCTTTGAAC  CTGCTGCTGA
251 TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301 GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTGT  TCAAACCT
351 TTCGCCGACC  AACCACTGGT  ATGTGCGCGT  GGAGGACGCG  GCAGGCGTGT
401 GGCAGCGTCG  GAACAAATGG  ATTACCAGCC  AAGGCAATGC  GGTGCGATTG
451 ACCCCGATGG  ACAAGCTTTT  CAATAATACT  GAAAGCAAAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDDY  YKDGKHIDIQ  LHRDEEAVRR
51  HIGVQVLISP  DMNAAKVFVG  GEFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101 GSAQNGRAEY  EAVFKTLSPT  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151 TPMDKLFNNT  ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
m274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLPPA					
m274	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDA AGVWRVENKW ITSQNAVDLT PMDKLFNNAGSKX					
m274	NHWYVRVEDA AGVWRVENKW ITSQNAVDLT PMDKLFNNATESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC  CGATTTTGT  CGTCATCGCC  AGCGTCGCTA  TGTTTTTGT
51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAAGACG
101 GCAAGCATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151 CATATCGGGG  TGCAGGTTCT  CATTCCCCC  GATATGAATG  CGGCAAAAGT
201 GTTTGTCGGC  GGCAGTTTG  ACGGCAAACA  GCCTTTGAAC  CTGCTGCTGA
251 TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301 GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTGT  TCAAACCCCT
351 TTCGCCGACC  AACCCTGGT  ATGTGCGCGT  GGAGGACGCG  GCAGGCGTGT
401 GGC GCGTCGA  GAACAAATGG  ATTACCAGCC  AAGGCAATGC  GGTGATTTG
451 ACCCCGATGG  ACAAACCTTT  CAATAATACT  GAAAGCAAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDY  YKDGKHIDIQ  LHRDEEAVRR
51  HIGVQVLISP  DMNAAKVFVG  GFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101 GSAQNGRAEY  EAVFKTLSPT  NHWYVRVEDA  AGVWRVENKW  ITSQGNVDL
151 TPMDKLFNNT  ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIVASVAMFFVAQQHATDLVTDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIVASVAMFFVAQQHATDLVTDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDAAGVWRVENKWTISQGNVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWTISQGNVDLTPMDKLFNNTESKX					
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWTISQGNVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWTISQGNVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgattttgc  cgccatccat  gacgatgatg  cggtcggcgg  attcgacggt
51  ggtcaggcgg  tgggcgacga  tgatgccggt  gcggttttcc  atcaggcggt
101 cgagcgcttg  ttggacgagg  cggttcggtt  cggtgtccaa  tgcgctggtg
151 gcttcgtcca  ataataatat  cggcgcgtct  tcaaaatgg  cgcgggcgat
201 ggcgacgcgt  tgccgctgtc  cgccggataa  gttgctgccg  ttcgatccga
251 tgggctggtg  cagtcggagc  ggggatgcgt  cgatcaggct  ttgcagggtg
301 gcggcttgga  gggcggacag  gacttcggct  tcgcccgcgt  cgggacggct
351 gtatcggacg  ttttcaaaca  ggggtgtcgt  aaacagggaat  acgtcttggt
401 agacgagggc  gaattgggag  cgcaggcagc  cgagtttgat  gtcggcgatg
451 tcgataccgt  ctatgcagat  gttgccggca  gacggttcga  caaagcgggg
501 cagaagggtg  acgacgggtg  atttgccgct  gccggaacgt  ccgaccaggg
551 cgacgcgttc  gccttgtctg  atgtcgaggt  tgaagtgttc  gagggctttg
601 atgccgtctg  aacggtattc  gacatcgacg  ttgcggaagc  tgatgcgccc
651 ttcgacacgc  tgcggcgcca  gcgtgccttt  gtctgttctg  ggcggggtgt
701 cgagaaatgc  acatacgccg  tcggcggcga  ggaacatcgt  ctgcataggg
751 atgctgatgt  tggcaaggct  tttgatgggg  gcgtacattt  gcagcatcgc
801 gacgatgaat  gccataaatt  cgccgatggt  ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

m276.seq

1	ATGATTTTGC	CGTCGTCCAT	CACGATGATG	CGGTCGGCCC	CTTCGATGGT
51	GGTCAGCGCG	TGGGCCACGA	TGATGCCGGT	GCGTTTTCC	ATCAGGCGTT
101	CGAGCGCCTG	TTGGACGAGG	CGTTCCGGAT	CGTTGTCTAA	TGCGCTGGTG
151	GCTTCGTCCA	ATAATAATAT	CGGCGCGTCT	TTCAAATATG	CGCGGCGCAAT
201	GGCGACGCGT	TGCCGTGTCT	CGCCGGATAA	GTGTGTCGCG	TTTCGATCCGA
251	TGGGCTGGTG	CAGTCCGAGC	GGGGAGCTGT	CAATCAGGCT	TTGCAGGTTG
301	GCGGTTTGGA	GGGCGAACAG	GACTTCGGCT	TCGCCCCGCT	CGGGACGGCT
351	GTATCGGACG	TTTTCAAACA	GGGTGTCTGC	AAACAGGAAT	ACGTCTTGGG
401	AGACGAGGGC	GAATTGGGCG	CGCAGCCGAT	CGAGTTTGAT	GTCGGCGCATG
451	TCGATAACCT	CTATGCAGAT	GTTGCCGCGA	GACGGTTCGA	CAAAGCGGGG
501	CAGCAGGGTG	ACGACGGTGG	ATTTGCCGCT	GCGGGAACGT	CGACCAAGGG
551	CGACGCGTTC	GCCTTGCTCT	ATGTCGAGGT	TGAAGTTGTC	GAGGGCTTTG
601	ATGCCGTCCT	AACGGTATTC	GACATCGACG	TTGCGGAAGC	TGATGCGCCC
651	TTCGACACGC	TGCGGTGCGA	GCGTGCCCTT	GTCTGTTCG	GCGGGGTGT
701	CGAGAAATGC	ACATACACCG	TCGCGGGCGA	GGAACATCGT	CTGCATAGGG
751	ATGCTGATGT	TGGCAAGGCT	TTGGATGGGG	CGGTACATT	GCAGCATCGC
801	GACGATGAAT	GCCATAAATT	CGCCGATGGT	GGTGTAG	

m276 . pep

1	MILPSSITMM	RSAPSMVVRR	WATMMPVRFS	IRRSACWTR	RSDSLSNALV
51	ASSNNNIGAS	FKMARAMATR	CRCPPDKLLP	FDPMGWCSPS	GELSIRLCRL
101	AVVRANRTSA	SPASGRLYRT	FSNRVSSNRN	TSWETRANWA	RQSSLSMSAM
151	SIPSMQMLPA	DGSTRKGRSL	TTVDLPLPER	PTRATRSPLC	MSRLKLSRAL
201	MPSERYSTST	LRKLMRPSTR	CASVPLSCS	GGVSRNAHTP	SAARNIVCIG
251	MLMLRLLMG	AYICSIATMNN	AGINPMVV*		

Homology with a predicted ORF from *N.gonorrhoeae*

m276/q276

		10	20	30	40	50	60
m276.pep	MILPSSITM	RSAFMSVVR	WATMMPVRF	SIRSSACWTR	RSDSL	SNALVASSN	NNIGAS
	:	:					
g276	MILPPSMT	MRSDSTVVR	WATMMPVRF	SIRSSACWTR	RSDSL	SNALVASSN	NNIGAS
		10	20	30	40	50	60
		70	80	90	100	110	120
m276.pep	FKMARAMA	TRCRCPPD	KLLPFDP	MGWCSPSG	ELSIRLCRL	AVWRANR	TSTSASPAG
g276	FKMARAMA	TRCRCPPD	KLLPFDP	MGWCSPSG	DASIRLCRL	AARADRT	SASPAGRLY
		70	80	90	100	110	120
		130	140	150	160	170	180
m276.pep	FSNRVSSN	RNTSWETR	ANWARROSSL	MSAMSIPSMQ	MLPADGSTK	RGRSLTTVD	LPLPER
g276	FSNRVSSN	RNTSWETR	ANWARROSSL	MSAMSIPSMQ	MLPADGSTK	RGRRLTTVD	LPLPER
		130	140	150	160	170	180
		190	200	210	220	230	240
m276.pep	PTRATRSP	CLMSRLKL	SRALMPSE	RYSTSTLR	KLMPSTRCG	ASVPLSCSG	GVSRNAHTP
g276	PTRATRSP	CLMSRLKL	SRALMPSE	RYSTSTLR	KLMPSTRCG	ASVPLSCSG	GVSRNAHTP
		190	200	210	220	230	240

	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```
a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTGCATGGT
51  GGTCAAGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTGTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCG AACCGTATTC GACATCGACG TTGCCGAAGC TGATGCCGCC
651 TTCGACACGC TGCGGTGCGA GCGTGCCTTT GTCCTGTTCG GCGGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```
a276.pep
1  MILPSSITMM RSAPSMVVRW WATMMPVRF SIRRSSACW TRSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGSR LTTVDLPLPER PTRATRSPLC MSRLKPSRAL
201 MPSEYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRF SIRRSSACWTRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRWATMMPVRF SIRRSSACWTRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGEL SIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGEL SIRLCRLAARADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGSR LTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGSR LTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLMSRLKLSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPLMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1 ..atggtacacg tcgcccgtagc ttacggtatt gccgtccggc gtttttgccc
51 aaacgaggtc atagacgttt tccacgcctt gcaggtagcat cgccaagcgt
101 tcgatgccgt aggtaatctt gccgagtagc ggcgtgcaat cgataccgcc
151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201 cttcccagcc caaaccacac gcaccgaggg tgggggtttc ccagtctgtc
251 tcgacaaagc ggatgtcgtg gactttggga tcgatgcca attcgcgcag
301 ggagtcgaga tagaggtctt ggatattggc gggggcgggt ttgagggcga
351 cttggaattg gtaatatgtg tgcaggcggc tgggggttgc gccgtagcgg
401 ccgtcttttg ggcggcggct gggttggacg taggcggcaa accaaggctc
451 ggggccgagc gcgcgcagc aggtggcggg atgggatgtg ccggcaccga
501 cttccatgtc gaagggttg atgacggtgc agcctttgtc tgcccagaag
551 gtttcagtt tgaagatgat ttgttgaag gtaagcatgg cttattgttc
601 gataaaataa aggttttatt ttactgttc catagccgct tgaatagatt
651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1 ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
51 DLLEIGKLG YFHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101 GVEIEVLDI GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPRL
151 GAERAQAGG MGCAGTDFHV EGLDDGAFFV CPEGLQFEDD LLEGKHGLLF
201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1 ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51 TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AGTCGCATC GCTGTATTCG AAGTTGTAGG TGGATTGCTC
151 GACTTCGTTT TGGTGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201 GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT AAATGGGTT ACTTCCATGC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCC ACGCCCGAG GGTGGGGTTT
401 TCCAGTTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451 CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG CCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GGCCGTCTTT GGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651 TGCCGCGACC GACTTCCATG TCGAAGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTGTCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GCCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1 MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVGI AVFEVVGGLL
51 DFLVHVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101 VDAADLLEIG KLGYPHAVEP DFPAQTPRAE GGVFPVFDK ADVVDFGIDA
151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201 KPRLGAECAQ AGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30
MVHVAVAYGIAVRRFCPNEVIDVFHALQVH



```

m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAVGDGVAVERFCNPENVVDVFYTLQVH
           30          40          50          60          70          80

g277.pep  RQAFDAVGNFAEYGRAIDTADLLEIGKLGIFYHAVEPDFPAQTPRTEGGVFVPVFDKADV
           40          50          60          70          80          90
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGIFYHAVEPDFPAQTPRAEAGGVFPVVF
           90          100         110         120         130         140

g277.pep  DFGIDAQFAQGVEIEVLDDIGGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGK
           100         110         120         130         140         150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m277      DFGIDAQFAQRVEIEVLDDIGGSGLEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGK
           150         160         170         180         190         200

g277.pep  GAERAQAGGGMGCGAGTDFHVEGLDDGAAAFVCPEGLQFEDDLLLEGKHGLL
           160         170         180         190         200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m277      GAECAQAGGGMGCGAGTDFHVEGLDDGAAAFVCPECLQFEDDLLLEGKHGLX
           210         220         230         240         250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1137>:

a277.seq

1	ATGCCCGCT	TTGAGGACAA	GCTCGTAGGC	AGGCAGGGCG	AGGGCGGCGT
51	TTTCTTCGGC	AAGCAGGCGT	TTGGCTTGC	CTTCGTAGTC	GTTGAACTGG
101	CGCAGCAGCC	AATCGGCATC	GCTGTATTCG	AAGTTGTAGG	TGGATTGTTT
151	GACTTCGTTT	TGGTGGTACA	CGTCGCCGTA	AGTTACTGTA	TTACCGTCCA
201	GCGTTTTTGC	CCAAACGAGG	TCATAGACGT	TTTCCACGCC	TTGCAGGTAC
251	ATCGCCAAGC	GTTTCGATGCC	TAGGTGATT	TCGCCGAGTA	CGGGGGTGCA
301	GTCGATGCCG	CCGACTTGTT	GGAAATAGGT	GAACTGGGTT	ACTTCCATAC
351	CGTTGAGCCA	GACTTCCCAG	CCCAAACCCC	ACGCGCCGAG	GGTGGGGTTT
401	TCCCAGTCGT	CTTCGACAAA	GCGGATGTCG	TGCACTTTGG	GGTCGATGCC
451	CAATTCGCGC	AGGGAGTCGA	GATAGAGGTC	TTGGATATTG	GCGGGAGCGG
501	GCTTGAGGGC	GACTTGGAAT	TGGTAATAGT	GTTGCAGGCG	GTTGGGGTTG
551	TCGCCGTAGC	GACCGTCTTT	GGGGCGGCGG	CTGGGTTGGA	CGTAGGCGGC
601	AAACCAAGGC	TCGGGGCCGA	GTGCGCGCAG	ACAGGTGGCG	GGATGGGATG
651	TGCCGGCACC	GACTTCCATG	TCGAAGGGTT	GGATGACGGT	GCAGCCTTTG
701	TCGTCCACAG	ATGTTTGCAG	TTTGAAGATG	ATTTGTTGGA	AGGTAAGCAT
751	GGCTTATAGA				

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

a277.pap

1	MPRFEDKLVG	RQEGGVVFFG	KQAFGLRFVV	VELAQQPIGI	AVFEVVGGLF
51	<u>DFVLVHVAV</u>	SYCITVQRFC	PNEVIDVFHA	LQVHRQAFDA	VGDFAEYGGG
101	<u>VDAADLLEIG</u>	ELGYFHTVEP	DFPAQTPrAE	GGVFPVVFDD	ADVVFHFGVDA
151	QFAQGVIEIV	LDIGSGGLEG	<u>DLELVIVLQA</u>	<u>VGVVAVATVF</u>	GAAAGLDVGG
201	KPRLGAECAQ	TGGMGMCAGT	DFHVEGLDDG	AAFVCPECLQ	FEDDLLEGKH
251	GL*				

m277/a277 92.5% identity in 252 aa overlap

	10	20	30	40	50	60
m277.pep	MPRFEDKLVGRQEGGVFFGKQAFGLRFV	VVELAQQPVGIAVF	EVVGGLLDFVL	VVHVAV		
a277	MPRFEDKLVGRQEGGVFFGKQAFGLRFV	VVELAQQPIGIAVF	EVVGGLLDFVL	VVHVAV		
	10	20	30	40	50	60
m277.pep	GDGVAVERFCPNEVV	DVFYTLQVHRQAF	DAVGDFAEYGRAV	DAADLLEIGKLG	YFHAVEP	
a277	SYCITVQRFCPNEVID	VFHALQVHRQAF	DAVGDFAEYGGAV	DAADLLEIGELG	YFHTVEP	
	70	80	90	100	110	120
	130	140	150	160	170	180

632

```

m277.pep    DFPAQT PRAEGGVFPVVDKADVVDFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQA
a277        DFPAQT PRAEGGVFPVVDKADVVHFGVDAQFAQGVIEVLDIGGSGLEGDLELVIVLQA
              130      140      150      160      170      180

              190      200      210      220      230      240
m277.pep    VGVVAVAAVFGAAAGLDVGGKPRLGAECAQAGGGMGCAGTDFHVEGLDDGAAFVCPCLQ
a277        VGVVAVATVFGAAAGLDVGGKPRLGAECAQTGGGMGCAGTDFHVEGLDDGAAFVCPCLQ
              190      200      210      220      230      240

              250
m277.pep    FEDDLLEGKHGLX
a277        FEDDLLEGKHGLX
              250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

g278.seq (partial)

```

1   ttgcgtgcaa tcacgccccg tgcgattttt tgcacagggg cggtcacaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcg tccgaccggca cttctaaaat acggccggta
151 caggtaaccg tgcgccttc tttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gagtgcgct ccagggttc cccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgtcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

g278.pep (partial)

```

1   LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

m278.seq..

```

1   TTGCGCGCAA TCACGCCCGG TGCGATTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCCGCT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTCAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTGTCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTGACCACT ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

m278.pep

```

1   LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPQVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLHLAD
201 LFGVQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVV	LIGPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVTVSPSLIC				
m278	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYSNNTTAPTESRSR	FIAPKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEITVPRVLTSAFT		
m278	SYSNNTTAPTESRSR	FIAPKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEITVPRVLTSAFT		
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGLSCMK	TKLLIRHSRVQSTQFALYRQIQNLITHFNF				
m278	DRFSILALIKSLISAGLSCMK	TKLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF				
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHLQ	LADLFVGQRIGTVNDGRFDMVE*				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

```

1  TTGCGCGCAA TCACGCCCGG TCGGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTCAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTGGC TTTAATCAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTGTGCG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

```

1  LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLIC SCSNNTTAPT ESRSRFIAPK KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRLQAD
201 LFVGQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
a278	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLIC				
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYSNNTTAPTESRSR	FIAPKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEITVPRVLTSAFT		
a278	SCSNNTTAPTESRSR	FIAPKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEITVPRVLTSAFT		
	70	80	90	100	110	120

	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLHLQADLFVQGRIQTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLRLQADLFVQGRIQTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1   atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 cgggcagcgg cagggcgcgt ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcggcggc gttgcctgca atcacgactt gtccgggcga
201 gttgaagttg acggcttcga ccacttcgac ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcacat tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcgacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1   MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCGELKL TASTTSPCAD SAQICLTCS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1   ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTC GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACC GGCTTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCCTGCA ATCAGGATTT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1   ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

635

```

m279.pep  ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g279       ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRTSLTA
           70      80      90      100     110     120

           130     140     150
m279.pep  SAKFNAPAATSAVYSPRLCPATAAGVLPASKX
           ||| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g279       SAKSNASAATSAVYSPRLCPATAAGVLPPTSKX
           130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1149>:

```

a279.seq
1  ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNN GGGCTTCGGC
51  GAGTTTGTCT GCGGCGGGTT TCATGAGGCT GCAATGGGA GGTACNGACA
101 CNGGCAGCGG CAGGCGCGCT TTGGCGCCG CTTCTTTGGC GGCAAGCATA
151 GCGCGCTCGA CCGCGGCGGC ATTGCCTGCA ATCAGCACT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTTAC CTGTTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCGCT
451 TCCGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1150; ORF 279.a>:

```

a279.pep
1  MTXICGCLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAT SAVYSPXLCP ATAAGVLPAP
151 SE*

```

m279/a279 88.2% identity in 152 aa overlap

```

           10      20      30      40      50      60
m279.pep  ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMARPTAAALPA
           :| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a279       MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA
           10      20      30      40      50      60

           70      80      90      100     110     120
m279.pep  ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
           || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a279       ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA
           70      80      90      100     110     120

           130     140     150
m279.pep  SAKFNAPAATSAVYSPRLCPATAAGVLPASKX
           ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a279       SAKSNAPAATSAVYSPXLCPATAAGVLPASEX
           130     140     150

```

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1   atgaaacacc tcaaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttcgag ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgctag ccgtacaaag cctcgtcgga
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttgagg cttgaagccg
251 ccgacatcca acgcgccgctc aaacagagca aagatcccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagcaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgacccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccata acgtcgctga aaccctgata aaggccgcat ccgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaatgcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtccctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 ccaaaacaagt cgccgccatc atccggcaaa tcaaacgcga aggcacataa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcatcgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcggca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1   MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EGGHHHDHHD HDHHDHDEGH HHDHGEYDPH VWNDPVLMSD
151 YAQNVAETLI KADPEGKVYY QORLGNYYMQ LKKLHSDAQA AFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQGVSSSE EPSAKQVAAI IRQIKREGIK
251 AVFTENIKDT RMDVRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNVE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1   ATGAAACACC TCAAACTCAC CCTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTACGATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGCTCAA CGGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCTT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCCTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCTTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GCGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1   MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EGGHHHDHHD HDHEGHHHDH GEYDPHVWND PVLMSAYAQN
151 VAKALIKADP EGKVVYQQL GNYQMQLKKL HSDAQAAFNA VPAKRKVLV

```

```

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAAIIRQI KREGIKAVFT
251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN
301 AMKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng) from *N. gonorrhoeae*:

 m_{280}/g_{280}

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTFSFILGDVAQIGGERVSIQSLVGANQDTHAYHM					
	: : : : :					
g280	MKHLKLTLIAALLATAATAAPLPVVTFSFILGDVAQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLLNGLGLEAADVQRADVSKVSYTEATKGIQPLKAEEEGGHHHDDH-					
	: : :					
g280	TSGDIKKIRSAKLVLLNGLGLEAADIQRADVSKVSYAEATKGIQPLKAEEEGGHHHDDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQORLGNYQM					
	: : : :					
g280	HDHDHDHGEGHHDHGEYDPHVWNDPVLMSDYAQNVATLIKADPEGKVYYQORLGNYQM					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFYSYGKRYHIEFIAPQGVSSSEAEPSAKQVAAI					
	: : : :					
g280	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFYSYGNRYNISFIAPQGVSSSEAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	: : : : :					
g280	IRQIKREGIKAVFTENIKDTRMVDRIKETGVNVSGKLYSDALGNAPADTYIGMYRHVE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKOX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AACTGCCGCC	CCCCTGCCGG	TTGTAACCAT	CTTCAGCATT	TTAGGCGACG
101	TAGCCAAAAC	AATCGGCGGA	GAGCGCATAT	CCATACAAAG	TTTGGTCGGA
151	GGCAACCAAG	ATACGCACGC	CTATCATATG	ACACGCGCGC	ACATTAAAAA
201	AATCCGCAGT	GCAAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CCGACATCCA	ACGTGCGCTT	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAGAAGCGCG	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCATGACCA	CGAAGGACAC	CACCCACGAC
401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCTC	TATGTCGGCC
451	TATGCCCAAA	ACGTCGCCGA	AGCCCTGATA	AAGGCGCGAC	CCGAAGGCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCAAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCAACAAGC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCTCTA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
701	CCAAACAAGT	CGCCGCGATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	GCCGTATTTA	CCGAAAAATAT	CAAGACACCC	CGCATGGTTG	ACCGCATCGC

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE EGGHHHDHD HDHDHDEGH HDHGEYDPH VWNDPVLMAS
 151 YAQNVAEALI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAKR
 201 KVLTHGDAFS YMGKRYHIEF IAPQGSSEA EPSAKQVAI IRQIKREGIK
 251 AVFTENIKDT RMVDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

m280.pep	10	20	30	40	50	60
	MKHLKLTLIAALLTASATAAPLPVVTSFSILGDAKQIGGERVSIQSLVGANQDTHAYHM					
a280	MKHPKLTLIAALLTTAATAAPLPVVTSFSILGDAKQIGGERVSIQSLVGANQDTHAYHM					
	10	20	30	40	50	60
m280.pep	70	80	90	100	110	120
	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280	TSGDIKKIRS AKLVLLNGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAE EGGHHHDHD					
	70	80	90	100	110	120
m280.pep	130	140	150	160	170	
	HDH---EGHHHDHGEYDPHVWNPVLMASAYQNVAKALIKADPEGKVYYQQRLGNYQMQ					
a280	HDHDHDEGHHDHGEYDPHVWNPVLMASAYQNVAEALIKADPEGKVYYQQRLGNYQMQ					
	130	140	150	160	170	180
m280.pep	180	190	200	210	220	230
	LKKLHSDAQA AFNAVPAKRKVLTHGDAFSYMGKRYHIEF IAPQGSSEA EPSAKQVAI					
a280	LKKLHSDAQA AFNAVPAKRKVLTHGDAFSYMGKRYHIEF IAPQGSSEA EPSAKQVAI					
	180	190	200	210	220	230
m280.pep	240	250	260	270	280	290
	IRQIKREGIK AVFTENIKDTRMVDRIAKET GNVVSGKLYS DALGNAPADTYIGMYRHNK					
a280	IRQIKREGIK AVFTENIKDTRMVDRIAKET GNVVSGKLYS DALGNAPADTYIGMYRHNK					
	240	250	260	270	280	290
m280.pep	300					
	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:
 g281.seq

1 atgcactacg ccctcgcatc cgtcttctgc ctgtccctca gcgccgcacc
 51 cgctcggcgta ttctctgcta tgcgcgctat gagcctgata ggcgacgcac
 101 tgagccacgc cgtcctgccc ggtgcccgcg tcggctacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtggcgagg tttgccgcg gtatgctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccacctg aaagaagatg
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgactgca actcatcgcc gccgtctccg
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa
 451 agcatagacc cccttttctc caagtcgctc aacggcaaa gcgggccttg

501 gcacgtcatt ttcctcatcc tcgtcggtat gaacctcgta tccggcttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccggt tatgggcaag aaatatgggg acgctcattc tgttgccgt
651 cctcatcgcc ctttttttgcg gtttgatcgg gctgctcatt tctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgacg cgtcctttat
751 ctttttttccg tcatactcgg caaagaagcg ggcattctgc ccaaatggtt
801 caaaaaccac cgccaccaca ccacctga

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.ppe

```

1  MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGVGG FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL
101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE
151 SIDPLFLKSV NGKGKGLWHVI FLILVVMNLV SGFQALGILM SVGIMMLPAI
201 TARLWARNMG TLILLVSLVIA LFCGLIGLLI SYHIEIPSGF AAILCCSVLY
251 LFSVILGKEG GILPKWFKNH RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

1	ATGCGCTACG	CCCTCGCATC	CGTCTTCTGC	CTGTCCCTCA	GTGCCGCACC
51	CGTCGGCGTA	TTCCTCGTCA	TGCGCCGTAT	GAGCCTGATA	GGCGACGCAT
101	TGAGCCACGC	CGTCCCTGCC	GGTGC CGCCG	TCGGCTACAT	GTTTGCCGGC
151	TTGAGCCTGC	CCCGCATGGG	TTTGGGCGCG	GTAGCCGCAG	GCATGCTGAT
201	GGCACGTGCT	GCCGGACTCG	TCAGCCGCTT	CACCACCCTG	AAGAAGATAG
251	CCAACTTTGC	CGCCTTTTAT	CTCAGCAGCC	TCGCCATCGG	CGTAGTCTCT
301	GTCAGCAAAA	ACGGGAGCAG	CGTCGATTTG	CTCCACCTCC	TTTTCGGGTC
351	TGTACTTGCC	GTCGATATTCT	CTGCCCTGCA	GCTCATCGCC	GCCGTCTCCA
401	GCCTCACGCT	CATTACCCTT	GCCGTACAT	ACCGCCCGCT	CGTACTCGAA
451	AGCATCGACC	CCCTGTTTCT	CAAAATCCGTC	GGCGGGCAAG	GCGGGCTTTG
501	GCACGTCCTC	TTTCTCGTCC	TGGTCGTCAT	GAACCTCGTA	TCCGGCTTTT
551	AAGCCCTCGG	CACACTCATG	TCCGTCGGAC	TCATGATGCT	GCCAGCCATT
601	ACCGCCCGCC	TGTGGGCGAA	GCATATGGGC	GCACTCATCC	TCCTATCCGT
651	TCTGACAGCC	CTCGTGTGCG	GCTTGAGCGC	ACTGCTCATT	TCTTACCACA
701	TCTGAAAATTC	TTCCGGTCCC	GCCATCATCC	TCTGTTGCAG	CGCTCTTTAT
751	CTCTTTTTCG	TCATACTCGG	CAAAGAAGGC	GGCATTCTGA	CC...

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGVMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTLTIL AVIYRPLVLE
151 SIDPLFLKSV GKGGLLWHVL FLVLVVMNLV SGFQALGTLM SVGLMMLPAI
201 TARLWAKHMG ALILSVLTA LLCGLSGLLI SYHIEIPSGP AIIICCSVLY
251 LFSVILKKEG GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSL	AAPVGVLV	MRRMSL	IGDALSHAVL	PGAAGVGM	FAGLSLPAMGLGG
	:					
g281	MHYALASVFCLSL	AAPVGVLV	MRRMSL	IGDALSHAVL	PGAAGVGM	FAGLSLPAMGVGG
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGL	VSFRFTTL	KEDANFAAF	YLSSLAIGV	VLVSKNGSSV	DLLHLLFGSVLA
g281	FAAGMLMALLAGL	VSFRFTTL	KEDANFAAF	YLSSLAIGV	ILISKNGSSV	DLLHLLFGSVLA
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAV	SSSLTLIT	LAVIYRPL	VLESIDPL	FLKSVGGK	GGLWHVLFVLVVMNL



640

				:						:		:	:				
g281	VDIPALQLTAAVSGLTLTITLAVIYRPLVLESIDPLFLKSVNGKGGWLHVIFLILVVMNLV																
	130			140			150			160			170			180	
	190			200			210			220			230			240	
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP																
g281	SGFQALGTLMSVGINMMLPAITARLWARNMGTLLILLSVLIALFCGLIGLLISYHIEIPSGP																
	190			200			210			220			230			240	
	250			260													
m281.pep	AIILCCSVLYLFSVILGKEGGILT																
g281	AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX																
	250			260			270										

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1161>:

a281.seq

```
1 ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51 CGTCGGCGTA TTCCTCGTCA TGCGCCGATG GAGCCTGATA GGGCAGCGAT
101 TGAGCCACGC CGTCCTGCCG GTTGCCGCGC TCGGCTAGAT GTTTGCCGGC
151 TTAAGCCTGC CGCCCATGGG TTTGGGCGCG GTAGCCGAGT GATATGCTGAT
201 GGCAC TGCTT GCCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG TGTAGTCCTC
301 GTCAGCAAAA ACGGCAGCAG CGTCGATTTC CTCACCTCGG TTTTCCGGCT
351 CGTACTTGCC GCTGATATTC CTGCCCTGCA ACTCATCGCC CGCGTATCCA
401 CCCTCACACT GCTTACCCTT GCCGTCATCT ACCGCCCCTG CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCTGTC GGGGGCAAAG GCGGGCTTTG
501 GCACGCTCCT TTTCTCGTCT TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACATCTATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGGCGAA TCCATGGGCG GCACTATCC TCCATCCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCT TCTGTTGAGG CGTCCTTTAT
751 CTCTTTTTCG TCATACTCGG CAAAGAAGCC GGCATTCTGA CCAAATGGCT
801 CAAAAACCA CAGCCACCA CCACTGA
```

This corresponds to the amino acid sequence <SEQ ID 1162; ORF 281.a>:

```

a281.pep
1  MRYALASVFC  LSLSAAPVGV  FLVMRRMSLI  GDALSHAVLP  GAAVGYMFAG
51  LSLPAMGLGG  VAAGMLMLAL  AGLVRSFTTL  KEDANFAAFY  LSSLAIGVVV
101 VSKNGSSVDL  LHLLFGSVLA  VDIPALQLIA  AVSTLTLLTI  AVIYRPLVLE
151 SIDPLFLKSV  GGGKGLWHVL  FLVLVVMNLV  SGFOALGTM  SVGLMMLPAI
201 TARLWAKHMG  ALLILSVLTA  LCLGLSGLLI  SYHIEIPSPG  AII LCSSVLY
251 LFSVILGKEG  GILTKWLKNH  RHHTT*

```

m281/a281 99.2% identity in 264 aa overlap

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVG	FLVMRRMSLIGDALSHAV	LPGA	AVGYMFAGLSLPAM	GLGG	
a281	MRYALASVFCLSLSAAPVG	FLVMRRMSLIGDALSHAV	LPGA	AVGYMFAGLSLPAM	GLGG	
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRFT	TLKEDANFAAFYLSSLA	IGVVLVSKNGSSVDLL	LHLFLFGSVLA		
a281	VAAGMLMALLAGLVSRFT	TLKEDANFAAFYLSSLA	IGVVLVSKNGSSVDLL	LHLFLFGSVLA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSLT	LITLAVIYRPLVLES	IDPLFLKSVGGKGL	LWHVFLVLVVMNLV		
a281	VDIPALQLIAAVSSLT	LITLAVIYRPLVLES	IDPLFLKSVGGKGL	LWHVFLVLVVMNLV		
	130	140	150	160	170	180

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1 atgggattgg gtatggaaat cggcaagctg attgtggctc ttttggtgct
51 gatcaatccg tttagcgcgt tgtcgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgac ggcggtgcgc tattgaaggt
201 tttgggcac agcgtcgggt cgtttcaggt cggcggcggg attttggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcggtccgg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttgta
501 tgccatttta atcgttgccg ggaaggctcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccgcg aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1 MGLGMEIGKL IVALLVLINP FSALSPLYLDL TNGHSTKERR KVARTAATAVAV
51 FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYT
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLR GATGLTILNR IMGMMLAAYS
201 VEIIVSGLKT IFFQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1 ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51 GATTAATCCG TTTAGCGCGT TGTGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GGCAGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTGCTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTC GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTAAACCGC ATTATGGGTA TGATGCTGGC GGCAGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1 MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAATAVAV
51 FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLR GATGLTILNR IMGMMLAAYS
201 VEIIVSGLKT IFFQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRLI					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRLI					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282.seq

```

1   ATGGGATTGG  GCATGGAAT  CGGCAAGCTG  ATTGTGGCTT  TTTGGTGCT
51  GATTAATCCG  TTTAGCGCGT  TGTCGCTTTA  CCTTGACCTG  ACCAACGGGC
101 ACAGCACGAA  GGAGCGCAGG  AAGGTCGCGC  GGACGGCCGC  CGTTGCCGTG
151 TTTGCCGTGA  TTGCGGTATT  TGCGCTGATC  GGCGGTACGC  TGCTGAAGGT
201 TTTGGGCATC  AGCGTCGGTT  CGTTTCAGGT  CGGCGGCGGA  ATTTTGGTGT
251 TGCTGATTGC  CATTTCGATG  ATGAACGGCA  ACGACAATCC  CGCCAAGCAG
301 AATCTCGGCG  CGCAGCCGGA  AACGGGGCAG  GTGCGCCCCG  CCCGCAATGC
351 CGGAGCGATT  GCCGTCGTGC  CCATCGCCAT  ACCGATCACC  ATCGGCCCGG
401 GCGGTATTTC  GACCGTGATT  ATTTACGCTT  CGGCGGCTAA  AACATACGGC
451 GACATCGCGT  TGATTATCGC  GGCCGGTTTG  GTGGTCAGTG  CGATTGTGTTA
501 TGCCATTTTA  ATCGTTGCCG  GGAAGGTCAG  CCGCCTGCTG  GGTGCGACGG
551 GGCTGACGAT  TTAAACCGT  ATCATGGGTA  TGATGCTGGC  GGCGGTATCG
601 GTGGAGATTA  TTGTGTCGGG  ACTGAAAATG  ATATTCCTCG  AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282.pep

```

1   MGLGMEIGKL  IVAFLVLINP  FSALSPLYLDL  TNGHSTKERR  KVARTAAVAV
51  FAVIAVFALI  GGTLLKVLGI  SVGSFQVGGG  ILVLLIAISM  MNGNDNPAKQ
101 NLGAQPETGQ  VRPARNAGAI  AVVPIAIPIT  IGPGGISTVI  IYASAAKTYG
151 DIALIIAAGL  VVSAICYAIL  IVAGKVSRLI  GATGLTILNR  IMGMLAAVS
201 VEIIVSGLKM  IFPQLAG*

```

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOVRPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
a282	GATGLTILNRIMGMLAAVSVEIIVSGLKMIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1   atgaactttg ctttatccgt catcacattt accctcgcct ctttcctgcc
51  cgtcccgccg gccggaaccg ccgtctttac ttggaagac ggcggcgcca
101 acagctattc ggatgtgccg aaacagcttc atcccgacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaaccg gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaacaagga tgatttgatc cgtaaatata
401 ataacgccgt aaacaatac tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1   MNFALSVITF TLASFLPVPP AGTAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRLTQTKP AVKPKFAVDN NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKKEENCR SKMNLKAVGN SNAKNKDDLI RKYNNAVNKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1   ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GCGCGCGGCA
101 ACAGCTATTC GGATGTACCG AACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGCG CGGATTTCAG AAATGAACCT
351 GAAGGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1   MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTQTKP AVKPAQADAG KRTDGAAQEN NPDTEKNRQ LEEKKRIAE
101 TERQNKKEEN RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRLTQTKP					
	: : : : : :					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRLTQTKP					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
		:	:	:	:	:
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKRIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNVAVNKYCRX					
g283	GNSNAKNKDDLIRKYNNVAVNKYCRX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1173>:

a283.seq

1	ATGAAC	TTTG	CTTTAT	CCGT	CATTAT	GTTG	ACCTC	GCCT	CTTCCT	GCC
51	CGTCC	CGCCT	GCCGG	AGCCG	CGTCT	TTTAC	TTGGA	AGGAC	GGCGG	CGGCA
101	ACAGCT	ATTG	GGATG	TACCG	AAACAG	CTTC	ATCCC	GACCA	AAGCC	AAATC
151	TTAAAC	CTGC	GGACG	CGCCA	AACCA	AACCG	GCGGT	CAAA	CCGCC	CAAGC
201	CGACG	CAGGG	AAGCG	CACAG	ACGGC	GCGGC	ACAGG	AAAAC	AATCC	GACAC
251	CTGCC	GAGAA	AAACG	GCAG	CTTGA	GGAAG	AAAAG	AAAAG	AATTG	CCGAA
301	ACCGA	ACGGC	AGAAC	AAAGA	AGAAA	ACTGC	CGGAT	TTCAA	AAATG	AACCT
351	GAAAG	CGGTG	GGAAA	TTCAA	ATGCA	AAAAA	CAAGG	ATGAT	TTGAT	TGCGA
401	AATAC	AATAA	CGCCG	TAAAC	AAATA	CTGCC	GTTAA			

This corresponds to the amino acid sequence <SEQ ID 1174; ORF 283.a>:

a283.pep

1	MNFALS	VIML	TLASFL	PVPP	AGAAV	FTWKD	GGGNS	YSYSD	VPKQL	HPDQS	QILN	LRTRQ	TKP
51	LNLRTR	QTKP	AVKPAQ	ADAG	KRTDGA	AQEN	NPDTAE	KNRQ	LEEEK	KRIAE			
101	TERQN	KEENC	RISKMN	LKAV	GNSNA	KNKDD	LIRKY	NNVAV	NKYCR	*			

m283/a283 100.0% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVMILTLASFLPVPPAGAAVFTWKDGGGNSYSYSDVPKQLHPDQSQILNLRTRQTKP					
a283	MNFALSVMILTLASFLPVPPAGAAVFTWKDGGGNSYSYSDVPKQLHPDQSQILNLRTRQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
a283	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNVAVNKYCRX					
a283	GNSNAKNKDDLIRKYNNVAVNKYCRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1175>:

g284.seq.

1	atgccgt	ctctg	aaactcg	aaa	tcggttt	cag	acggcatt	gg	tttacgc	ggc
51	aggttgg	gggc	ttagcgg	tct	ttgtaac	ggc	attcgttt	tt	gcctgca	aaa
101	gagtcgc	ccgg	ctttgcg	ttt	gcctttg	aag	ccttcgc	ccg	ttttttg	aa
151	actgtct	tttc	ttaaagc	ctt	ctttctg	aa	accttcg	ccg	cgcgttt	gc
201	cgccga	aagcc	ttctttg	ccc	ggtttat	gat	cgccgcg	ccg	gccgcgg	gat
251	ttcctat	cg	cccagcg	ccc	tttgcct	ttc	ggcttg	ccgc	ctgcgga	tt
301	gcgtttg	ccg	gcggctc	ca	tgccctc	gat	ggtcagt	tcg	ggcagtt	gc
351	ggttaat	gta	tttttcg	att	ttgtgg	actt	tgacgt	tattc	gttcact	tcg
401	gcaaacg	taa	tcgcaat	acc	cgtgcgg	cct	gcgcgg	ccg	tgccccc	gat
451	gcggtgg	acg	tagtctt	ccg	cctgttt	cgg	caggtcg	tag	tttatgc	agt

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```

501 gggtaaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaatatttgc agcggccttt acgcaaatcc gtcagcgtgc ggttgcgcca
601 gccctgcggc atatcgccgt gcaggcagtt ggcggcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggtcatcg ctttggtgga cgtgaaaatc
701 acacattggt cgatgttggc atcgcgagg atgtggtcga gcaggcggtt
751 tttgtggcgc atatcgctgc agtacaacaa ctgctcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcctt ggtcagtttg
851 cgcgccagtt tgccgactgc gccgtcccaa gtggcggaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51 TVFLKAFFLE TFAARFAAEA FFARFMIAAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD GQFGQFAVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDVGNNG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHREFG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LLFDLALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
1 ATGCCGCTCG AAACGCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51 AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTTCGAA
151 ACCGTCTCTC TTAAAGCCTT CTTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTATTGAT CGCCGCGCCA ACCGCCGAT
251 TTACGATCGC CCCAGCGGCC TTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTTCGG GTCGGTCCA TGCTTCGAT GGTCAGTTCG GGCAGTTTTC
351 GGTAAATGTA TTTTCGATT TTGTGGACT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGCCCT GCGCGGCCGG TCGGCCCGAT
451 GCGGTGGACG TAGTCTTCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCCTT ACGCAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TGCGGCGAAA CCTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTCATGG CTTTGGTGA CGTGAAATC
701 ACGCATGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATT CAGGGTCTTT GGTCAGTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGGCGTTG CTTCCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTGGCC GCTTTCATC AGGTCCATCA GACGGCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCCGACG ATGCTGACGG TGCGGAACCA ACGCATATTT
1151 TTGGCATACG CCAGCGGCTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGGCCTTT GCCCGGTTT TCGCTGCGTT
1251 TGGTCAGTTT TTGCAAAGTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDVGNNG RYVDTACGNI GGNQNFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFEG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVNQ HFQTFKINFA ALHQVHQTAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284 . pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284 . pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAAGFPIAPAAFAFRLAACGFAFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284 . pep	FFDFVDFDFVHFVHGKRNTRAACAGAPDAVDVFRFRQVVVDVNGRNVDTACGNI					
g284	FFDFVDFDFVHFVHGKRNTRAACAGAPDAVDVFRFRQVVVDVNGRNVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284 . pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284 . pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFRFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLFFDFALAVHAFDFDNRFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284 . pep	LTVARRCFHDGFDVVDKAHIQHTVGTVQNVQHFQTFKINFAALHQVHQTARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284 . seq
1  ATGCCGCTCG AAACGCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTGTGAA
151 ACCGTCTCTC TTAAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTGC
201 CGCCGAAGCC TTCTTTGCTC GGTTCATGAT CGCCGCGCCA ACCGCCGGAT
251 TTACGATCGC CCCAGCCGCG TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGC GGTCGGTTCCA TGCTTCGAT GGTCAGTTTC GGCAGTTTTT
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCT GCGCGGCCGG TCGCCCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACGTC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT GCGCAAATCC ATCAGCGTGC GGTTCGCCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT GCGGCGGAAA CCTTTTTCGT
651 ACAATTCATC CGCGATGACT TCGGTCATGG CTTTGGTGGG CGTGAAAATC
701 ACGCATTGAT CGATGTCGCG ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTCTTCG ATTTTGCCTT
801 GGTCGTCCAC GCGTTCGACT TCGATGATTT CAGGGTCTTT GGTCACTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCT TCCGGCGTGG CTTTCGACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAG
1001 CGGGCGAAAT CGACTTTGCC GCTTTCATC AAGTCCATCA GACGGCCCCG
1051 CGTGCGGACA ATCAGATCGA CCGGTTTGCT CAGGGCGCGG GTTGGTAGC
1101 CGAACGATGC ACCACCGACG ATGCTGACGG TACGGAACCA ACGCATATTT
1151 TTGGCATAAC CAGCGCGGTT TTTCTCGACT TGAGCCGCCA ATTCGCGGGT
1201 CGGCGTCAAC ACCAACGCGC GCGGGCCTTT GCCCGGTTTT TCGTGCCTT
1251 TGGTCAGTCG CTGCAAAGTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284 . pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE

```


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```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNG HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

m284.pep	10	20	30	40	50	60
a284	10	20	30	40	50	60
m284.pep	70	80	90	100	110	120
a284	70	80	90	100	110	120
m284.pep	130	140	150	160	170	180
a284	130	140	150	160	170	180
m284.pep	190	200	210	220	230	240
a284	190	200	210	220	230	240
m284.pep	250	260	270	280	290	300
a284	250	260	270	280	290	300
m284.pep	310	320	330	340	350	360
a284	310	320	330	340	350	360
m284.pep	370	380	390	400	410	420
a284	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

```

151 tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gtttcgggct
201 gtaccaaate ccgtcctggt tcggcgtaaa catttcctcc caaaacctca
251 aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
301 gagggggcag accttaaaat cagccgcttc cgcttcgctt ggaaaccgtc
351 cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
401 tcgcatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa
451 ggccctgccg acagcataga cctgcccgcc gctgtctatc tcgaccgctt
501 cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaacctgtc
551 atctcgaacg cctcaacgcg gcataccgtt acgaccgtaa agggcaccgc
601 ctcgacctga agggccgccg cagcccggtg agcagttcgt cggggtcagc
651 ctcgctcgcc ttgaaaaaac cgtttgcctt cgataccgcc atttacacca
701 aaggcggtt cgaaggcgaa accatacaca gtacggcgcg gctgagcgcg
751 agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801 cctctcggga aaatccgtca tccaccggtt tgccgaatca ttggataaaa
851 cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901 gtgccttccc tgcccgatgc cgggtggaat ttcgacctga ccgccatccc
951 gtcgttttca gacggcatcg cgctggaagg ctcgctcgat ttgaaaaaca
1001 ccaaagcccg ctttgcgcac cgcaacggca tccccgtccg tcaggttttg
1051 ggcggctttg tcatccggca ggacggcacg gtgcataatc gcaatacgtc
1101 cgccgccctg ctcggaaggc gcgccatcag gctgtcgggc aaaatcgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatacaatc cgtcggcgcg
1201 gaagacgtgc tgcaaacgcg gttcaaaagg aggttgacg gcagcatcgg
1251 catcggcgcc acgaccgcct cgcccaaaat ctcttggaac ctcggcaccg
1301 gcacggcacg cagcgacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtggt cgacacgcgc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgctca
1451 agctggacat ccgttcccgc gcattcgacc cttcgcgcac cgatccgcaa
1501 tttcggcgag gcaatatcaa cggttcgatt catcttgccg gtgaactggc
1551 aaaagagaaa tttacgggca aaatgcgttt tttgccgggt acgttcaacg
1601 gcgtgccgat tgccggcagc gccgacattg tttacgagtc ccgccacctt
1651 ccgcgcgcgc ccgtcgattt gcggttgagg cggaaacatc tcaaaaacaga
1701 cggcggttcc ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
1751 ccgatttatc ccgttcgggt ttcggactcg cggggtcttt aaatgtacgc
1801 ggacaccttt ccggcgattt ggacggcgcc atccgaacct ttgaaaccga
1851 cctttccggc acggcgcgca acttacacat cggcaaaagc gcagacatcc
1901 gttcgcctca ttttaccctc aaaggctcac ccggcacaag ccgcccgatg
1951 cgcccgata tcaaggcgcg ccgcctttcc ctgtcgggcg gcgcggcggt
2001 tgtcgatacc gccggcctga cgctggaagg tacggcgcgcg cagcaccgca
2051 tccgcacaca ccgcgccatg acgctggacg gcaaaccgtt caaactcgat
2101 ttggacgctt caggcgccat caacagggaa cttaccgatg ggaaaggcag
2151 catcggcatc ctcgacatcg gcggcgcatc caacctcaag ctgcaaaaacc
2201 gtatgacgct cgaagccggg gcggaacacg tggcggaag tgccggcaaat
2251 tggcaggcaa tgggcggcag cctcaacctg caacactttt cttgggacag
2301 gaaaaccggc atatcggaac aaggcggcgc acgcggcctg cacatcgccg
2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgcta cgggcacaa gcgcggcggt acctcaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcatt ttccctgaaa acgcgcttcc aaaacgaccg catcggaatc
2551 ctgcttgacg gcggcgcgcg tttcgacggt attaacgccg atttggcatc
2601 cggcaacgcc ttcggcgcca atatggcaaa tacaccgctc ggcggcagga
2651 ttacagcctc ccttcccgcg ttggcgcatg tgaagccctt tctgcccgcc
2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcgcgcg
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggg agcagcaact
2801 acgggaaaat caacggcaat atcacgctcg ggcaaaagcc ctccttcgat
2851 accgcacctt tggcgggcag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttcctaccgg tcggacaaac cgtcaaaggc agcctgaatg
2951 ccgccgtaac cctcggcgcc agcatcgccg acccgcaact gggcggcagt
3001 atcaacggcg acaagctcta ttaccgcaac caaaaccaag gcatactctt
3051 ggacaacggc tcgctcggtt cgcatattgc aggcaggaaa tgggtaatcg
3101 acagcctgaa attccggcac gaagggacg cggaactctc cggcacgggtc
3151 agcatggaaa acagcgtgcc cgatgtcgat atcggcgcgg tgttcgacaa
3201 ataccgcata ctgtcccgcc ccaaccgccg cctgacgggt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
3301 aaaactgatc aggggctggt cggttcgcaa aaatcctcga tgccgtccgt
3351 cggcgacgat gtcgtcgtat tgggcgaagt caagaaagag gcggcgccat
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

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3451 ttctccggct acggcgcgga cgttaccata ggccgcaaac tgacctgac
3501 cgcgcaaccg ggccgaaatg tgcgtggggg gggcacggtc cgcgtcatca
3551 aagggcggtta caaagcatat gggcaggatt tagacattac caaaggcaca
3601 gtctcccttg tcggcccgct caacgacccc aacctgaaca tccgcgccga
3651 acgcccgcct tcccccgctg gtgcgggctg ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaanaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcggca gcagcggcga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgcagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcgggtg cccgtatcgg cagccgttcg tcggcgccgc agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

```

g285.pep
1  MTDTPPTDPT PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRLSHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDREFETG KISMGTDFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTFW SSSSGSASVG LKPPFALDTA IYTKGFEFE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGS LD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGTGARTDGL SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTGGGF GKKGDRNLNL ITAPDLRFGL FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLTG TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRSL LSGGAADVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSLNL QHFSWDRKTG ISAKGGARGL HIAELHNFVK PFPEHNLVLN
801 GDWDVAYGHN ARGYNISRQ SGDAVLPGGG ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVQGSRSFD
951 TAPLGGRNLN TVADAEAFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGG
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
1051 SMENSVPDVT IGAVFDDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GGKLTTLTAQP GGNVRGVGTV RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNAAL LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRLEGSDDK DSAGNGKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

```

m285.seq
1  ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACCGG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTCCTCG GCTGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAACCGTC
351 CGAACTGATG CGCCGACGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAGC CTTTGACAAA CAAACCGCTC
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCCGTGG AGCAGTTCGT CGGGGGCGGC
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC
901 GTGCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCa GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGCTCCG TCAGGTTTTA
1051 GGCGGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC
1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTGCGGC AAAATCGACA
1151 CCGAAAAAGA CATCTCGAT TTAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAT CTCTTGCAA CTGCGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTGACCC CTTGCGCGAT CGATCCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 CCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACACAGA
1701 CCGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC
1751 CCGATTTATC CCGTTTCGGT TTCGGAATCG CCGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA
1851 CTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA
1951 CGCGCCGACA TCAAAGGCAG CCGCTTTTCG CTGTGCGGCG GAGCGGCGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGCGGCAAG TGCGGCAAAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCAGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GGCGACTGGG ATGTGCGCTA CCGGCGCAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCGG ATTTGGGCAT
2601 CGCCAACGCC TTCGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
2651 TTACCGCCTC CTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
2701 GCGGCGCAA ACATTACCGG CAGCTGAAT GCCGCGCGC AAATCGGCGG
2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAATA CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCCGCAAC TTCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCGTAAC CCTCGGCGGC AGCATCGCGC ATCCGCACTT GGGCGGCAGC
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGTGCCTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CCGAACTCTC CGGTACGGTC
3151 GGTATGGAAG ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGACAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCGC CCGTACGGTT TCCGGCAACA
3251 CCCGCTGCG CTATTCGCGC CAAAAGGCA TATCCGTTAC CCGGATGATT
3301 AAAACGGATC AGGGGCTGTT CCGTTCGCAA AAATCCTCGA TGCCGTCCGT
3351 CGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGTCCCGCT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
3451 TTCGCCGCT ACAGCGCGGA CGTTACCATA GCGGCAAC TGACCCTGAC
3501 CGCCCAATCG GCGGAAGCG TACGGGGCGT GGGCAGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCCTTG TCGGCCGCT CAACGATCC AACCTCAACA TCCGCGCCGA
3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAATATTG GGCAGCCTCA
3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAGAGAC
3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA
3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAATCA
3851 ACGACCGCAT CCGGCTGGTG GATGATTTGG GCTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCGGAACAGG TGCTGACCGT
3951 CCGCAACCAA CTGACCGGCA AACTCTACAT CCGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAATGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCG CAGCCGTTTC TCGGCGGCG AGCTGACATA

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACGGCAA AGGAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
1 MTDAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWLAGE AGLRFLYQI PSWFGVNIS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPELMM RRLSHITEIS AGDIAIVTKP TPPKEERPPL
151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
301 VPSLPDAGLN FDLTAIPSF S DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTGGGF GKKGDRNLN ITAPDLRSRFG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAADVDT ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSNLN QHFSWDKKTG ISAKGGAHL HIAELHNFFK PPFENLVLN
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSEF
951 TAPLGGRLNL TVADAEVERN FLPVGGTVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPVSGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GKKLTTLTAQS GGSVRGVGT VIKGRYKAY QDLDITKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSKK DSAGNGKKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

m285.pep	10	20	30	40	50	60
	MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
g285	MTDTTPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
m285.pep	70	80	90	100	110	120
	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPELMM					
g285	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPELMM					
	70	80	90	100	110	120
m285.pep	130	140	150	160	170	180
	RRLSHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAYLDRLFETGKISMKGAFDK					
g285	RRLSHITDISAGDIAIVTKPTPPKEERPPQGLPDSIDLPAAYLDRLFETGKISMKGTFDK					
	130	140	150	160	170	180
m285.pep	190	200	210	220	230	240
	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
g285	QTVYLERLNAAARYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
m285.pep	250	260	270	280	290	300
	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

[illegible]

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g285	AAQNITGSLNASQAQIGGRVGSFSPVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLNL	910	920	930	940	950	960
m285.pep	TVADAEVFRNFLPVGQTVKGSLSNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG	970	980	990	1000	1010	1020
g285	TVADAEVFRNFLPVGQTVKGSLSNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG	970	980	990	1000	1010	1020
m285.pep	SLRSHIAGRKWWIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV	1030	1040	1050	1060	1070	1080
g285	SLRSHIAGRKWWIDSLKFRHEGTAELSGTVSMENSVDPVDIGAVFDKYRILSRPNRRLTV	1030	1040	1050	1060	1070	1080
m285.pep	SGNTRLRYSYPQKGISVTGMIKTDQGLFGSQKSSMPSVGDDVVVLGEVKKEAAAPLPVNMN	1090	1100	1110	1120	1130	1140
g285	SGNTRLRYSYPQKGISVTGMIKTDQGLFGSQKSSMPSVGDDVVVLGEVKKEAAASLPVNMN	1090	1100	1110	1120	1130	1140
m285.pep	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTIKGT	1150	1160	1170	1180	1190	1200
g285	LTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVRGVGTVRVIKGRYKAYGQDLDTIKGT	1150	1160	1170	1180	1190	1200
m285.pep	VSVFGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLIILNRA	1210	1220	1230	1240	1250	1260
g285	VSVFGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLIILNRA	1210	1220	1230	1240	1250	1260
m285.pep	GGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ	1270	1280	1290	1300	1310	1320
g285	GGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ	1270	1280	1290	1300	1310	1320
m285.pep	LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFGSDKK	1330	1340	1350	1360	1370	1380
g285	LTGKLYIGYEGISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFGSDKK	1330	1340	1350	1360	1370	1380
m285.pep	DSAGNGKGKX	1390					
g285	DSAGNGKGKX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

```

a285.seq
1  ATGACCAGATA  CCGCACCGAC  AGATACCGAT  CCGACCGAAA  ACGGCACGCG
51  CAAATGTGCC  TCTGAACACC  GCCCTACCCC  GCCGGCAAAA  AAACGCGCCC
101 CGCTGCTGAA  GCTGTCGGCG  GCACTGCTGT  CTGTTCTGAT  TTTGGCAGTA
151 TGTTTTCTCG  GCTGGCTCGC  CGGCACGGAA  CGGGGTTTGC  GCTTCGGGCT
201 GTACCAAATC  CCGTCTTGGT  TCGGCGTAAA  CATTTCTCTC  CAAAACCTCA
251 AAGGCACGCT  GCTCGACGGC  TTCGACGGCG  ACAACTGTCT  GATAGAAACC
301 GAGGGGGCAG  ACCTTAAAAA  CAGCCGCTTC  CGCTTCGCGT  GGAAACCGTC
351 CGAACTGATG  CGCCGACGCC  TGCACATTAC  CGAAATTTCC  CGCGGCAGAC
401 TCGCCATCGT  TACCAAACCG  ACTCCGCCTA  AAGAAGAACG  CGCGCCGCTC
451 AGCATTCCCC  ACAGCATAGA  CCTGCCTGCC  GCCGTCTATC  TCGACCGCTT
501 CGAGACGGGC  AAAATCAGCA  TGGGCAAAGC  CTTTGACAAA  CAAACCGTCT
551 ATCTCGAAGC  GCTGGATGCT  TCATCATGCT  ACGACCCGCA  AGGACACCGC
601 CTCGACCTGA  AGGCTGCCGA  CAGCCGCTGG  ACGAGTTTCG  CGGGGTGACG

```

651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
801 CCTCTCGGGA AAATCCGTCA TCCACCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCCTTC
901 GTGCCTTCCC TGCCCCGATG CGGGCTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTC AAGGCGCATG CGCTGGAAGG CTCGCTCGAT TTGAAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGTCCG TCAGGTTTTA
1051 GGCAGCTTTG TCATCCGGCA GGACGGCAG GTGCATATCG GCAATACGTC
1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTGCGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAATATAG GCATCAATC CGTCGGCGCG
1201 GAAGACGTAC TGCAAAACCG GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCCACAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTGACG CTTGCGCAT CGATCCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTGCGC GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGGTGCGCG CCGTCGATTT GCGGTGCGG CGGAACATTA TTAACACAGA
1701 CGGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCACAC
1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
1851 CCTTTCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCGATA
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTGCGGCG GAGCGGAGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGBA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGCAAG TGCGGCAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GCGGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTCGGGCGG ATTAACGCGG ATTTGGACAT
2601 CCGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
2651 TTACCGCCTC CCTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC
2701 GCCGCGCAA ACATTACCGG CAGCCTGAAT GCCCGCGCG AAATCGGCGG
2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGAAAAAT CAACGCGCAAC ATCACCCTCG GGCAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCCGCAAC TTCTTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCGGTAAC CCTCGGCGGC AGCATCGCGC ATCCGCACTT GGGCGGCAGC
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
3151 GGTATGGAAC ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTCCGACA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCGC CCTGACGGT TCCGGCAACA
3251 CCCGCCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CCGGATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTGCGAA AAATCCTCGA TGCCGTCCGT
3351 CCGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAGAG GCGGCGGCAC
3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC
3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCCTGAC
3501 CGCCCAATCG GCGGGAAGCG TCGGCGGCGT GGGCAGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA
3651 ACGCGCCTT TCCCGCTCG GTGCGGCGT GGAATATTG GGCAGCCTCA
3701 ACAGTCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAGAAAGC
3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA
3801 CAATGCCGCC CTGTCCGCG CCGCGGCGC GCTGCTTGCC GGGCAATCA
3851 ACGACCGCAT CCGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

3951 CGGCAAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
 4001 CCAGCGCGGA ACAGTCCGTC AACTGATTT ACCGGCTGAC CCGCGCCATA
 4051 CAGGCGGTG CCGTATCGG CAGCCGTTG TCGGGCGGCG AGCTGACATA
 4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
 4151 GAAACAGCAA AGGAAATATA

This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

a285.pep
 1 MTDAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTFW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRLELA IDGGNIRLSG KSVIHPPAES LDKTLEEVLV KGFNINPSAF
 301 VPSLPDAGLN FDLTAIPSFS DGIALEGLSD LENTKAGFAD RNGIPVRQVL
 351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQGSLLT AQGYLELFKD RLLKLDIRSR AFDPSTRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIKTGDDG GKKGDRNLN ITAPDLRFSG FGLAGSLNVR
 601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPTDSRPI
 651 RADIKGSRLS LSGGAEVVDL ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKGSGI LDIGGAFLNK LQNRMTLEAG AERVAASAA
 751 WQAMGGSLLN QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENHLVLN
 801 GDWDVAYGRN ARGYLNISRO SGDAVLPGGQ ALGLNAFLSK TRFQNDRIGI
 851 LLDGGAREFR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSD
 951 TAPLGGRLNL TVADAEVFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGS
 1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRITV SGNTRLRYSP QKGISVTGMI
 1101 KTDQGLFGSQ KSSMPVSGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR
 1151 FAGYGADVTI GGLTLTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTIKGT
 1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
 1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
 1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISSAEQSV KLIYRLTRAI
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNSKKG*

m285/a285 99.4% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
a285	MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	10	20	30	40	50	60
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRAWKPSSELM					
a285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRAWKPSSELM					
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRAWKPSSELM					
a285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRAWKPSSELM					
	70	80	90	100	110	120
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMKGAFDK					
a285	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMKGAFDK					
	130	140	150	160	170	180
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMKGAFDK					
a285	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMKGAFDK					
	130	140	150	160	170	180
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
a285	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK					
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK					
a285	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK					
	190	200	210	220	230	240
m285.pep	TIHSTARLSGSLKDVRLELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF					
a285	TIHSTARLSGSLKDVRLELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF					
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRLELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF					
a285	TIHSTARLSGSLKDVRLELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF					

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a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHFAESLDKTL EEVLVKGFNINPSAF
	250 260 270 280 290 300
	310 320 330 340 350 360
m285.pep	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
	: : : : :
a285	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
	370 380 390 400 410 420
m285.pep	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	: : : : :
a285	VHIGNTSVALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
	430 440 450 460 470 480
m285.pep	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKVLDTVNIAAGQGS LTAQGYLELFKD
	: : : : :
a285	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKVLDTVNIAAGQGS LTAQGYLELFKD
	430 440 450 460 470 480
	490 500 510 520 530 540
m285.pep	RLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	: : : : :
a285	RLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	490 500 510 520 530 540
	550 560 570 580 590 600
m285.pep	ADIVYESRHLPRAAVDLRLGRNIIKT DGGFGKKGDRNLNITAPDLSRFGLAGSLNVR
	: : : : :
a285	ADIVYESRHLPRAAVDLRLGRNIIKT DGGFGKKGDRNLNITAPDLSRFGLAGSLNVR
	550 560 570 580 590 600
	610 620 630 640 650 660
m285.pep	GHLSGDL DGGIRT FETDL SGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	: : : : :
a285	GHLSGDL DGGIRT FETDL SGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	610 620 630 640 650 660
	670 680 690 700 710 720
m285.pep	LSGGA VVD TADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSIGI
	: : : : :
a285	LSGGA EVVD TADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSIGI
	670 680 690 700 710 720
	730 740 750 760 770 780
m285.pep	LDIGGA FNKLQNRMTLEAGAERVAASAANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
	: : : : :
a285	LDIGGA FNKLQNRMTLEAGAERVAASAANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
	730 740 750 760 770 780
	790 800 810 820 830 840
m285.pep	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	: : : : :
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	790 800 810 820 830 840
	850 860 870 880 890 900
m285.pep	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
	: : : : :
a285	TRFQNDRIGILLDGGARFGRINADLDIGNAFGGNMANAPLGGRITASLPDLGTLKPFLPA
	850 860 870 880 890 900
	910 920 930 940 950 960
m285.pep	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYKINGNITVGQSRSFDTAPLGGRNLN
	: : : : :

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a285      AAQNITGSLNAAQIGGRVGSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
           910      920      930      940      950      960

           970      980      990      1000     1010     1020
m285.pep  TVADAEVFRNFLPVGQTVKGSLSNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
           |||||
a285      TVADAEVFRNFLPVGQTVKGSLSNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
           970      980      990      1000     1010     1020

           1030     1040     1050     1060     1070     1080
m285.pep  SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRIILSRPNRRLTV
           |||||
a285      SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRIILSRPNRRLTV
           1030     1040     1050     1060     1070     1080

           1090     1100     1110     1120     1130     1140
m285.pep  SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
           |||||
a285      SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
           1090     1100     1110     1120     1130     1140

           1150     1160     1170     1180     1190     1200
m285.pep  LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
           |||||
a285      LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
           1150     1160     1170     1180     1190     1200

           1210     1220     1230     1240     1250     1260
m285.pep  VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLIILNRA
           |||||
a285      VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLIILNRA
           1210     1220     1230     1240     1250     1260

           1270     1280     1290     1300     1310     1320
m285.pep  GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
           |||||
a285      GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
           1270     1280     1290     1300     1310     1320

           1330     1340     1350     1360     1370     1380
m285.pep  LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
           |||||
a285      LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
           1330     1340     1350     1360     1370     1380

           1390
m285.pep  DSAGNGKGKX
           |||||
a285      DSAGNSKGKX
           1390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1   CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 AACTGCTCG ACGGCTTCGA CGGCACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCCGCG CAGCCTGCAC ATCACCACA TCTCCGCCG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAGGCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAACAAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGACGATCGA CGCGGCAAT ATCCGCTCT
701 CGGGAATC CGTCATCCAC CCGTTTCCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGG TGAATTTGCA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA
901 GCGGGTTTGG CCGACCGCAA CGGCATCCCC GTCCGTGAGG TTTTGGGCGG
951 CTTTGTCTAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCTGTCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTGC GCGCGAAGA
1101 CGTGTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGACCCCG CAAACGAACA
1251 GCGGAAACTG GTGTTGACA CCGTCAACAT CTCCGCCGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATT CGACCTTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGCGat atCAACGGTT CGATTCTCT TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTCG CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCC GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 CGCCGCGCTG GATTTCGGGT TGGGGCGGAA CATCGTCAAA ACAGACGGCG
1601 GCTTCCGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGCG GATTTCGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CGGCGACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTCC
1801 CTCGATTTTA CCCTCAAAGG CTCACCCGGC ACAAGCGGCC CGATGCGCGC
1851 CGATATCAAG GCGGGCGGCC TTTCCCTGTC GGGCGGCGCG GCGGTTGTCG
1901 ATACCGCCGG CTTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC
1951 ACACACGCGC CATGACGCT GGACGGCAAA CCGTTCAAAC TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTTCTTGG GACAGGAAAA
2201 CCGGCATATC GGCAAAAGGC GCGCGACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGAAACAC AATCTGGTTT TAAACGCGCA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCGGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCTC TGAACACGCG CTTTCAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTTC GGCATCGGCA
2501 ACGCCTTCGG CCGCAATATG GCAAATACAC CGCTCGGCGG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTCTGCG CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CGCGCAAAAT CCGGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCGGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCATACCCG
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCCCTC GCGGCAGCAT CGCCGACCCG CACTTGGGCG GCAGTATCAA
2901 CGGCGACAAG CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGA
2951 ACGGCTCGCT GCGTTCGCAT ATTGCAGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCG GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTGAGCAT
3051 GGAAAACAGC GTGCCGATG TCGATATCGG GCGGTTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCAAC CCGCGCTGTA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCAGTA TGATTAACAA
3201 TGATCAGGGG CTGTTTCGGT CGCAAAATC CTCGATGCCG TCCGTGCGCG
3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCAGGCGG AAATGTGCGT GGGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTACAAAG CATACGGGCA GGATTTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTCCGG CCGCTCAACG ACCCAACCT GAACATCCCG GCCGAACGCC
3551 GCCTTTCCCG CGTCGGTGGC GCGGTGGAAT TATTGGGCGC CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GTGCCGCGAG CGGCAGCAGC GCGGCAATG
3701 CGGCCCTGTC CGCAGCCGCA GCGCGCTGCT TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCGCCGGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACCTGAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACCT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTTCGCCGT ATCGGCAGCC GTTCGTGCGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTCTTTC GGTTCGGACA AAAAAGACTC CGCAGGAAAC
4051 GGCAAGGGA AATAA

This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pep

```

1  LKLSAALLSV LILAVCF LGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGF DGDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAYYLD RFETGKISMG KTFDKQTVYL
151 ERLNAARYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKG FNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGTGT
401 ARTDGS LAIA SDPANEQRKL VFDTVNISAG EGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAG E LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLSG DLDGGI RTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGSPG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLNQRM
701 TLEAGAEHVA ASAANWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISROSGDAV LPGGQALGLN
801 AFSLKRTRFQ N DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAAQNI TGSLSNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRNLNLTVADA EAFRNFLPVG QTVKGS LNAA
951 VTLGGS IADP HLGGSINGDK LYRNRQTQGI ILDNGLSLRSH IAGRKKWIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAASL
1101 PVMNMLTDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIK
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKD KLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNP AEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GK GK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTGCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAG CGCTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCGCG CGACATCGCC
301 ATCGTATACCA AACCGACTCC GCCTAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCTTGA
501 CCTGAAGGCC GCCGACAGC CGTGGAGCAG TTCGTCGGGG GCGGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGAATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAATAAT CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGAC TGAATTCGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACCG CATCGCGCTG GAAGGTTTCG TCGATTGGA AAACACCAAA
901 GCCGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCGG
951 CTTTGTATC CGGCAAGGAC GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAAT TATAGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAG CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAATAAT GTGCTCGACA CCGTCAACAT CGCCGCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGCGGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAAGTCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGGTC GATTGCGGC TGGGGCGGAA CATTATTAAC ACAGACGGCG
1601 GCTTCGGCAA AAAAGCGCAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGT GATTGAGAC GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCC
1801 CTCGATTCCA CGCTCAAAGG TTCGCCGAC ACAAGCGGCC CGATACGCGC
1851 CGACATCAAA GGCAGCGGCC TTTGCTGTGC GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG GCGTGAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAATTTGGCA

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTC TCAAACCGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCCGCG GGCAGGCTTT GGGTTTGAAC
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2451 TGACGGCGGC GCGCGTTTCG GCGCGATTAA CGCCGATTGG GGCATCGCCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GGCAAAACATT ACCGGCAGCC TGAATGCCG CCGCAAAATC GCGGACGCGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCCCTC GCGGCAGCAT CGCCGATCCG CACTTGGGCG CAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTC GGCACGAAG GACGGCGGAA CTCTCCGTA CGGTCCGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CCGGTGTTC GACAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCTGA CGGTTTCCGG CAACACCGC
3151 CTGCGCTATT CGCCGAAAA AGGCATATCC GTTACCGGGA TGATTA AAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGG GAAGTCAAAA AAGAGGCGCG GGCACCGCTC
3301 CCCGTCATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTACGG GCGGTGGGCA CGGTCCGCGT CATCAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGG CCGCTCAACG ATCCCAACCT CAACATCCCG GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGG GCGGTGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTTGGGTC ATCCTCAACC GCGCCGCGAG CCGCAGCAGC GGCAGCAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCCGCGCA ACAGGTGCTG ACCGTCGGCA
3851 AACCACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGGCCCGT ATCGGCAGCC GTTCGTCGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 GGCAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

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1 LKLSAALLSV LILAVCF LGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGF DGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPE ERPLSLPDS IDLPAAYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTFWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKG FNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGS LAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHL SG DLDDGGIRTFE TDLGSAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVDTADLML DGTGVQHRIR
651 THAAMTL DKG PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAANWQAMG GSLNLQHFWS DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGS LNAAAI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVQG SRSFDTAPLG GRLNLTVADA EVFRNPLPVG QTVKGS LNAA
951 VTLGGS IADP HLGGSINGDK LYRNTQGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVMNLTLDL NDGIRFAGY ADVTIGGKLT LTAQSGGSVR GVGTVRVIK
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAG GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 GRGK*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

[illegible]

662

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	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGGRITASLPDLGALKPFLPAAAQINITGSLNAAQIGGRVGSPPSVNAAVNGSSNYG					
m285-1	ANAPLGGGRITASLPDLGALKPFLPAAAQINITGSLNAAQIGGRVGSPPSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVQSRSFDTAPLGGRLNLTVADAEAFRNFPLVPGQTVKGSLNAAVTLGGSIADP					
m285-1	KINGNITVQSRSFDTAPLGGRLNLTVADAEVFRNFPLVPGQTVKGSLNAAVTLGGSIADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWWIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWWIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVGIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVGIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGK GK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGK GKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

```

1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTT CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGCCA CGAAGCGGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAGGCC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATCGCGCG CAGCCTGCAC ATTACCGAAA TTTCGCGCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCGCGC CGCTCAGCCT
351 TCCCAGACAG ATAGACCTGC CTGCGCGCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTG CCGTACCGCC ATCCCGTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTTGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTGAGG TTTTAGGCAG
951 CTTTGTGATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAACCGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTACAG AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGCTG GATTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGC GATTGAGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGCGCGGGC GCGCAACCTG CACATCGGCA AGGCGGCGA CATCCGTTG
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGCGC
1851 CGCATCAAAA GGCAGCCGCC TTTGCTGTC GGGCGGAGCG GAGGTTGTG
1901 ATACCGCGCA CCGTATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCCTGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAATTTGGCA
2151 GGCATATGGG GGCAGCCTCA ACCTGCAACA CTTTCTTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAAACGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACACGCG CTTTCAAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGGCGG GCGGTTTCG GCGGATTAA CGCCGATTG GACATCGGCA
2501 ACGCCTTCGG CCGCAATATG GCAATGACG CGCTCGGCGG CAGGATTACC
2551 GCGTCCCTTC CCGACTTGGG CACATTGAAG CCCTTCTCG CCGCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CACATACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG CCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTGCGAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTGCGTAT
3051 GGAAAAACAG GACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTGCGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGCGCG AAGCGTGGCG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGAGC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCAAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAA TATTGGGCGG CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 TCCTTGGCTC ATCTCAACC GCGCCGGCAG TGGCAGCAGC GGCACAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGTC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGGCAAAAC GGCAGAACTCA ACCCCGCGCA ACAGGTGCTG ACCGTGCGCA
3851 AACCACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGCGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCTG CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

a285-1.pep

```

1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGDN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGTTASP KISWQLGIGT
401 ARTDGSIAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLGAARNL HIGKAADIRS
601 LDFTLKGSPP TSRRIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNEFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPPGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGMM ANAPLGGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSLNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGG SRSFDTAPLG GRLNLTVADA EVFRNFPVG QTVKGSLNAA
951 VTLGGSIADP HLGGSSINGDK LYRNRQTQGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDDVVVLG EVKKEAAAPL
1101 PVMNMTLDDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSRV GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLMIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAG GALLAQIIND
1251 RIGLVDDLGF TSKRSRQAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRDFRFS GSDKKDSAGN
1351 SKGK*

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a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	IDLPAAYLDLRFETGKISMKGAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG					
m285-1	IDLPAAYLDLRFETGKISMKGAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK					
m285-1	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	LTAAQGYLE	FKDRLLK	LDIRSR	AFDPSRID	PQLPAGNINGS	INLAGE
m285-1	VLDTVNIAAGQGS	LTAAQGYLE	FKDRLLK	LDIRSR	AFDPSRID	PQLPAGNINGS	INLAGE
	430	440	450	460	470	480	
a285-1.pep	490	500	510	520	530	540	
a285-1.pep	LAKEKFTGKMR	FLPGTFNGV	PIAGSADI	VYESRHL	PRAAVDL	RRLGRNII	KTDGGFGKKGD
m285-1	LAKEKFTGKMR	FLPGTFNGV	PIAGSADI	VYESRHL	PRAAVDL	RRLGRNII	KTDGGFGKKGD
	490	500	510	520	530	540	
a285-1.pep	550	560	570	580	590	600	
a285-1.pep	RLNLNITAPD	LSRFGFLA	GS LNVR	GHLSGD	LDGGIRT	FETDLSGA	ARNLHIGKAADIRS
m285-1	RLNLNITAPD	LSRFGFLA	GS LNVR	GHLSGD	LDGGIRT	FETDLSGA	ARNLHIGKAADIRS
	550	560	570	580	590	600	
a285-1.pep	610	620	630	640	650	660	
a285-1.pep	LDFTLKGS	PDTSRPI	RADIKGS	RLSLSGG	AEVVD	TADLMLD	GTGVQHRIRTHAAMTLDGK
m285-1	LDFTLKGS	PDTSRPI	RADIKGS	RLSLSGG	AEVVD	TADLMLD	GTGVQHRIRTHAAMTLDGK
	610	620	630	640	650	660	
a285-1.pep	670	680	690	700	710	720	
a285-1.pep	PFKFDLDAS	GGINREL	TRWKG	SIGILD	IGGAFNL	KLQNRMT	LEAGAERVAASAANWQAMG
m285-1	PFKFDLDAS	GGINREL	TRWKG	SIGILD	IGGAFNL	KLQNRMT	LEAGAERVAASAANWQAMG
	670	680	690	700	710	720	
a285-1.pep	730	740	750	760	770	780	
a285-1.pep	GSLNLQHFS	WDKKTGI	SAKGG	AHGLHIA	ELHNFF	KPPFEHNL	VLNGDWDVAYGRNARGYL
m285-1	GSLNLQHFS	WDKKTGI	SAKGG	AHGLHIA	ELHNFF	KPPFEHNL	VLNGDWDVAYGRNARGYL
	730	740	750	760	770	780	
a285-1.pep	790	800	810	820	830	840	
a285-1.pep	NISRQSGDA	VLPGGQ	ALGLNA	FSLKTR	FQNDRI	GILLDGG	ARFGRINADLDIGNAFGGNM
m285-1	NISRQSGDA	VLPGGQ	ALGLNA	FSLKTR	FQNDRI	GILLDGG	ARFGRINADLDIGNAFGGNM
	790	800	810	820	830	840	
a285-1.pep	850	860	870	880	890	900	
a285-1.pep	ANAPLGG	RITASL	PDGLTK	PFLPAA	AQNI	TGSLNAA	QIGGRVGS
m285-1	ANAPLGG	RITASL	PDGLTK	PFLPAA	AQNI	TGSLNAA	QIGGRVGS
	850	860	870	880	890	900	
a285-1.pep	910	920	930	940	950	960	
a285-1.pep	KINGNITV	GQSR	SFDTAP	LGGRLN	LTVADA	EVFRN	FLPVGQTVKGS
m285-1	KINGNITV	GQSR	SFDTAP	LGGRLN	LTVADA	EVFRN	FLPVGQTVKGS
	910	920	930	940	950	960	
a285-1.pep	970	980	990	1000	1010	1020	
a285-1.pep	HLGGSING	DKLYYRN	QTQGI	ILDNGS	LRSHI	AGRKW	VIDSLKFRHEGTAELSGTVGMENS
m285-1	HLGGSING	DKLYYRN	QTQGI	ILDNGS	LRSHI	AGRKW	VIDSLKFRHEGTAELSGTVGMENS
	970	980	990	1000	1010	1020	
a285-1.pep	1030	1040	1050	1060	1070	1080	
a285-1.pep	GPDVDIG	AVFDKY	RILSR	PNRRL	TVSGN	TLRYS	PQKGISVTGMIKT
m285-1	GPDVDIG	AVFDKY	RILSR	PNRRL	TVSGN	TLRYS	PQKGISVTGMIKT
	1030	1040	1050	1060	1070	1080	
a285-1.pep	1090	1100	1110	1120	1130	1140	
a285-1.pep	SVGDDVV	VLGEV	KKAAAP	LPVNM	NLTLD	LDNG	GIRFAGYGADVTIGGKLT
m285-1	SVGDDVV	VLGEV	KKAAAP	LPVNM	NLTLD	LDNG	GIRFAGYGADVTIGGKLT
	1090	1100	1110	1120	1130	1140	
a285-1.pep	1150	1160	1170	1180	1190	1200	
a285-1.pep	GVGTVR	VIKGRY	KAYQD	LDITK	GTVSF	VGPLND	PNLNIRAERRLSPVGAGVEILGSLNS
m285-1	GVGTVR	VIKGRY	KAYQD	LDITK	GTVSF	VGPLND	PNLNIRAERRLSPVGAGVEILGSLNS

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTAN	EPSEKDKLSWL	ILNRAGSGSSGDNAAL	SAAAGALLAGQ	INDRIGLVDD	DLGF
m285-1	PRITLTAN	EPSEKDKLSWL	ILNRAGSGSGDNAAL	SAAAGALLAGQ	INDRIGLVDD	DLGF
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQ	TGELNPAEQVLT	VGKQLTGKLYIGYEYS	ISSAEQSVKLI	YRLTRAIQAVAR	
m285-1	TSKRSRNAQ	TGELNPAEQVLT	VGKQLTGKLYIGYEYS	ISSAEQSVKLI	YRLTRAIQAVAR	
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYT	IRFDRFSGSDKKDS	AGNSKKGKX			
m285-1	IGSRSSGGELTYT	IRFDRFSGSDKKDS	AGNSKKGKX			
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

```

1 atgcagaaca cgggtacccat gatgatcaaa ccgaccgccc tgctcctgcc
51 ggctttatatt ttctttccgc acgcatacgc gcctgcccgc gacctttccg
101 aaaacaaggc ggcggttttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtca aattaaaacc caaattcccc gtccgcatcg acacgcagga
201 cagtgaatc aaagatatgg tcgaagaaca cctgcccgtc atcacgcagc
251 agcaggaaga ggttttgat aaggaacaga cgggattcct tgcccagaag
301 gcaccggaca acgttaaaac aatgctccgc agcaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacgggt cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctgaaaaa
501 ctggcagcag ccggtaggca gcgatttcga tcaggacagt tgggaaaaca
551 gcaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta cccgcttgcc
601 aagctcgga acaccgggc ggccgtcaac cccgataccg ccaccgcga
651 tttgaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcaccgg cacacagcgt taccgccaac aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcatatttc cggcgcgctc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaa tcagcgtaac
901 cgaggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcggtcgt ctgggatatg gacaatacgc aaaccacgct
1051 tgccgcggc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaaacgcgc
1151 ttctccggcg gcatctggtg tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggcg gaatttctcg cagaaggccg gaaaatcccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaacgc
1301 cagctgctca acaacgtgct gcaccccgaa aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaattc
1401 gcacctctgc ccgcgcaggt tatttcttca cgcccgaaaa caaaaactc
1451 ggcacgttca tcatacgcgg acaagcgggt tacaccgttg cacgcgacaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcggcggc gcgtcttccg
1551 tgcgcggtta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

```

1 MQNTGTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAIVT HITPGPRTKI ANVGVAIGLD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201 KLGNTRAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQTVSGLA
251 RFQPGTPYDL DLLLDFQQAL EQNGHYS GAS VQADFRLPR GPRPRQSQRN
301 RGQTPQTRNR HPPRFGIRFG RQNRLLRLQP LQQLYRLGR LGYGQIRNHA
351 CRRHQPAQQL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRCQ
401 AGGGISRRRP ENPRLGCRFG QPRHDAADRL LETPAAQORA APRKRPLPRR

```

451 QNRDDFGHIP VLHRANPHLC PRRFLHARK QKTRHVHHTR TSGLHRCTRQ
501 CRCPLGADVP QRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

```
m286.seq
1  ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51  GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGGTTC GCATTGTCA AAAACAAAAG CCCCACACCC
151 GAATCAGTCA AATTAACC CAAATCCCC GTCCTCATCG ACACGCAGGA
201 CAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTCAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAATA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA
551 GCAAACTTTC CGTCCTCGGC GCGGTAAACG GCAAAGCCTA CCGCTTGCC
601 AAGCTCGGCA ATACGCAGGC GGCCGTCAAC CCCGATACCG CCACGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GGCGACTTTG
701 AAATCACCGG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGCG
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAAACT CGAAACCGGC ATCCGCCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAAATACGA AACCACGCTT
1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCCGCT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGGCGG AATTTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGCTGT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCTCT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCGAAA ACGGCCATTA CCTCGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGT ACACCGTTGC CCGCGACAAT
1501 GCCGACGTTT CTTAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGCGCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTT CACGATATGG GCGATGCCGC
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTCGGGA CTGGGCGTGC
1751 GCTGGTTTCA CCCGCTTGGC CCGTTTCTCT TCGACATCGC CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

```
m286.pep
1  MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLEAE
101 APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAI LGD
151 ILSDGNLA EY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLLDFQQAL EQNGHYS GAS VQADFDR LQG DRVVPKVS VT
301 EVKRHKLETG IRLDSEYGLG GKIA YDYYNL FNKG YIGSVV WDMDKYETTL
351 AAGISQPRNY RGN YWTSNVS YNRSTQNL E KRAFSGGVWY VRDRAGIDAR
401 LGAEFLA EGR KIPGSAVDLG NSHATMLTAS WKRL LNNVL HPENGHYLDG
451 KIGTTLGTFL SSTALIR TSA RAGYFFTPEN KKLGTFIIRG QAGYT VARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTL SGAVF HMDGDAANF KRMKLKHGSG LGVRWFSP LA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*
```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

668

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKNKS	PDTESVKLKPKFP				
g286	MQNTGTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKSKSPD	TESVKLKPKFP				
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLR	SKGYFSSKVS				
g286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLR	SKGYFSSKVS				
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEEYRNALENWQ	PVGSDFDQDS				
g286	LTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEEYRNALENWQ	PVGSDFDQDS				
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVVD	SGRPIAFGDFEITGTQR				
g286	WENSKTSVLGAVTRKGYPLAKLGNTAAVNPDATADLNVVVD	SGRPIAFGDFEITGTQR				
	190	200	210	220	230	240
	250	260	270	280	290	299
m286.pep	YPEQIVSGLARFQPGMPYDLDLLDFQQALEQNGHYS	GASVQADFRL-QGDRVPVKVSV				
g286	YPEQTVSGLARFQPGTPYDLDLLDFQQALEQNGHYS	GASVQADFRLPRGPRRQSQRN				
	250	260	270	280	290	300
	300	310	320	330	340	350
m286.pep	TEVKRHKLETGIRLDSEYGLGGKIADYDYNLFNKGYIGSVVWMDKYETTLAAGISQPRN					
g286	RGQTPQTRNRHPPRFGIRFGRQNRLLQLQRLYRLGRLGYGQIRNHACRRHQPA	QAL				
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1197>:

a286.seq

1	ATGCACGACA	CCCGTACCAT	GATGATTAAA	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTTCCG
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTTCA	AAAACAAAAG	CCCCGACACC
151	GAATCAGTTA	AATTAATAAC	CAAATCCCC	GTCCGCATCG	ACACGCAGGA
201	TAGTGAAATC	AAAGATATGG	TCAAGAACA	CCTGCCGCTC	ATCACGCAGC
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA
301	GCACCGGACA	ACGTAAAAAC	AATGCTCCGC	AGCAAAGGCT	ATTTACAGCAG
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGAGC	TTATACGGTA	CACATCACAC
401	CGGGCCCGCG	CACCAAAATC	GCCAACGTCG	GCGTCGCCAT	CCTCGGCGAC
451	ATCCTTTTCAG	ACGGCAACCT	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA
501	CTGGCAGCAG	CCGGTAGGCA	GTGATTTCGA	TCAGGACAGT	TGGGAAAAACA
551	GCAAACTTC	CGTCTCGGC	GCGGTAACGC	GCAAAGCCTA	CCCGCTTGCC
601	AAGCTCGGCA	ACACCGGGC	GGCCGTCAAC	CCCGATACCG	CCACCGCCGA
651	TTTGAACGTC	GTCGTGGACA	GCGGCCGCC	CATCGCCTTC	GGCGACTTTG
701	AAATTACCGG	CACGCAGCGT	TACCCGAAC	AAATCGTCTC	CGGCTTGGCG
751	CGCTTCCAAC	CGGGCACGCC	CTACGACCTC	GACCTGCTGC	TCGACTTCCA
801	ACAGGCGCTC	GAACAAAACG	GGCATTATTC	CGGCGCGTCC	GTACAAGCCG
851	ACTTCGACCG	CCTCCAAGGC	GACCGCGTCC	CCGTCAAAGT	CAGCGTAACC
901	GAGGTCAAAC	GCCACAAGCT	CGAAACCGGC	ATCCGCCTCG	ATTCGGAATA
951	CGGTTTGGGC	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTCAACAAAG
1001	GCTATATCGG	TTCGGTCGTC	TGGGATATGG	ACAAATACGA	AACCACGCTT
1051	GCCGCCGGCA	TCAGCCAGCC	GCGCAACTAT	CGGGGCAACT	ACTGGACAAG
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCCT
1151	TCTCCGGCGG	CATCTGGTAT	GTGCGCGACC	GCGCGGGCAT	CGATGCCAGG
1201	CTGGGGGCGG	AGTTTCTCGC	AGAAGGCCGG	AAAATCCCCG	GCTCGGATAT
1251	CGATTTGGGC	AACAGCCACG	CCACGATGCT	GACCGCCTCT	TGGAAACGCC
1301	AGCTGCTCAA	CAACGTGCTG	CATCCCGAAA	ACGGCCATTA	CCTCGACGGC

```

1351 AAAATCGGTA CGACTTTGGG CGCATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTACGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGACGCCCG
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTTCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGF LAEE
101 APDNVKTMLR SKGYFSSKVS LTKDGAYTV HITPGPRTKI ANVGVA ILGD
151 ILS DGNLA EY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLG NTRAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQA L EQNGHYS GAS VQADFDRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKG YIGSVV WMDMKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNLE KRAFSGGIWY VRDRAGIDAR
401 LGA EFLA EGR KIPGSDIDL G NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGAFL SSTALIRTS A RAGYFFTPEN KKLGTFIIRG QAGYT VARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRL SGAVF HDMGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

```

m286/a286 98.7% identity in 615 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP					
a286	MHDTRTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGF LAEEAPDNVKTMLRSKGYFSSKVS					
a286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGF LAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKD GAYTVHITPGPRTKIANVGVA ILGDILSDGNLA EY YRNALENWQQPVGSDFDQDS					
a286	LTEKD GAYTVHITPGPRTKIANVGVA ILGDILSDGNLA EY YRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVDSGRPIAFGDFEITGTQR					
a286	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVDSGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m286.pep	YPEQIVSGLARFQPGMPYDL DLLLDFQQA L EQNGHYS GAS VQADFDRLQGDRVPVKVSVT					
a286	YPEQIVSGLARFQPGTPYDL DLLLDFQQA L EQNGHYS GAS VQADFDRLQGDRVPVKVSVT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m286.pep	EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKG YIGSVVWMDMKYETTLAAGISQPRNY					
a286	EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKG YIGSVVWMDMKYETTLAAGISQPRNY					
	310	320	330	340	350	360
	370	380	390	400	410	420

670

m286.pep	RGNYWTSNVSYNRSTTQNLKRAFSGGVWYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLKRAFSGGIWIYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRQLNNVLHPENGHYLDGKIGITTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRQLNNVLHPENGHYLDGKIGITTLGAFLLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSDIAYGH
a286	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTFRFX
a286	SDKKIRWHISLGTFRFX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

```

1 atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcggtggcg gatcgccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggccgcccc gttgttgctg aaaatgccgg ggaaggggtg
151 ctgccgaaaag aaaagaaaaga tgaggaggca gcggcggtg cgccgcaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcgccag
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgcccgcca
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 ccccgcgctc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 gttgaccac tgtaaaaggc attctgttaa tggtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaaagcat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttccggcc
751 gagattccgc tgattcccgat caatcaggcc gatacgtgta ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcgatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttgg
951 cacggccgtg tacaacggcg aagtgtgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaaa cggctttaag gggacttggg
1151 cggaataatg cggcggggat gtttccggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

```

1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV
51 LPKEKKDEEA AGGAPQADTQ DATAGEGSD MAVSAENTG NGGAATTNPF
101 KNEDAGAQND MPQNAAESAN QTGNQPAGS SDSAPASNP PANGGSDFGF

```


151	TNVGNSVVVID	GPSQNTLTTH	CKGDSCNGDN	LLDEEAPSKS	EFEKLSDEEK
201	IKRYKKDEQR	ENFVGLVADR	VKKDGTNKYI	IFYTDKPPTR	SARSRRSLPA
251	EIPLIPVNQ	DTLIVDGEAV	LDTHSGNIF	APEGNYRYLT	YGAELKPGGS
301	YALRVQGEPA	KGEMLVGTAV	YNGEVLHFHM	ENGRPPYPSGG	RFAAKVDFGS
351	KSVDDGIIDSG	DDLHMLTQKF	KAADIGNGFK	GTWTENGGGD	VSGRFYGPAG
401	EEVAGKYSYR	PTDAEKGKGF	VFAGKKDRD*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```
m287.seq
1    ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTGT  CCCTTTTCAGC
51   CTGCGGGGGC  GGCCTGTGGC  GATCGCCCCG  TGTCAAGTGC  GCGGCAGACG
101  TGTCAAAAAC  TGCCGCCCCC  GTTGTTTCTG  AAAAAAGAGC  AGAGAGCAAAG
151  GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201  AGGCAGTCAA  GATATGGCGG  CGGTTCGGA  AGAAAATACA  GGCAATGGCG
251  GTGCGGTAAC  AGCGGATAAT  CCCAAAAATG  AAGACGAGGT  GGCACAAAAAT
301  GATATGCCGC  AAAATGCCCG  CGGTACAGAT  AGTTCGACAC  CGAATCACAC
351  CCGGGATCCG  AATATGCTTG  CCGGAAATAT  GGGAAATCAA  GCAACGGATG
401  CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451  GACGGAATGC  AGGGGGACGA  TCCGTCGGCA  GGCGGGCAAA  ATGCCGCGAA
501  TACGGCTGCC  CAAGGTGCAA  ATCAAGCCGG  AAACATCAA  AGCCGCCGGT
551  CTTCAGATCC  CATCCCGCG  TCAAACCCCTG  CACCTGCGAA  TGGCGGTAGC
601  AATTTTGGA  GGGTTGATTT  GGCTAATGGC  GTTTTGATTG  ACGGGCCGTC
651  GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGGAATA
701  ATTTCTTGG  TGAAGAAGTA  CAGCTAAAT  CAGAATTTGA  AAAATTTAAGT
751  GATGCAGACA  AAAAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAAAT
801  TGTCGGTTTG  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851  TTATCTTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901  GCACGGTCGA  GGCGETCGT  TCCGCCCGAG  ATGCCGCTGA  TTCCCGTCAA
951  TCAGGCGGAT  ACGCTGATTG  TCGATGGGGA  AGCGGTGACG  CTGACGGGGC
1001 ATTCCGGCAA  TATCTTCGCG  CCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051 GGGGCGGAAA  AATTGCCCGG  CGGATCGTAT  GCCCTTCGTG  TTCAAGGCGA
1101 ACCGGCAAAA  GGCGAAATGC  TTGCGGGCGC  GGCGGTGTAC  AACGGCGAAG
1151 TACTGCATT  CCATCGGAA  AACGGCCGTC  CGTACCCGAC  CAGGGGCGAG
1201 TTTGCCGAA  AATCGATT  CGGCAGCAA  TCTGTGGACG  GCATTATCGA
1251 CAGCGGCGAT  GATTTCATA  TGGGTACGCA  TAAATTCAAA  GCGGCATCG
1301 ATGGAACGG  CTTTAAGGG  ACTTGGACGG  AAAATGGCAG  CGGGGATGTT
1351 TCCGGAAAGT  TTTACGGCCC  GGCGGCGCAG  GAAGTGGCGG  GAAAATACAG
1401 CTATCGCCG  ACAGATCGG  AAAAGGGCGG  ATTCGGCGTG  TTTGCCGGCA
1451 AAAAACAGCA  GGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```
m287.pep
  1  MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51  EDAPQAGSQG QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGDT SSTPNHPTDP NMLAGNMENQ ATDAGESSQP ANQPDFMANAA
151 DGGQDDPSA  GGNAGNTAA  GGGQAAGNNQ  AAGSSDPIPA  SNFPADNGGS
201 NFGRVDLANG VLIDGPSQNI  TLTHCKGDSC  SGNNFLDEEV  QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL  VADSVQMKGI  NQYIIFYKPK  PTSFARFRRS
301 ARSRRLPAE  MPLIPVNQAD  TLIVDGEAVS  LTGHSGNIFA  PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK  GEMLAGAAYV  NGEVLHFHTE  NGRPYPTRGR
401 FAAKVDFGSK SDVGIIISGD  DLHMTQKFEK  AAIDNGNGFKG  TWTENGSGDV
451 SGKFYGPAGE  EVAGKYSYRP  TDAEKGKGFV  FAGKKEOD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

      10      20      30      40      49
m287.pép MFKRSVIAMACIFALSACGGGGGSPDVKSadTLskPaAPVvSE-----KETEA
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      MFKRSVIAMACIFPLSACGGGGGSPDVKSadTPskPaAPVvAENAGEGVLpKEKKDEEA
      10      20      30      40      50      60

```

672

	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQGQGPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMDMPQNAAGT						
	: :: :						
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQNMDMPQNA--						
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDFNMLAGNMENQATDAGESSQPANQPDMANAADMGGDDPSAGGQNAGNTA						
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQINITLTHCKGDS						
	:: : : : : :						
g287	-ESANQTGNNQPAGSSDSAPASNPAPANGGSDFGRITNVGNSVVIDGPSQINITLTHCKGDS						
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP						
	: : : : : : : : : : :						
g287	CNGDNLLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD						
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFARFRRSARRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNRYRLT						
	: :						
g287	KPPT-----RSARRSLPAEIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNRYRLT						
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTGRFRAAKVDFGS						
	: : :						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMEGRPYPSGGRFRAAKVDFGS						
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSFGKFGPAGEEVAGKYSYR						
	: : :						
g287	KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSGRFGYPAGEEVAGKYSYR						
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKGFGVFGAKKEQDX						
	:						
g287	PTDAEKGFGVFGAKKDRDX						
	420	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1203>:

a287.seq

1	ATGTTTAAAC	GCAGTGTGAT	TGCAATGGCT	TGTATTGTTG	CCCTTTCAGC
51	CTGTGGGGGC	GGCGGTGGCG	GATCGCCCGA	TGTTAAGTCG	GCGGACACGC
101	TGTCAAAACC	TGCCGCCCTT	GTTGTTACTG	AAGATGTCGG	GGAAGAGGTG
151	CTGCCGAAAG	AAAAGAAAGA	TGAGGAGGCG	GTGAGTGGTG	CGCCGCAAGC
201	CGATACGCAG	GACGCAACCG	CCGAAAAGG	CGGTCAAGAT	ATGGCGCAG
251	TTTCGCGAGA	AAATACAGGC	AATGGCGGTG	CGGCAACAAC	GGATAATCCC
301	GAAAATAAAG	ACGAGGGACC	GCAAAATGAT	ATGCCGCAAA	ATGCCGCCGA
351	TACAGATAGT	TCGACACCGA	ATCACACCCC	TGCACCGAAT	ATGCCAACCA
401	GAGATATGGG	AAACCAAGCA	CCGGATGCCG	GGGAATCGGC	ACAACCGGCA
451	AACCAACCGG	ATATGGCAAA	TGCGGCGGAC	GGAATGCAGG	GGGACGATCC
501	GTCGCGAGGG	GAAAATGCCG	GCAATACGGC	AGATCAAGCT	GCAAATCAAG
551	CTGAAAACAA	TCAAGTCGGC	GGCTCTCAAA	ATCCTGCCTC	TTCAACCAAT
601	CCTAACGCCA	CGAATGGCGG	CAGCGATTTT	GGAAGGATAA	ATGTAGCTAA
651	TGGCATCAAG	CTTGACAGCG	GTTCCGAAAA	TGTAACGTTG	ACACATTGTA
701	AAGACAAAGT	ATGCGATAGA	GATTTCTTAG	ATGAAGAAGC	ACCACCAAAA
751	TCAGAATTTG	AAAAATTAAG	TGATGAAGAA	AAAAATAATA	AATATAAAAA

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801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CGCGATTGAG GCGTTCTGCA CCGTCGAGGC GGTGCGCTTC
951 GGCCGAGATG CCGCTGATTG CCGTCAATCA GGCGGATACG CTGATGTGCG
1001 ATGGGGAAGC GGTGAGCCTG ACGGGGCATT CCGGCAATAT CTTCGCGCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGGCGG
1101 ATCGTATGCC CTCAGTGTGC AAGGCGAACC GGCAAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGTGACAAAC GCGGAAGTGC TGCATTTCCTA TATGGAAAAC
1201 GGCCGTCCGT CCCCCTCCGG AGGCAGGTTT GCCGCAAAAG TCGATTTCGG
1251 CAGCAAATCT GTGGACGGCA TTATCGACAG CCGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGAAA ATGGCGCGCG GATGTTTCC GGAAGGTTT ACGGCCCGCG
1401 CCGCGAAGAA GTGGCGGGAA AATACAGCTA TCGCCCGACA GATCGCGAAA
1451 AGGCGCGATT CGCGGTGTTT GCCGGCAAAA AAGAGCAGGA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1204; ORF 287.a>:

a287.pep

```

1 MFKRSVIAMA CIVALSGCG GGGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
151 NQPDMANAAD GMQGGDPSAG ENAGNTADQA ANQAENNQVG GSQNPASSTN
201 PNATNGGSDF GRINVANGIK LDGSGENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIIYKDKSAS
301 SSSARFRRSA RSRRLPAEM PLIPVNQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEN
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGD LHMGTQKFKA VIDGNGFKGT
451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEKGGFGVF AGKKEQD*

```

m287/a287 77.2% identity in 501 aa overlap

```

10 20 30 40 49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KTEA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 MFKRSVIAMACIVALSGCGGGGGSPDVKSADTLSKPAAPVVTEDVGEEVLPKEKKDEEA
10 20 30 40 50 60

50 60 70 80 90 100 109
m287.pep KEDAPQAGSQGQAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
||||| :| |::|:||||| |||||:|:|:|:|:| ||||| |
a287 VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPENKDEGPQNDMPQNAADT
70 80 90 100 110

110 120 130 140 150 160 169
m287.pep DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDPSAGGQNAGNTA
||||| ||| :| ||| |||||:||||| |||||:||||| |||||
a287 DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGGDPSAG-ENAGNTA
120 130 140 150 160 170

170 180 190 200 210 220 229
m287.pep AQGANQAGNNQAGSSDPIPASNPANGGSNFGVRDLANGVLIDGPSQNTLTHCKGDS
|:|||| |||:|:|:| :||| :|||:|:|:|:|:|:| :|: |:|:|:|
a287 DQAANQAENNQVGGSQNPASSTNPNATNGGSDFGRINVANGIKLDGSGENVTLTHCKDKV
180 190 200 210 220 230

230 240 250 260 270 280 289
m287.pep CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP
|: :||||| ||||| :|:|:|:| : :|:|:|:| |:| |:|:|:|
a287 CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVKNGTNKYVIIYKD
240 250 260 270 280 290

290 300 310 320 330 340
m287.pep KP--TSFARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNRYR
| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 KSASSSARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNRYR
300 310 320 330 340 350

```

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	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVVDGIIDSGDDLHMGTKQFKAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGGFGVFAGKKEQDX					
a287	YRPTDAEKGGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1   atgcacaccg gacaggcggg aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgctcaag caacctaccg gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggtg cgcccttacc gcaccttttc
201 acccttgccg gtgctgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgccg ttaaccggca ttctaccctg
301 cggagcccgg actttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacagggt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgct caagtcgccc tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1   ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTCGGTCT TGCTCCGAAT GGGGTTCGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTC CTTTCTGTTC
251 CACTTTCCTG CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/q288 97.8% identity in 181 aa overlap

		10	20	30	40	50	60
m288.pep		MHTGQAVSRVLSRTVIPLGIPLVCSNL	PERSAGSVIAFCLVLLRMGFGLPHIVTKAV				
g288		MHTGQAVSRVLSRTVIPLGIPLVCSNL	PERSAGSVIAFCLVLLRMGFGLPHIVTKAV				
		10	20	30	40	50	60
		70	80	90	100	110	120
m288.pep		RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288		RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
		70	80	90	100	110	120
		130	140	150	160	170	180
m288.pep		PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFGVADFVACTQVF					
g288		PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
		130	140	150	160	170	180
m288.pep	DTX						
	:						
g288	DAX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGTCTAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTCGCGCATA TTGTTACCAA ATCGCGCGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCGT GTGCTGCCAA AGCAGCCATC GGGCGTTTTC CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCTCG
301 CGGAGCCCGG ACTTTCTCTC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAACG GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCCGT CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

a288.pep

1	MHTGQAVSRV	LSRTVIPLGI	PLPVCSSNLP	ERSAGS <u>VIAF</u>	CLVLLRMFGF
51	LPHIVTKCAV	RPYRTFSLP	VLPKQPSAVL	LSVPLSVALP	RPAVNRHSTL
101	RSPDFPPRMP	YAIRGDCPLP	PCAARIITRN	AKMPSETVQV	SDGIQPKLHA
151	LFOAGDFKAV	OVAVOYGFVG	ADFVACAQVF	NA*	

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIP	LPVCS	SNLPERSAGSVIA	FCVL	LRMGFGLPHIV	TKCAV
a288	MHTGQAVSRVLSRTVIPLGIP	LPVCS	SNLPERSAGSVIA	FCVL	LRMGFGLPHIV	TKCAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVL	PKQPSAVLLSV	PLSVALPRPAVNR	HSTLRSPDFPP	RMPIAIRG	DCLPV
a288	RPYRTFSPLPVL	PKQPSAVLLSV	PLSVALPRPAVNR	HSTLRSPDFPP	RMPIAIRG	DCLPV
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNT	KMPSETVQVSD	GIQPKLHALFQAG	FDEAVQVAIQY	GFGVADFVACTQ	VF

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a288 PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFAVACAQVF
 130 140 150 160 170 180

m288.pep DTX
 ::
 a288 NAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

g290.seq
 1 atggcaaaaa tgatgaaatg ggcggtctgtt gcggcggtcg cggcggcagc
 51 ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
 101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
 151 ggcgagattt cgccgtccaa cctggtatcg gtcggcgcgc aggcttcggg
 201 gcagattaaa aagctttatg tcaaactcgg gcaacaggtc aaaaagggcg
 251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
 301 gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat
 351 tgcatgtggc agcgcggaaa aaaaatataa gcgtcaggcg gcgttggtga
 401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
 451 gccgcccga aagccaatgt tgccgagttg aaggctttaa tcagacagag
 501 caaaatttcc atcaataaccg ccgagtcgga tttgggctac acgcgcatta
 551 ccgcgacgat ggacggcacg gtggtggcga ttcccggtga agagggcgag
 601 actgtgaacg cggcgcgatc tacgccgacg attgtccaat tggcgaatct
 651 ggatatgatg ttgaacaaaa tcgagattgc cgaggcgat attaccaagg
 701 tgaaggcggg gcaggatatt tcgtttacga tttgtccga accggatacg
 751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
 801 gtcggggcgc tacaacagca gtacggatac ggcttccaat gcggtctatt
 851 attatgccg ttcgtttgtg ccgaatccg acggcaaat cgccacgggg
 901 atgacgacg agaatacggg tgaatcgac ggtgtgaaaa atgtgttgc
 951 tattccgtcg ctgaccgtga aaaatcgcg cggcaaggcg ttcgtacgcg
 1001 tgttgggtgc ggacggcaag gcagtggaac gcgaaatccg gaccggtatg
 1051 aaagacagta tgaataccga agtgaagaag ggggtgaaag agggggacaa
 1101 agtggtcac tccgaataaa ccgcgcgcca gcagcaggaa agcggcgaa
 1151 gcgccttagg cggcccgcg cgccgataa

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

g290.pep
 1 MAKMMKWAAY AAVAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
 51 GEISPSNLVS VQAQASGQIK KLYVKLGQV KKGDLIAEIN STTQNTIDM
 101 ESKKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL
 151 AAAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
 201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
 251 PIKAKLDSVD PGLTMSGG YNSSTDASN AVYYIYARFV PNPDKLATG
 301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
 351 KDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

m290.seq (partial)
 1 ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
 51 ACTCGGGCAA CAGGTTAAAA AGGGCGATTT GATTGCGGAA ATCAATTCGA
 101 CCTCGCAGAC CAATACGCTC AATACGAAA AATCCAAGTT GGAACGTAT
 151 CAGGCCAAGC TGGTGTCCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
 201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
 251 ATTTGGAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
 301 GAGCTGAAGG CTTTAATCAG ACAGAGCAA ATTTCCATCA ATACCGCCGA
 351 GTCGGAATTG GGCTACACGC GCATTACGCG AACGATGGAC GGCACGGTGG
 401 TGGCGATTCT CGTGGAAGAG GGCAGACTG TGAACGCGGC GCAGTCTACG
 451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
 501 GATTGCCGAG GCGATATTA CCAAGGTGAA GGCGGGGCG GATATTTCTG
 551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
 601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GGCGGTTACA ACAGCAGTAC
 651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTCG TTTGTGCCGA

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701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAATAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGGTGTT GGGTGGCGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
  1  .VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
 51  QAKLVSAQIA LGSAEKYKQR QAALWKENAT SKEDLESAQD AFAAAKANVA
101  ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151  PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201  VDPGLTTMSS GGYNSSDTA SNAVYYYARS FVPNPDGKLA TGMTTQNTVE
251  IDGVKNVLII PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301  KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep                                10      20      30
                                      VSVGAQASGQIKILYVKLGQVKKGDLIAE
g290                                PQAAYITEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQVKKGDLIAE
30      40      50      60      70      80

m290.pep                                40      50      60      70      80      90
INSTSQNTNLNTEKSKLETYQAKLVSAQIALGSAEKYKQRQAALWKENATSKEDLESAQD
g290                                INSTTQNTNIDMEKSKLETYQAKLVSAQIALGSAEKYKQRQAALWKDDATSKEDLESAQD
90      100     110     120     130     140

m290.pep                                100     110     120     130     140     150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
g290                                ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPVEEGQTVNAAQST
150     160     170     180     190     200

m290.pep                                160     170     180     190     200     210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
g290                                PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
210     220     230     240     250     260

m290.pep                                220     230     240     250     260     270
GGYNSSDTASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIIPSLTVKNRGG
g290                                GGYNSSDTASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
270     280     290     300     310     320

m290.pep                                280     290     300     310     320     330
KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
g290                                KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
330     340     350     360     370     380

m290.pep                                PPRRX
g290                                PPRRX
390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GCGGGCTGTT GCGGCGGTCG CGGCGGCAGC
51  GGT TTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAC GGT CAGGCGC GCGGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAAC TTTATG TCAAAC TCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTGGA AAAGCGCACA GGATGCGCTT
451 GCGCGCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATTA
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTGTCCGA ACCGGATACG
751 CCGATTAAAG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TCGTTTGTG CCGAATCCGG ACGGCAAACG CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTGGGTGCG AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCGCA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWAAV AAVAAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STSQTNTLNT
101 EKSLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSG YNSSTDASN AVYYYARFV PNPDGKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTCM
351 RDSMNTEVKS GLKEGDKVVI SEITAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

```
m290.pep
10 20 30
VSVGAQASGQIKLYVKLGQOVKKGDLIAE
|||||
a290 PQAAYITETVRRGDISRTVSATGEISPSNLVSVAQASGQIKLYVKLGQOVKKGDLIAE
30 40 50 60 70 80

40 50 60 70 80 90
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
|||||
a290 INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD
90 100 110 120 130 140

100 110 120 130 140 150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||
a290 ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
150 160 170 180 190 200

160 170 180 190 200 210
PTIVQLANLDMMLNMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||||
a290 PTIVQLANLDMMLNMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
210 220 230 240 250 260

220 230 240 250 260 270
```


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```

m290.pep      GGYNSSTDASNAVYYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               |||||||
a290          GGYNSSTDASNAVYYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTVEVKSGLKEGDKVVISSEITAAEQQESGERALGG
               :|||||
a290          KAFVRVLGADGKAAEREIRTGMRDSMNTVEVKSGLKEGDKVVISSEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               ||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaa gcaaatccc ggctcgccgc agcatctgcg acaatcccgt
651 cgcgaaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaac cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSVASLKR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRNGNKLKV AVFSDPDCCF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCTGCA CCCCAGTGCC GCGCGCAAGG
551 CGCAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAAATCCC GGTCGGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC

```

751 CAACTGGAGG AAATCATCCG CAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```
m292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFGVGLIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

m292.pep	10	20	30	40	50	60
	MKTKLIKILTPFTVLPLLACGQTPVSNANAEP	PAVKAESAGKSVAAASLKARLEKTYSAQDL				
g292	10	20	30	40	50	60
	MKTKLIKILTPFTVLPLLACGQTPVSNANAES	AVKAESAGKSVAAASLKARLEKTYSAQDL				
m292.pep	70	80	90	100	110	120
	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYM	FGVGLINIDTRKNLTEERAADLNKIDF				
g292	70	80	90	100	110	120
	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYM	FGVGLINIDTRKNLTEERAADLNKIDF				
m292.pep	130	140	150	160	170	180
	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKR	LEHEFEKMTDVTVYSFMMPIAGLHPDA				
g292	130	140	150	160	170	180
	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKR	LEHEFEKMTDVTVYSFMMPIAGLHPDA				
m292.pep	190	200	210	220	230	240
	ARKAQILWCQPDRAKAWTDWMRKGFVPVGG	SICDNPVAETTS	SLGEQFGFNGTPTLVFPNG			
g292	190	200	210	220	230	240
	ARKAQILWCQPDRAKAWTDWMRKGFVPVGG	SICDNPVAETTS	SLGEQFGFNGTPTLRLPQR			
m292.pep	250	260				
	RSQSGYSPMPQLEEIIRKNQX					
g292	250	260				
	AHPKRLQPDAPTGGNHPQKPAVNPQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```
a292.seq
  1  ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101  TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151  TTGGAAAAAA CCTATTCCGC CCAAGATTTG AAAGTGTTGA GCGTCAGCGA
201  AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251  TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301  ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351  AATCGACTTC GCCTCCCTGC CTTTGACAA AGCCATCAAA GAAGTGCGCG
401  GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451  TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501  CAGCTTTATG ATGCCCATTT CCGGCCTGCA CCCCATGCCG GCGCGCAAGG
551  CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601  ATCGGTAAAG GCAAATTTCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651  CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701  CCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751  CAACTGGAGG AAATCATCCG CAAAATCAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLAKAR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

m292/a292    100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep      MKTKLIKILTPFTVLPLLACGQTPVSNANAEP AVKAESAGKSVASLAKARLEKTYSAQDL
              |||||||
a292           MKTKLIKILTPFTVLPLLACGQTPVSNANAEP AVKAESAGKSVASLAKARLEKTYSAQDL
              10      20      30      40      50      60

              70      80      90     100     110     120
m292.pep      KVLVSSETPVKGIYEVVVSQ RQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              |||||||
a292           KVLVSSETPVKGIYEVVVSQ RQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              70      80      90     100     110     120

              130     140     150     160     170     180
m292.pep      ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              |||||||
a292           ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep      ARKAQILWCQPDRAKAWTDWMRKGFVPVGG SICDNPVAETTS LGEQFGFNGTPTLVFPNG
              |||||||
a292           ARKAQILWCQPDRAKAWTDWMRKGFVPVGG SICDNPVAETTS LGEQFGFNGTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep      RSQSGYSPMPQLEEIIRKNQX
              |||||||
a292           RSQSGYSPMPQLEEIIRKNQX
              250     260
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtcctggtc
51  ggttcgggct gtcagaacat catcgaaccg ctttctcgcg gcgttacgac
101 gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151 tggcatcggg tgccggcggt caagtcgaat cggcggagcg gtggcgtgaa
201 gccgttgaaa aaaccttatac tggcgagggg ggcggaatgc agatgcaggc
251 gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301 ccgaggcggt gcgggaagcg gtatgcggac atcggggggc atagtgtatac
351 aatccgtatc cgagttttcc ggttggagca tcgtatgagt atttatgccg
401 tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcggtg
451 ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgtcgcg
501 cgaggcgcg cgcgaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551 tgatgccgtt tgcggtcgga ctgctgttcg ccagggaac tctagagtcg
601 actgcagcag catgccctc...
  
```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
1  MRITCAPMSL LSAAVWSVRA VRTSSNRFFA ALRRYSAPRP TIFPKPAGTP
51  WHRVRFRFSN RRTRGVKPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
101 PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151 FFEVLVLSVL HTGRVSRREAR REVEKAMSYR AVRVMFPAVG LLFARGTLLES
201 TAAACP....
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

682

m294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
151 TGGCATCGGG TCGGGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCCG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC GGTCCGTTGG
751 TCGAAATACA TACACGCCGT CGTCTTACC CATATGCTGC TGATTGTCTT
801 TTGGCAAAA GCGATGTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep

```

1  MRITCAPMSL LSAAVWSIRV VRTSSNRFP AFRYSAFPQ TIFPKPADTP
51  WHRVRRFKSN RMRGGKPLK KPYRPRGGC RCRRWTALS HNIAERARE
101 PRRCGRYAD IGGDSDTIRI RVFRLEHRMS IYVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
201 ANRYSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
251 SKYIHAVVET HMLLIVFLAK AMFYISW*

```

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSAAVWSVRAVRTSSNRFPALRRYSAPRPTIFPKPAGTPWHRVRRFKSN					
m294	MRITCAPMSLLSAAVWSIRVVRTSSNRFPAAFRYSAPQPTIFPKPADTPWHRVRRFKSN					
	10	20	30	40	50	60
g294.pep	RRTRGVKPLKKPYLARGAECRCRRWTALSHNIAERARESPRRCGRYADIGGDSDTIRI					
m294	RRMRGGKPLKKPYRPRGGCRRWTALSHNIAERARESPRRCGRYADIGGDSDTIRI					
	70	80	90	100	110	120
g294.pep	RVFRLEHRMSIYVAHIIHLYCATAFVGGVFFEVVLVLSVLHTGRVSREARREVEKAMSYR					
m294	RVFRLEHRMSIYVAHIVHLYCAIAFVGGVFFEVVLVLSVLHTGRVSREARREVEKAMSYR					
	130	140	150	160	170	180
g294.pep	AVRVMFVAVGLLFARGTLESTAAACP					
m294	AVRVMFVAVGLLFASGIVMAANRYSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
151 TGGCATCGGG TCGGGCGGTT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
201 GCCGTTGAAA AAAACTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GGTGGAGTA CCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCCG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

```

683

701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAFRP TIFPKPAGTP
 51 WHRVRRFKSN RRTGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
 101 PRYRGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LFFASGIVMA
 201 ANRYSILGE PFATSFGTML TLKILLAFSV LAHFIAIVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

m294.pep	10	20	30	40	50	60
	MRITCAPMSLLSAAVWSIRVVRTSSNRFPAAFRYSAFQPTIFPKPADTPWHRVRRFKSN					
a294	MRITCAPMSLLSAAVWSIRAVRTSSNRFPAAFRYSAFRPTIFPKPAGTPWHRVRRFKSN					
	10	20	30	40	50	60
m294.pep	70	80	90	100	110	120
	RRMRGGKPLKKPYRPRGGCRRRAWTALSHNIAERARESPRCGKRYADIGGDSDTIRI					
a294	RRTGGKPLKKTYPRAECRRARTALSHNIAERARESPRYGKRYADIGGDSDTIRI					
	70	80	90	100	110	120
m294.pep	130	140	150	160	170	180
	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVLVLSVLHTGRVSREARREVEKAMSYR					
a294	RVFRLEYRMSIYAVAHIVHLYCAIAFVGGVFFEVLVLSVLHTGRVSCEARREVEKAMSYR					
	130	140	150	160	170	180
m294.pep	190	200	210	220	230	240
	AVRVMFVVGLLFASGIVMAANRYSILGEPFATSFGTMLTLKILLAFSVLAHFIAIVVK					
a294	AVRVMFVVGLLFASGIVMAANRYSILGEPFATSFGTMLTLKILLAFSVLAHFIAIVVK					
	190	200	210	220	230	240
m294.pep	250	260	270			
	MARSTLTVGWSKYIHAVVETHMLLIVFLAKAMFYISWX					
a294	MARSTLTVGWSKYIHTVVETHMLLIVFLAKAMFYISWX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcggga tggcgcggca cgacggccag caggcgcacg ccgcgatatt
 51 gttgccacgc cgccagcagt ttttcgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgcc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
 301 acggatcagg cggcggactt tcagataacc gttcagcgat ttttcgaca
 351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgcgc gcattccttc
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcggggc
 451 gtgttcgcgc aaaaactgcc gtaccacagt tttttgtca tacggaagat
 501 agcggcattg cgcacgcgga aacagaactt gcgcggttcc ccgtcccgtc
 551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaac gccgcgcgaa
 601 ctgcggtatc aagggtctgg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcgcgggta acgggattcg gatgcggcgt gccgaaacgc
 701 tcgtccctat gcgcccggta tgcgggggca cttccggagc gtttgcctaa
 751 ataacgcgt atccatctcg gcgcaagcag ccacaataca tcataaagcc
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacgggtc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

684

g295.pep

```

1  MLGMARHDDQ QGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK
51  LPRQRFHVF RHOVVFGLAA HLHGCRAQFR QPRRIRLRLR QTARQSRGCG
101 TDQAADFQIT VQFFFRQPRI RQQRHTRSP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

```

1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTCA TCTGTTCCGA CGGTATGATG TCGTATTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTGACGGAAG CGCGCGCAGG
301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC
401 ATCAGGTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGCGC
451 GTGTTCCGCG AAAAAGTGGC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG CGCATCGGGA AACAGAACTT GCGCGGTTT CCGCCCCGTC
551 GGGGTATCT GCGTCATCAG CAGCGGCGCA TCGGAAAAC GCCGCCGCAA
601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT GCGCCCGATA TGCCGGGGCA CTTCGGGAGC GTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTCTATTT CTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGGCAACGG AATCAATAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep

```

1  MLGMARHDDQ QRIAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK
51  LPRQRFHLFR RYDVVFGLAA HLHGCRAQFR QPRRIRLCLR QTPRQSRGGR
101 TDQAADFQIT VQFFFRQPRI RQQRHTRAP AFPHQVGPDE GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PPRRGLRHQ QRRIGKTPPQ
201 LAYQGLGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV XTQTAFRQR NQIS*

```

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQRIAAILLPRRQOFFRLVTFPINARAAAHGNRPASDAFFKLPQRQFHLFR					
g295	MLGMARHDDGQGGIAAILLPRRQOFFRLVFA PINARAAAHGNRPASDAFFKLPQRQFHVFR					
	10	20	30	40	50	60
m295.pep	RYDVVFGLAAHLHGCRAQFRQPRRIRLCLROTTPRQSRGGRTDQAADFQITVQFFRQPRI					
g295	RHQVVFGLAAHLHGCRAQFRQPRRIRLRLRQTARQSRGGTDDQAADFQITVQFFRQPRI					
	70	80	90	100	110	120
m295.pep	RQQRHTRAPAFPHQVGPDEGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
g295	RQQRHTRSPAFHLHQIGPDFGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
	130	140	150	160	170	180
m295.pep	PPRRGHLRHQRRIGKTPPQLAYQGLGTRFSDRNGVYPNRAGNGIRIRLAETLVPMRPI					
g295	PSRRGHLRHQRRIGKTPPQLAYQGLGTRFSDRNGVYPNRAGNGIRMRLAETLVPMRPV					
	190	200	210	220	230	240
m295.pep	CRGTSGAFVQITPYPYRRKQPQYIIPLEHLSISCKTNAVXTQTAFRQRNQISX					
g295	CRGTSGAFVQITPYPYRRKQPQYIIPLEHLSISCKTNAVXTQTAFRQRNQIS					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1 ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51 GTTGCCACGC CGCCAGCAGT TTTTCCGCTT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATGTCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTT GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAAGTCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTT CCGTCCCGTC
551 GGGGTATCT GCGTCATCAG CAGCGGCGCA TCGGAAAAC GCTGCCGCAA
601 CTCGCGTATC AAAGTTGGG CGGCACGCGT TTCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTCT GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCGATA TGCAGGGGCA CTTCCGGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1 MLGMARHDDQ QGIAAILLPR ROQFFRLVFT PINARAAAHG NLPVSDAFFK
51 LPRQRFHLFR RHQVVFQIAA HLHGCRAQFR QPRRIRLRLC QTARQSSGGR
101 TDQAADFQIT V*RFRRQPRI RQKQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPO
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQ	RIAAILPR	ROQFFRLVFT	PINARAAAHG	NRPASDAFFK	LPRQRFHLFR
a295	MLGMARHDDQ	QIAAILPR	ROQFFRLVFT	PINARAAAHG	NLPVSDAFFK	LPRQRFHLFR
	70	80	90	100	110	120
m295.pep	RYDVVFQIAA	HLHGCRAQFR	QPRRIRLRLC	QRTARQSSGGR	TDQAADFQIT	VQRFRRQPRI
a295	RHQVVFQIAA	HLHGCRAQFR	QPRRIRLRLC	QRTARQSSGGR	TDQAADFQIT	VXRFFRQPRI
	130	140	150	160	170	180
m295.pep	RQKQRHTRAP	AFPHQVGF	DFGFHQNAE	HRAVFAQK	LPYPFFVIR	KIAALRIGKQNL
a295	RQKQRHTRAP	AFPHQVGF	DFGFHQNAE	HRAVFAQK	LPYPFFVIR	KIAALCIRKQNL
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQ	QRRIGKTP	PQLAYQGL	GGTRFSDR	NGVYPNR	RAGNGIRIRLAETL
a295	PSRRGHLRHQ	QRRIGKTP	PQLAYQGL	GGTRFSDR	NGVYPNR	RAGNGIRIRLAETL
	250	260	270	280	290	
m295.pep	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	XTVQTA	FRQRNQISX
a295	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	RTVRTA	FRQRNQISX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1 ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

```

51 GCTTGCCGTT TCGATTATTC TGGTGtcgGC GGCATACATT Gcttcgacag
101 aggggaccga gcgcgtcaga ccgcAGCGCG Tggaacaaa ACTGCCGCCG
151 CTGTCTTGGg gcggcaacgg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGGcatt tGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttaC CGACGAAGAC GGCAGGCGCA
401 aTctGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 CAAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701 CAACCCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgag CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 CAAGGCAATG TGCAGCGCGG CGAGGTATC GGTTTTGTG GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCGGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

```

g297.pep
1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PORVEQKLPP
51 LSWGNGVQY AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGS A REVQFTDED GERNLVALEK KGGIWRRSAS
151 DADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHQQVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYDEDGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTTPVRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

```

m297.seq
1 ATGGCTGTCT TCCCACCTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51 GCTTGCCGTT TCGATTATTT TGGTGTCGCG GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGAACAAAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCAGGCGCA
401 ATCTGGTCGC TTTGGAAAAG AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TGCAGCGCGG CGAGGTATC GGTTTTGTG GTTCGACCGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCGGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

```

m297.pep
1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERVR PORVEQNLPP
51 LSWGSGVQY AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGS A REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

```


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201 EGDVRLMYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
 251 GNYDDEGKV LQEKGGFNI PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTVPRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVPVSV ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHRKYALRALAVSIILVSAAYIASTERTERVPRQVEQNLPPLSWGSGVQT					
g297	MAVFPLSAKHRKYALRALAVSIILVSAAYIASTEGTERVPRQVEQKLPPLSWGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTTDEDGERNLVALEKKGGIWRRSASEADMKVLPPLRSVVVKTSARGSLARAEVVP					
g297	REVQFFTTDEDGERNLVALEKKGGIWRRSASDADMKVLPPLRSVVVKTSARGSLARAEVVP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQAAGDILAAEVVKGTRHQAFY					
g297	EIRESLSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQQAAGDILAAEVVKGTTHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGNYYDEDGKVLQEKGGFNIPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGNYYDEDGRVLQEKGGFNIPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTVPVASADGVITFKGRKGGYGNVIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTVPVASADGVITFKGRKGGYGNVIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVPVSVVALPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPVPVSVVALPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1 ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
 51 GCTTGCCGTT TCGATTATTT TGGTGTCGGC GGCATACATT GCTTCGACAG
 101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA ACTGCCGCCG
 151 CTGTCTTGGG GCGGCAGCGG TGTTCAGACG GCATATTGGG TGCAGGAGGC
 201 GGTGCAGCCA GGCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
 251 CGCGGGACGA AATTGCCCGA ATAACGAAA AATATGGCGG CGAAGCCGAT
 301 TTGCGGCATT TCGTGCCGA CCAGTCGGT CATGTTTGG TCGCGGCGA
 351 CGGCGGCGCG CGCGAAGTGC AGTTTTTAC CGACGAAGAC GGCGAGCGCA
 401 ATCTGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
 451 GAGGCGGATA TGAAGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
 501 GTCGCGCGC GGTTCGCTGG CGCGGCGGCA AGTGCCCGTC GAAATTCGCG

688

```

551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGCG
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGCGCGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTACGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TCGCGGCGCG CGAGGTCATC GGTTTTGTCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GGCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1 MAVFPLSAKH RYALRALAV SIILVSAAYI ASTERTVRV RQVEQKLPP
51 LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGA REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGG
251 GNYDEDGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGPVRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPNVPSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

```

          10      20      30      40      50      60
m297.pep  MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTVRVPQVEQNLPLPSWGGSGVQT
          |||
a297      MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTVRVPQVEQKLPLPSWGGSGVQT
          10      20      30      40      50      60

          70      80      90      100     110     120
m297.pep  AYWVQEAQVPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGA
          |||
a297      AYWVQEAQVPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGA
          70      80      90      100     110     120

          130     140     150     160     170     180
m297.pep  REVQFTDEDGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVPV
          |||
a297      REVQFTDEDGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVPV
          130     140     150     160     170     180

          190     200     210     220     230     240
m297.pep  EIRESLSGIFAGRFSLDGLKEGDVRLMYDSLYFHGQQAAGDILAAEVVKGGTRHQAFY
          |||
a297      EIRESLSGIFAGRFSLDGLKEGDVRLIYDSLYFHGQQAAGDILAAEVVKGGTRHQAFY
          190     200     210     220     230     240

          250     260     270     280     290     300
m297.pep  YRSDKEGGGGNYDEDGKVLQEKGGFNIEPLVYTRISSPFGyRMHPILHTWRLHTGIDY
          |||
a297      YRSDKEGGGGNYDEDGRVLQEKGGFNIEPLVYTRISSPFGyRMHPILHTWRLHTGIDY
          250     260     270     280     290     300

          310     320     330     340     350     360
m297.pep  AAPQGPVRAADGVITFKGRKGyGNAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
          |||
a297      AAPQGPVRAADGVITFKGRKGyGNAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
          310     320     330     340     350     360

```

689

	370	380	390	400	410	420
m297.pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298.seq

```

1 ATGAAAAACT TTCTTCCCT TTTCCGCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcggcgaaa ggCTCAAGAC GGCAGTTCGG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGCGCGGC
301 GGAACAGAAT GGAACAAGG CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTCGCCGAG ATTCTGCTGAT GCAGGGCGTT GCGCTTTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCGGAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTC CCGTCGGCAA ACGTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACTT GAAAGGCAA ATCATCTGA TTCCACCGC
801 GCAAACTACT AGCGGCGGGA AAGGccGCTA CACCGATTCC GTCACGTC
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298.pep

```

1 MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51 SGAALQENAY ALSDGIKTFI SGETPPTAQD GGSADMPPEA AASEAPPAG
101 GTEWKQGETA AAVRSGDKVF FAGDSLMOGV APFVQKSLKQ QYGI SANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRIE AAHTRVQVW WLGI PYMKKV KLDGQMR YLD
251 KLLSEHLKGI IILIPTAQL SGGKGRYTDV VNVNGKPVRY RSKDGIHFTA
301 EQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298.seq

```

1 ATGAAAAACT TTCTTCCCT TTTCTCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCGGAC GGCTCAAGAC GGCAGTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCT TCAAACCGGT
301 GAAACAGAAT GGAACAAGA CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTCGGCG ACTCGCTGAT GCAGGGCGTT GCCCCTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCGGAAAAC
501 GATTGAAGAA ACCCTGCAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATGCTTT CGGAACATTT GAAAGGCAA ATCATCTGA TTCCACCAC
801 GCACACCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTC
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAATAATA ATGGAATAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep
 1 MKNFLSLFSS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
 51 SGAAALQENAY ALSDGIKAFV SGETPPTAQD GGSADMPSEA AASEAVPQTG
 101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
 151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDF WDFPVGKLYL
 201 KFASDEWAQE YLKRVDRIE AAHTRVQVW WLGIPYMKKA KLDGQMRVLD
 251 KLLSEHLKKG IILPTHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
 301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

m298/g298 94.8% identity in 327 aa overlap

m298.pep	10	20	30	40	50	60
	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	10	20	30	40	50	60
	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
m298.pep	70	80	90	100	110	120
	ALSDGIKAFVLSGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	70	80	90	100	110	120
	ALSDGIKTFVLSGETPPTAQDGGSDMPPEAAASEAAPPAGGTEWKQDTEAAAVRSGDKVF					
m298.pep	130	140	150	160	170	180
	FVGDSLMOGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	130	140	150	160	170	180
	FAGDSLMOGVAPFVQKSLKQYQYIESANLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
m298.pep	190	200	210	220	230	240
	LAVFLGPNDFWDFPVGKLYLKFASDEWAQEYLKRVDRIEAAHTRVQVWVWLGIPYMKKA					
g298	190	200	210	220	230	240
	LAVFLGPNDFWDFPVGKRYLKFASDEWAQEYLKRVDRIEAAHTRVQVWVWLGIPYMKKV					
m298.pep	250	260	270	280	290	300
	KLDGQMRVLDKLLSEHLKKGKIIILPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
g298	250	260	270	280	290	300
	KLDGQMRVLDKLLSEHLKKGKIIILPTAQTLSGGKGRYTDVNVNGKPVRYRSKDGIHFTA					
m298.pep	310	320				
	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	310	320				
	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq
 1 ATGAAAACT TTCTTCCCT TTTGCCTCC ATACTGATGT CTGCCCTGAT
 51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
 101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
 151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
 201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GCGGTTTCGG
 251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACTGGC
 301 GAAACAGAAAT GGAAACAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
 351 CAAAGTCTTT TTCGCCGCG ACTCGCTGAT GCAGGCGGTT GCACCCTTCG
 401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
 451 AAACAAAGCA CGGGCTGTC CTACCCCTCA TTCTCGACT GGCCGAAAAC
 501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
 551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC
 601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
 651 CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
 701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

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751 AAACGCTTT CGGAATATTT GAAAGGCAAA ATCATCCTGA TTCCACCGC
801 GCACACCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1  MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AAPETAPQTG
101 ETEWKQNTA AAVRTGDKVF FAGDSLMQGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAE YLKRVDRIE AAHthyVQVW WLGIpYMKA KLDGQmRYLD
251 KLLSEYLK GK ILIPIAHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFESSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFISGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTAEEAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDLSLMQGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMQGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWFDFPVGKLYLKFADEWAEYLKRVDRIEAAHthrvQVWVWLGIpYMKA					
a298	LAVFLGPNDPWFDFPVGKRYLKFADEWAEYLKRVDRIEAAHthyVQVWVWLGIpYMKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQmRYLDKLLSEHLKGIILIPHTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
a298	KLDGQmRYLDKLLSEYLKGIILIPHTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1  ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CCGCCACGCA
51  GGCGAAGCC CTGCCCCTCG CCTCCGTCAG CCCCGACACC GTTACCGTTT
101 CCCCGTCCG CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCGCC CCTCGCCTTG GATGAAAAA CTCCGATCCG TCGCACAAGG
201 CAGCGCGCAG GCCTTCCGCA TCCTGCAAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACGCC CTGCGCAAAAC GCCTGCAAAA AACATGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCCGTC CGTCACAGCG GCAACTGGCA AAGCTTCACC AGCAGGAACA
401 ATACCGGAGA TTTCCCGCTC GCGCGCATCC TCGCCCAAC CGGCAGCGGC
451 GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

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501 TTCCCTGTTT GCCAAACCGC TGCTCGCCGA ACAAACCTTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGCGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCTGGCCAT ACAGACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTGACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCC TTCAACAACA ACATCGACAT TGCCGATACC GAACAAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCCGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACGCGCCCC GTCTCTCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCC
1001 CCCGTCAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC AATGGGCGGC
1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCGC CCAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGGCGGAA ATGCTTGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCGCGCGC CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

g299.pep

```

1  MNPKHFIAFS ALFAATQAEA LPVASVSPDT VTVSPSAPYT DTNGLLTDYG
51  NAAASPWMKK LRSVAQGSSE AFRILQIGDS HTAGDFFTDA LRKRLQKTWG
101 DGGIGWVYPA NVKGQRMMAV RHSGNWQSFT SRNNTGDFPL GGILAQTGSG
151 GGMTLTASDG KTGKQRVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLAIQTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRTP VLLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNWLNQ GWAADKGVHF SAQGYRRAE MLADSLEELV RAAAIRQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

```

1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCC CCGCCACGCA
51  GGCAGAAGCC CTACCTGTGC CCTCCGTGAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTGCAAAA AACTTGGGGC
301 GACGCGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GCGGCGCGTC CGGCACAACG GTAAGTGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTCGTC GCGCGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGCGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTCG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCT TTCAACAACA ACATCGACAT TGCCGACACC GAACAAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCTGC CGCCGGCATC
901 CTCATCATCG GCGCACCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCC
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC CATGGGCGGC
1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCGC CCAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGGCGGAA ATGCTGCGCC
1151 ACAGCCTCGA AGAACTCGTC CGCTCGCTG CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

m299.pep

```

1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51  NASASPWMKK LQSVAGGSSE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101 DGGIGWVYPA NVKGQRMMAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151 GSMTLTASDG IASKQRVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRTP VRLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNWLNQ GWAADKGVHF SAKGYRRAE MLADSLEELV RAAAIRQ*

```

m299/g299 95.5% identity in 397 aa overlap

```

10      20      30      40      50      60
m299.pep  MNPKHLIAFSALFAATQAEALPVASVSLDTVTVPSPAPYDTNGLLTDYGNASASPWMKK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

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g299	MNPKHFIASFALPAATQAEALPVASVSPDVTVTSPSAPYTDNGLLTDYGNAASPWMKK
	10 20 30 40 50 60
m299 . pep	LQSV AQSGSETFRILQIGDSHTAGDFFTD SLRKLQKTWGDGGIGWVYPANVKGQRM AAV
g299	LR SVAQSGSEAFRILQIGDSHTAGDFFTDALRKLQKTWGDGGIGWVYPANVKGQRM AAV
	70 80 90 100 110 120
m299 . pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMILTASDGIASKQRVSLFAKPLLAEQTL
g299	RHSGNWQSFTSRNNTGDFPLGGILAHTGSGGSMILTASDGTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299 . pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
g299	TVNGNTVSANGGGWQVLDTGAAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299 . pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299 . pep	LIIGAPESLKNLTGVCGTRPVRLTEVQQMORRVARQGQTMFWSWQNAMGGICSMKNWLNQ
g299	LIIGAPESLKNLTGVCGTRPVLLTEVQQMORRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299 . pep	GWA AKDGVHFSAGYRRAEMLADSLEELVRSAAIRQX
g299	GWA AKDGVHFSAGYRRAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

```

a299.seq
1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCC CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCC CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GCGGCGCGTC CGGCACAACG GTAAC TGGA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCCGCTC GCGCGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTT CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCGGCATC
901 CTCATCATCG GCGGCGCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGCGGCG
1051 GTTTGCAGCA TGAAAACTG GCTCAACCAC GGATGGGCCG CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGA ACTCGTC CGTCCGCTG CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSVAGGSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101  DGGIGWVYPA NVKGORMAAV RHNGNWQSLT SRNNTGDFPL GGILAHGTSG
151  GSMTLTASDG IASKQRVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRTP VRLTEVQQMQ RRIARQGQTM FWSWQAMGG
351  VCSMKNWLNH GWAADGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

m299.pep	10	20	30	40	50	60
	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
a299	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
	10	20	30	40	50	60
m299.pep	70	80	90	100	110	120
	LQSVAGGSGETFRILQIGDSHTAGDFFTDSLRLQKTWGDGGIGWVYPANVKQORMAAV					
a299	LQSVAGGSGETFRILQIGDSHTAGDFFTDSLRLQKTWGDGGIGWVYPANVKQORMAAV					
	70	80	90	100	110	120
m299.pep	130	140	150	160	170	180
	RHNGNWQSLTSRNNTGDFPLGGILAHGTSGGSMTLTASDGIASKQRVSLFAKPLLAETL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHGTSGGSMTLTASDGIASKQRVSLFAKPLLAETL					
	130	140	150	160	170	180
m299.pep	190	200	210	220	230	240
	TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
m299.pep	250	260	270	280	290	300
	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIDIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
m299.pep	310	320	330	340	350	360
	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRVARQGQTMFWSWQAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRRIARQGQTMFWSWQAMGGVCSMKNWLNH					
	310	320	330	340	350	360
m299.pep	370	380	390			
	GWAADGVHFSAGYRRAEMLADSLEELVRSAAIRQX					
a299	GWAADGVHFSAGYQRSAEMLADSLEELVRSAAIRQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGTTGGGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
```



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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTTATT CGCTCGGCCG CCATCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACCTG TTTTATATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGT CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTTAT TTCTGTGTGT
1001 TTGCGCTGCC GGGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTGCGA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGCGGCAG TGTGTTGTTT ATCGGTTTAA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCTT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATT CTATGATGT GCCGTATTCC
1501 GCTTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATT GGGTATTTGT
1551 TTTGGGTCTG CCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTSPRK LTTFMVVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYL IIFFAAQFVA FFWNTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFILICAPI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNIITPM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGTPTFY PVP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATTATT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTTATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAAATC ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCTG
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGT ACTGAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTGTG ACAAGAAGAA AAAGACATC GGCATTCCAA
801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTGGGCT GCGGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGA GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGT TCCGGTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTTTATT TCTTGTGTT TGAAGTGCY GGCmTTGTTT
1001 ATGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

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1051 ATGCCCGAAT CGATGAGTAC TCTGGsGCTT TmTTTGswCA kcATCTTTTT
1101 TGCCGCACAG TTGTTCGCAT TTTTAAATG GACGAATATT GGGCAATATA
1151 TTGCCGTAA AGGGCGGACG TTCTAAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTTGTTA TCGGTTTTAT TTTAATTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TCGCCCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCGG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GCGGTGGGTA
1451 CGCTGATTTC TATGATGTTG CCGTATTCCG CTTTCTTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTG GGTATTTGTT TTGGGCTGCG CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

```

1 MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDPRVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAST FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVFFALSAL LAWSIVPADG
301 ILRHPTGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXIXFFAAQ FVAFFNWTNI GQYIAVKGAT FLKEVGLGGS
401 VLFIGFILIC AFINLMIGSA SAQWAVTAPI FVPMMLAGY APEVIQAAAYR
451 IGDSVTNIIT PMMSYFGLIM ATVIKYKKA GVGTLISMML PYSAFFLIAW
501 IALFCIWVVFV LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from *N. gonorrhoeae*:

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
m302.pep	SVPDPRVGA KGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
g302	SVPDPRVGA KGRADDGLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
	70	80	90	100	110	120
m302.pep	EKSGLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL					
g302	EKSGLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL					
	130	140	150	160	170	180
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
m302.pep	ALIGYFVTEKIVEPQLGPGYQSDLSQEEKDIRHSNEITPLEYKGLIWA GVVFFALSALLAW					
g302	ALIGYFVTEKIVEPQLGPGYQSDLSQEEKDIRHSNEITPLEYKGLIWA GVVFFALSALLAW					
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQLGPGYQSDLSQEEKDIRHSNEITPLEYKGLIWA GVVFFALSALLAW					
g302	ALIGYFVTEKIVEPQLGPGYQSDLSQEEKDIRHSNEITPLEYKGLIWA GVVFFALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

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```

m302.pep  SIVPADGILRHPETGLVSGSPFLKSI VVFI FLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SIVPADGILRHPETGLVAGSPFLKSI VVFI FLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLXIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGILICAFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAFLKEVGLGGSVLFIFIGILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      NLMIGSASAQWAVTAPIFVPMMLAGYAPQVIQAAAYRIGDSVTNIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKDAGVGTLSMMLPYSAFFLIWIALFCIWVFLGLPVGPAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      IKYKKDAGVGTLSMMLPYSAFFLIWIALFCIWVFLGLPVGPPTPTFFYPVPX
          490      500      510      520      530

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTCAC GTTGTCAGCC
251 TGTCGATGTC TGACGGTTTG ATCAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGCGCT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 TTCGCGCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCGGCGGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCT TAGGCCCTGA AGCCAACTGG TTTTTATGG
701 TAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTGCGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCTGAAA CAGGATTGGT
951 TTCCGGTTTC CCGTTTAA AATCAATTGT TGTTTTATT TTCTTGTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGG
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTTTAATT
1151 GGACGAATAT TGGCAATAT ATTGCCGTTA AAGGGCGCAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTTT ATCGGTTTA TTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCCCGGAT TTTCGTCCCT ATGCTGATGT TGGCCGCTA CGGCCCGGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTACCA ATATTATTAC
1401 CCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATT CTATGATGT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATT GGGTATTTGT
1551 TTTGGGCTG CCCGTCGGTC CCGGCGGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQDTQRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLTKSPRK LTTFMVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMEE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIITPM SYFGLIMATV IKYKKGAVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	QTDGRFLRTVEW	LGNMLPHPVTLF	IIIFIVILLIAS	AVGAYFGL	
a302	MHSIYFFKEKQMSQTD	QTDGRFLRTVEW	LGNMLPHPVTLF	IIIFIVILLIAS	AAGAYFGL	
	10	20	30	40	50	60
m302.pep	70	80	90	100	110	120
	SVPDPRPVGAKGRADD	GLIYIVSLLNAD	GFIKILTHTVKN	FTGFAPLGTVLV	SLLGVGIA	
a302	SVPDPRPVGAKGRADD	GLIHVVSLDAD	GLIKILTHTVKN	FTGFAPLGTVLV	SLLGVGIA	
	70	80	90	100	110	120
m302.pep	130	140	150	160	170	180
	EKSGLSALMRLLLT	TKSPRKLTTFMV	FTGILSNTASEL	GYVVLIPLSAI	IFHSLGRHPL	
a302	EKSGLSALMRLLLT	TKSPRKLTTFMV	FTGILSNTASEL	GYVVLIPLSAI	IFHSLGRHPL	
	130	140	150	160	170	180
m302.pep	190	200	210	220	230	
	AGLAAAFAGVSGGYS	ANLFLSTIDPL	LACITHQAA-----	VVGPEANWFFM	VASTFVI	
a302	AGLAAAFAGVSGGYS	ANLFLGTIDPL	LAGITQQAQIIHP	DYVVGPEANW	FFMFASTFVI	
	190	200	210	220	230	240
m302.pep	240	250	260	270	280	290
	ALIGYFVTEKIVEP	QLGPYQSDLSQ	EKDIRHSNEIT	PLEYKGLIWAG	VVFVALSALLAW	
a302	ALIGYFVTEKIVEP	QLGPYQSDLSQ	EKDIRHSNEIT	PLEYKGLIWAG	VVFVALSALLAW	
	250	260	270	280	290	300
m302.pep	300	310	320	330	340	350
	SIVPADGILRHPET	GLVSGSPFLKS	SIVVFIFLLFAL	XGXVYGRVTR	SLRGEQEVVNAMEE	
a302	SIVPADGILRHPET	GLVSGSPFLKS	SIVVFIFLLFAL	PGIVYGRVTR	SLRGEQEVVNAMEE	
	310	320	330	340	350	360
m302.pep	360	370	380	390	400	410
	SMSTLXLXLIFFAA	QFVAFFNWTN	IGQYIAVKGAT	FLKEVGLGGSV	LFIGFILICAFI	
a302	SMSTLGLYLVIIFF	AAQFVAFFNWTN	IGQYIAVKGAT	FLKEVGLGGSV	LFIGFILICAFI	
	370	380	390	400	410	420
m302.pep	420	430	440	450	460	470
	NLMIGSASAOAVT	APIFVPMMLAG	YAPEVIQAAYR	IGDSVTNIITP	MSYFGLIMATV	
a302	NLMIGSASAOAVT	APIFVPMMLAG	YAPEVIQAAYR	IGDSVTNIITP	MSYFGLIMATV	
	430	440	450	460	470	480
m302.pep	480	490	500	510	520	
	IKYKKGAVGTLISM	MMLPYSAFFLI	AWIALFCIWV	FLGLPVGPGAP	TFYPAPX	
a302	IKYKKGAVGTLISM	MMLPYSAFFLI	AWIALFCIWV	FLGLPVGPGAP	TFYPAPX	
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

g305.seq

```

1 ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CGGTTTTTGGC GGTAGTGTTT GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GACAAACAAA TCAAAGAGTA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GTGTTGCCCA AGTGTTCGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGCCCG TCCGATGAT GGTTCAGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTCCT GGTTCGGTAG
701 CGGTTAAAGC ACTGCTGAAG TTGTTTCCA AGAAAACTA TATCCCGTTT
751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGGTTGTC
801 GGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51 QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 QKQIKEXLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1 AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CAGTTTTTGGC GGTAGTGTTT GAATACCGGC AACGTTTCAG
201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCawACAAA TCAAAGAGyA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTyTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTTCGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGAAAAA
551 CTGCGACAGA ATTCTCGTTT TTCTTGCTG TGCCGATGAT GGTTCGCCCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTCCTA GGCTTGGTAG
701 CGGTAAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51 QLGAVLAVVF EYRQRFNSVL HGLGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60

700

	70	80	90	100	110	120
g305.pep	BYRQRF	SNVLHG	VGKDRK	ANRFVL	NLAIAFI	PAAVMGL
m305	BYRQRF	SNVLHG	LKGKDR	KANRFVL	NLAIAFI	PAAVMGL
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFIL	WVEKRQ	SRAEPK	IAVDAL	RPIDAL	MIGVAQ
m305	XGFXIL	WVEKRQ	SRAEPK	IAVDAL	RPIDAL	MIGVAQ
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTAT	EFSSFL	AVPMMV	AATAYD	VLDKHY	RFFTLH
m305	ERKTAT	EFSSFL	AVPMMV	AATAYD	VLDKHY	RFFTLH
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKN	YIPFAY	YRIVFG	IVIIIL	WLSGWI	SWEX
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1  ATGGATTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTCG
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTG GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGG GCTGTGTTC
301 GGCAAACAAA TCAAAGAGTA TCTGTTTAA CCCTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TTATTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTTGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCCA AGTGTGTCG CTGGTCCAG GTACGTCGCC
501 TCGGGCAGT ACGATTATG GCGGGATGCT TTGGGGAATC GAGCGGAAA
551 CGGCAACGGA GTTTTCATTT TTCTGGCCG TTCCGATGAT GGTGTCAGCA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTGTTTCA GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRF SNVL HGVGKDRKAN RFVLNLAIAF IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIV	LKALMM	GLVEGF	TEFLPI	SSSTGHL	IVFGNL
a305	MDFLIV	LKALMM	GLVEGF	TEFLPI	SSSTGHL	IVFGNL
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRF	SNVLHG	LKGKDR	KANRFVL	NLAIAFI	PAAVMGL
a305	EYRQRF	SNVLHG	VGKDRK	ANRFVL	NLAIAFI	PAAVMGL

701

	70	80	90	100	110	120
m305.pep	130	140	150	160	170	180
	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
a305	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
	130	140	150	160	170	180
m305.pep	190	200	210	220	230	240
	ERKTATEFSFFLAVPMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGVLVAVKALLR					
a305	ERKTATEFSFFLAVPMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGVLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

g306.seq

```

1   ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCCG
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAATTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GCGGGAAGCC  AACGCATTAT
651 CTGCAAAATG  GCGCGTATGC  CGAACCCCG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTTCCGA  AGTGGTCGGC  TATCAGCGCG
751 GACATAAAAC  GCTTTACCGC  GTGCAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

g306.pep

```

1   MFMNKSQSG  KGLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILK  LK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREED  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

m306.seq (partial)

```

1   ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCmAwAA  CCAGCYTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCAGG
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAAGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCTCAACA  GCGGCAGCAT  CGAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

702

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
 701 GCGGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)
 1 ..GLFFGLILAT VIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPXNQXK
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
 101 EREEPDQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
 151 SKEEKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
 201 IICKWARMPT VRARKGSVPN WQSWAYLPRW SVIRIRDIKRF TGCKAAICLP
 251 MR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

m306.pep	10	20	30	40
	GLFFGLILATVIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPX			
g306	: : : : : : : : : :			
	10	20	30	40
	MFMNKFSSQSGKLSGFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAET EILKLK			
	50	60	70	80
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEPD			
	: : : : : : : : :			
g306	NQPKEDIQPEPADQNALSEPDAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEPD			
	70	80	90	100
	110			
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAKEKVAPKP			
	: : : : : : : : :			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKKAVKPSKETEKKASKEEKAAKEKVAPKP			
	130	140	150	160
	170			
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSVPNWQSWA			
	: : : : : : : : :			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGGGSQRIICKWARMPTNPGARKGSVPNWQSWA			
	190	200	210	220
	230			
m306.pep	YLPRWSVIRIRDIKFTGCKAAICLPMRX			
	: : : : :			
g306	YLPKWSAIRIRDIKFTACKAAICPPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq
 1 ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT
 51 CTTCCGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTTATC
 101 TGAACCAGAG CGGTCAAAT GCGTTCAAAA TCCCGGTTCC GTCGAAGCAG
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCTA AGGAAGACAT
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
 251 AAGAGGCAGA GCAGTCGAT GCGGAAAAAG CTGCCGACAA GCAGCCGTT
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA
 351 AAAGTCGGAC GGACAGGCAG TCGCAAGAA AGCACTGACG GAAGAGCGTG
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
 451 AAACAAGCGG TAAAAACATC TAAAGAAACA GAGAAAAAG CTTCAAAGA
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCGGAAC
 551 AAATCTCAA CAGCGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA


```

601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTCCAAGGT GGTCTGGTAT CAGGCGGGAC
751 ATAAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
1 MFMNKFSQSG KGLSGFFFL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD GQAVRKALT EEREQTVGEK AQKDAETVK
151 KQAVKPSKET EKKASKEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

m306.pep          10      20      30      40
                  GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPKX
a306              10      20      30      40      50      60
                  MFMNKFSQSGKGLSGFFFLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
                  10      20      30      40      50      60

m306.pep          50      60      70      80      90      100
                  NOXKEDIQXPADQNALSEPDAATEAEQSDAEKXADKQPVADKADEVEEKAGEPEREEDP
a306              50      60      70      80      90      100      110      120
                  NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
                  70      80      90      100      110      120

m306.pep          110     120     130     140     150     160
                  GQAVRKALTEEREQTVREKAQKDAETVKXQAVKPSKETEKKASKEKKAAKEKVAPKP
a306              110     120     130     140     150     160     170     180
                  GQAVRKALTEEREQTVGEKAQKDAETVKKQAVKPSKETEKKASKEKKAAKEKVAPKP
                  130     140     150     160     170     180

m306.pep          170     180     190     200     210     220
                  TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY
a306              170     180     190     200     210     220     230     240
                  TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
                  190     200     210     220     230     240

m306.pep          230     240     250
                  LPRWSVIRRDIKRTGCKAAICLPMRX
a306              230     240     250
                  LPRWSVIRRDIKRTGCKAAICLPMRX
                  250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
1 atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
51 cgcagcctgc ggcgggtcaaa aagacagcgc gccgcagcc tctgcccgcg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaatggt cgaatttacc gactatgtgc
251 gcccgaaatc ggcatggcgc gagggcgagt tggacatcaa cgtcttccaa
301 cacaaccctc atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgcgca ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
451 gaccctgcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
501 gatcaaaact aaagacggca tcaatccgct gaccgatcc aaagccgaca
551 tcgcggaata cctgaaaaac atcaaatcgc tcgagcttga agccgcacaa
601 ctgccgcgca gccgcgcgca cgtggatttt gccgtcgta acggcaacta
651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

```

704

```

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc
751 caatggccta aagacgtaac cgaggcctat aactccgacg cgttcaaagc
801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
851 aaggcgacg caaataa

```

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

```

g307.pep
1  MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSADNG AAKKEIVFGT
51  TVGDFGDMVK EQIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFO
101 HKPYLDDFKK EHNLDITEAF QVPTAPLGLY PGKLKSLEEV KDGSTVSAPN
151 DPSNFARALV MLNELGWIKL KGINPLTAS KADIAENLKN IKIVELEAAQ
201 LPRSRAVDVF AVVNGNYAIS SGMKLTEALF QEPSFAYVNW SAVKTADKDS
251 QWLKDVTEAY NSDAFKAYAH KRFEGYKYP A WNEGAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

```

m307.seq (partial)
1  ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
51  CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCTGCC GCATGGAATG
101 AAGGCGCAGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

```

m307.pep (partial)
1  ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA A WNEGAAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng) from *N. gonorrhoeae*:

m307/g307

m307.pep				10	20	30
				QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA		
g307	SGMKLTEALFQEPSFAYVNW	SAVKTADKDS	QWLKDVTEAYNSDAFKAYAHKRFEGYKYP			
	230	240	250	260	270	280

m307.pep		39
	AWNEGAAXX	
g307	AWNEGAAXX	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

```

a307.seq
1  ATGAAAACCT TCTTCAAAC CCTTCCGCC GCCGCACTCG CGCTCATCCT
51  CGCCGCCTGC GGCGGTCAA AAGATAGCGC GCCCGCCGCA TCCGCTTCTG
101 CCGCCGCCGA CAACGGCGCG GCGAAAAAG NAATCGTCTT CGGCACGACC
151 GTCGGCGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA
201 GAAAAAAGGC TACACCGTCA AACTGGTCGA GTTTACCGAC TATGTGCGCC
251 CGAATCTGGC ATTGGCTGAG GCGGAGTNGG ACATCAACGT CTTCACACAC
301 AAACCCATC TTGACGACTT CAAAAAAGAA CACAATCTGG ACATCACCGA
351 AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCGG GGCAAGCTGA
401 AATCGCTGGA AGAAGTCAA GACGGCAGCA CCGTATCCGC GCCCAACGAC
451 CCGTCCAAC TCGCCCGCGT CTTGGTGATG CTCGACGAAC TGGGTTGGAT
501 CAAACTCAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG
551 CCGAAAAACCT GAAAAACATC AAAATCGTCG AGCTTGAAGC CGCGCAACTG
601 CCGCGTAGCC GCGCCGACGT GGATTTTGN C GTCGTCAACG GCAANTACGC
651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT
701 TTGCCTATGT CAACTGGTCT GCCGTCAAAA CCGCCGACAA AGACAGCCAA
751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA
801 CGCGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG
851 GCGCAGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

```

a307.pep
1  MKTFFKTLA AALALILAAC GGQKDSAPAA SASAADNGA AKKXIVFGTT

```

```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLKN  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                                QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
           220      230      240      250      260      270

           39
m307.pep      AWNEGAAX
           |||||
a307      AWNEGAAX
           280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCTT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGCGCT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCCCT  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCCCT  CGATGTACCG  CAAGCCGCG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTGCGTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVFYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RRMVVRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPK
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTCTT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTCGGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGCGCT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGCT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GAAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCCCT  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTGCGTGTT
651 CGGAATCGAT  ACGCCGGATT  CCGCGGAATG  GCAGGGAATG  gCG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTTIA  GLPLQAVLWE  RMMVRRLLI
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADVFHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  XTEMGGVVFP  PVPAMYRKQP
201 TADDIVAHSV  AHALSLFGID  TPDSA EWQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKQPTADDIVAHSAHALSLFGIDTPDSA EWQGM A					
g308	VTEMGGVVFPVPAMYRKQPTADDIVAHSAHTLSLFGIDTPDLA EWQGM ADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTCTT  GTTTTTTAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTTC  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCAG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTGCTGTT
651 CGGAATCGAT  ACGCCGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIA  GLPLQAVLWE  RMMVRRLLI
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXIARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMXR  VTEMGGVVFP  PVPAMYRKQP
201 TADDIVAHSV  AHALSLFGID  TPDSA EWQGM  AD*

```

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRV	FYRIL	GVADN	LYPRL	SDFCF	FTIIA
a308	MLNRIF	YRILGV	ADNLYP	YLSDFC	FTIIA	GLPLQ
	10	20	30	40	50	60
m308.pep	GVKALE	LLRAQ	DVETH	LVVSK	GAEMAR	ASETAY
a308	GVKALX	LLRAQ	DIETH	LVVSK	GAEMAR	SETXYA
	70	80	90	100	110	120
m308.pep	KT	DGMLV	APCSM	R	TLASV	AHGFG
a308	KT	DGMLV	APCSM	R	TLASV	AHGFG
	130	140	150	160	170	180
m308.pep	KT	DGMLV	APCSM	R	TLASV	AHGFG
a308	KT	DGMLV	APCSM	R	TLASV	AHGFG
	190	200	210	220	230	
m308.pep	XTE	MGGV	VFPVP	PAMYR	KPQT	AD
a308	VTE	MGGV	VFPVP	PAMYR	KPQT	AD

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTTC TTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGAACT
201 TTTGCGCGCG CAAGATGTGC AAACGCACCT TGTGGTATCG AAAGCGCGCG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTGCGGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGCGGCGGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACGCG TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RMMVRRLLII
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTTC TTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGAACT
201 TTTGCGCGCG CAAGATGTGC AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTGCGGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGCGGCGGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTIIA GLPLQAVLWE RMMVRRLLII

```

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51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
 101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKQP
 201 TADDIVAHSV AHALSLFGID TPDSA EWQGM AD*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRV	FYRIL	GVADN	LYPRL	SDFCFF	FTIIAGL
	10	20	30	40	50	60
g308-1	MLNRV	FYRIL	GVADN	LYPCL	SDFCFF	FTIIAGL
	10	20	30	40	50	60
m308-1.pep	GVKALE	LLRAQ	DVETH	LVVSK	GAE	MARASE
	70	80	90	100	110	120
g308-1	GVKALE	LLRAQ	DVETH	LVVSK	GAE	MARASE
	70	80	90	100	110	120
m308-1.pep	KTDGML	VAPCS	MRTL	ASVA	HGFG	DNLLT
	130	140	150	160	170	180
g308-1	KTDGML	VAPCS	MRTL	ASVA	HGFG	DNLLT
	130	140	150	160	170	180
m308-1.pep	VTEMG	GVVFP	PVPAM	YRKQP	TADDI	VAHSV
	190	200	210	220	230	
g308-1	VTEMG	GVVFP	PVPAM	YRKQP	TADDI	VAHSV
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTGCGC ACAATTTGTA
 51 TCCGATTTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTGTGCGCT
 101 TGCAGCGCGT TTTATGGGAA AGCGGATGA TGGTACGCGC TTTGATAATC
 151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGANCT
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
 301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGCGCT GCATTGCCAG
 351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
 401 CGCTTGCCCT GGTGCTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
 451 CCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCAGCA
 501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
 551 TGGCGGCGGT GGTGTTTCCC CCTGTTCCTG CGATGTACCG CAAACCGCAG
 601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT
 651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTTII GLPLQAVLWE RMMVRRLLI
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVVH GFGDNLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLDNMXR VTEMGGVVFP PVPAMYRKQP
 201 TADDIVAHSV AHALSLFGID TPDSA EWQGM AD*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIF	YRILG	VADNLY	PYLSDF	CFFTTII	AGLPLQ
	10	20	30	40	50	60
m308-1	MLNRVF	YRILG	VADNLY	PRLSDF	CFFTTII	AGLPLQ
	10	20	30	40	50	60
a308-1	GVKALX	LLRAQ	DIETH	LVVSK	GAE	MARASE
	70	80	90	100	110	120
m308-1	GVKALE	LLRAQ	DVETH	LVVSK	GAE	MARASE
	70	80	90	100	110	120
a308-1	KTDGML	VAPCS	MRTL	ASVV	HGFG	DNLLT
	130	140	150	160	170	180
m308-1	KTDGML	VAPCS	MRTL	ASVV	HGFG	DNLLT
	130	140	150	160	170	180

```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPVPFAMRYRKPQTADDIVAHSAHALSLFGIDTPDSAEOGMADX
              |||||
m308-1      VTEMGGVVFPVPFAMRYRKPQTADDIVAHSAHALSLFGIDTPDSAEOGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

```

g311.seq
1   atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgcgtgcgc gcgcgctttg ggtgttttgg
101 gtttggaacac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggagc gcattctgat tgaaacagtc agggcgggcg gtaaacgggt
201 tgccgtgggtc ggtatcggca tcaatttcgt gctgccaacg gaagtggaaa
251 acgcccgttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgtgtgt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggtaaaaggc gtggacggac gaggcgttct
501 gcacttggaac acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgctgttggg aggcgggaac agccggctca agtgggcgtg
651 ggtggaacaa ggcacgttcg caaccgtggg cagcgcgcgc taccgcgatt
701 tgcgcctttt gggcgcgagc tgggcggaaa aggcggatgg aaatgtccgc
751 atcgtcgggt gcgcccgtgt cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgcga caggctttgg
851 gcatacgcaa ccaactaccg caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct cgcgtcgtcg
951 cagttgcggc acggcggtta cggttgacgc gctcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggtt
1151 gcggctcgat aatgatgatg caccgcccgt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcggcgcgg cgaaagtccg
1251 cgaagccctg ccgcctgcat ttttgcgga aaataccgtg cgcgtggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

```

g311.pep
1   MFSFGWAFDR POYELGSLSP VAALACRRAL GCLGLETLQIK WPNDLVVGRD
51  KLGGILITV RAGGKTAVV GIGINFVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LLAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVHLHLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLEGGN SRLKWAVVEN GTFATVGSAP YRDLSPLGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNR AGKRYPFPTT TGNASGMM DAVCGSIMM HGRLKEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

```

m311.seq (partial)
1   ATGTTCAAGT TTGCTGGGT GTTGACCGG CCGCAGTATG AGTTGGGTTT
51  GCTGTCGCCT GTTGCGCAG TGGCGTTCG GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCATATTAG TGGCCCAATG ATTTGGTTGT CCGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
301 CCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CGTGnCGAAG CCGCGGGATT

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710

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401 CGGAACGTTT TCTGCTGTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAG ACGGCACGTT CGCAACCGTC GGTCAGCGCG CGTACCgCGA
501 TTTGTGCGCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TGCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCCGACC
701 GCTGGTCAA CGCCTTGGG AGCCGCCGCT TCAGCCGCAA CGCyTGCgTC
751 GTCGTCAGTT GCGGCACGGC GGTAACGGT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCGG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCGT CCGAACCGCC AACCTCAACC GGCACGCCG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTCGCGC TCGGTTATGA TGATGCACGG GCGTTTGAAG GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATT CCGCGCGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGG GCGGAAAATA CCGTGCGCGT
1101 GCGGACAAC CTCGTCATT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGAATA TGAACAT....

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
  1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
 51 KLGGILIETV RTGGKTAVV GIGINFLPX EVENAASVQS LFQTASRRGN
101 ADAVLLXXX XXXXEISLR SDXRPVSXK RRDSEFLLL DGGNSRLKWA
151 WVENGTATV GSAPYRDLSP LGAWEAKAD GNVRIVCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTGNV ASGMMDAVCG SVMMHGRLK EKTGAGKPD VIITGGGAAG
351 VAEALPPAFL AENTVRVADN LVIYGLNMI AAEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311

      10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRDKLGGILIETV
          10      20      30      40      50      60

      70      80      90      100     110
m311.pep RTGGKTAVVVGIGINFLPXEVENAASVQSLFQTASRRGNADAAVLLXXX-----
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKTAVVVGIGINFLPKEVENAASVQSLFQTASRRGNADAAVLLLETLAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXX
g311      YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDGRGVLHLETAEGEQTVVS
          130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep XEISLRSDXRPVSXKRRDSEFLLLDGGNSRLKWAWVNGTFATVGSAPYRDLSPLGAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      GEISLRPDNRSVSVKRPDSEFLLLEGGNSRLKWAWVNGTFATVGSAPYRDLSPLGAE
          190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCVCGEFKKAQVQEQELARKIEWLPSSAQALFGIRNHYRHEEHGSDR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      WAEKADGNVRIVGCVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHEEHGSDR
          250     260     270     280     290

```


711

```

                240      250      260      270      280      290
m311.pep      WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR
                |||||
g311          WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR
                300      310      320      330      340      350

                300      310      320      330      340      350
m311.pep      HAGKRYPFPTTTGNVAVSGMMDAVCGSVMMHGRLEKKTGAGKPVVDVITGGGAAKVAEA
                |||||
g311          PAGKRYPFPTTTGNVAVSGMMDAVCGSIMMHGRLEKKTGAGKPVVDVITGGGAAKVAEA
                360      370      380      390      400      410

                360      370      380      389
m311.pep      LPPAFLAENTVRVADNLVIYGLLNMIAAEGREYEH
                |||||
g311          LPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
                420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAC   GCAAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAACCGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTCGT  GCTGCCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTGCT  GGAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTGCAA  TATGCGCGGG ACGGATTGCG GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC  GTGGACGGAC AAGGCGTTCT
501 GCACTTGGA  ACGGCAGAGG GCAAACAGAC GGTCGTCAGC GGCGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTCCG  TGCCGAAGCG GCGGGATTCT
601 GAACGTTTTC TGCTGTGGA  CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAAC  GGCACGTTCT CAACCGTCGG TAGCGCGCCG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGTT  GCGCCGTGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAATCG  AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGAAG  AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGCAGCCG CCGCTTCAGC CGCAACGCCT GCGTCGCTGT
951 CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTCACCAGT GACGGACATT
1001 ATCTCGGGGG AACCATCATG CCCGGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCCGAA CCGCCAACT  CAACCGGCAC CGCGGTAAAG GTTATCCTTT
1101 CCCGACCACA ACGGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCGGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GGCGGCGCGG CAAAAGTTGC
1251 CGAAGCCTG  CCGCCTGCAT TTTTGCGCGA AAATACCGTG CGCGTGGCGG
1301 ACAACCTCGT CATTACGGG  CTGCTGAACC TGATTGCCGC  CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGILITV   RTGKTVAVV  GIGINFLPK  EVENAASVQS LFQTASRRGN
101 ADAAVILETL LAELDAVLLQ YARDGFAPFV AEYQANRDH  GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLLE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
201 ERFLLDGGN  SRLKWAVVEN GTFATVGSAP YRDLSPGAE WAEKVDGNVR
251 IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFRS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRH AGKRYPFPTT TGNVAVSGMM DAVCGSVMMH HGRLEKKTGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFDRLPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV					
a311	MFSFGWVFDRLPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADAVALXXXXXX----					
a311	RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADAVALLETLLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVDGQGVLLHLETAEGKQTVVS					
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDXRPVSVXKRRDSEFLLLDGGNSRLKWAWVNGTFATVGSAPYRDLSPLGAE					
a311	GEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVNGTFATVGSAPYRDLSPLGAE					
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPPEHGS DR					
a311	WAEKV DGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHPPEHGS DR					
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSRFRSRNACVVVSCGTAVTVDA L TDDGHYLG GTIMPGFHLMKESLAVRTANLNR					
a311	WFNALGSRFRSRNACVVVSCGTAVTVDA L TDDGHYLG GTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPV DVIITGGGA AKVAEA					
a311	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPV DVIITGGGA AKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPFAFLAENTVRVADNLVIYGLLN MIAAEGREYEH					
a311	LPFAFLAENTVRVADNLVIHGLLN LIAAEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GAAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACCACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCT GATGTTCACT TTCGGCTGGG CGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGGGCA CTGCGTGCC GCGCGCTTT
501 GGGGTGTTTG GGTTCGAAA CGCAAATCAA GTGCCCAAAC GATTGTCG
551 TCGGACGCGA CAAATTGGGC GCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAAACCGG TTGCCGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTCAGTC GCTGTTTCAG ACGGCATCGC
701 GGCGGGGCAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGCGGAA
751 CTGGGCGCGG TGTTCGAAAC ATATGCGGAA GAAGGTTTCG CGCCATTTTT

```

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGGCGGACGG CGAAACCGTG TGGCAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGGTT TGCACCTGGA AACGGCAGaa ggCGAACAg cggtcGtcag
951 cggcGaaaTC AGccTGCGGc CCGacaacag gtcggtttcc GTgccaagc
1001 gGccggaTTC GgaacgttTT tTGCTgttgg aaggcgggaa cagccggctc
1051 aAGTGGcggt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGcGCC
1101 gtaCCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAAAT CAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCga
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAAC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCTT TCCCGACCAC AACGGGCAAC GCCGTCGCAA CGGCATGAT
1551 GGACGCGGTT TCGGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTVLKPSHWR VLAELADGLP QHVSQAREA DMKPQOLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPOY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGDRDLG GILLETVRAG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVDDG
301 RGVHLHLETAE GEQTVVSGEI SLRPDNRSVS VPKRPDSERF LLEGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAAL GIRNHYRHE EHGSDRWENA LGSRRFRSNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMGPF HLMKESLAVR TANLNRPAKG
501 RYFPPTTTGN AVASGMMDAV CGSIMMHGR LKEKNGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGTTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGGCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACCGGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGGCGC CATTGGCGGT
201 TTTGCATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTCAGAA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGACCGC GCCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGGTGC GGCAGCGCTT
501 GTCGCGTTTA GGTGTTGATG TGCAGATTAA GTGGCCCAAT GATTGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTGGA AACGGCAGAG GGCAACAGA CGGTCGTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTTC GTGCCGAAGC
1001 GCGGGGATTG GGAACGTTTT CTGCTGTTGG ACGCGGCGAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCCTGTGTT GCGGAGAAAT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCga
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAAC TCAACCGGCA CGCCGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCAA CGGCATGAT
1551 GGATGCGGTT TCGGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACGGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDRFPQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILLETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVGDG
301 QGVHLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAWVENGTF ATVGSAFYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQQLARKI EWLPSAQAL GIRNHYRHPE EHGSDRWFNA LGSRRFRSNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFPTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

	10	20	30	40	50	60
m311-1.pep	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m311-1.pep	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m311-1.pep	GRGRQGRKWSHRLGECLMFSFGWVDRFPQYELGSLSPVAACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRFPQYELGSLSPVAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m311-1.pep	DLVVGRDKLGGILLETVRTGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGILLETVRAGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m311-1.pep	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
g311-1	AVLLETLLAELGAVLEQYAEAGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m311-1.pep	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLDGGNSRLKWAWVENGTF					
g311-1	RGVHLHLETAEGEQTVVSGEISLRPDNRVSVPKRPDSERFLLLEGGNSRLKWAWVENGTF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m311-1.pep	ATVGSAFYRDLSPPLGAEWAEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
g311-1	ATVGSAFYRDLSPPLGAEWAEKADGNVRIVGCAVCGESKKAQVQEQQLARKIEWLPSSAQAL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m311-1.pep	GIRNHYRHPEEHGSDRWFNALGSRRFRSNAACVVVSCGTAVTVDALTDGHHYLGTTIMPGF					
g311-1	GIRNHYRHPEEHGSDRWFNALGSRRFRSNAACVVVSCGTAVTVDALTDGHHYLGTTIMPGF					
	430	440	450	460	470	480
	490	500	510	520	530	540
m311-1.pep	HLMKESLAVRTANLNRHAGKRYFPFPTTGNASGMMDAVCGSVMMHGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYFPFPTTGNASGMMDAVCGSIMMHGRLEKKTGAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	

```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
              |||||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTTCG GGTTCACAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTCGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGCGCA GTGGCGTGCC GGCGCGCCTT
501 GTCGCGTTTG GGTTCGAAA CGCAATCAA GTGCCAAAC GATTGGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACCGCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGAAA TGCCGATGCC GCGGTGTGTC TGGAACGCTT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGACGCGA
901 CAAGGCGTTC TGCACTTGGG AACGCGAGAG GGCAACAGA CGGTCGTCAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGCGGATTG GGAACGTTT CTGCTGTTGG ACGCGGCGAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGAATA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGSTGGATG
1151 GAAATGTCGG CATCGTCGGT TGGCGCGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACTGTATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTCGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACGCG GCTGTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTVLKPSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECMLFS FGWVFDPRQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGDRKLG GILIEVTRTG
201 GRTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVILLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVVDG
301 QGVHLLETAE GKQTVVSGEI SLRSDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAAL GIRNHRYRHE EHGSDFWFA LGSRRFRSNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYPFPTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

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a311-1/m311-1 98.5% identity in 591 aa overlap

```

              10      20      30      40      50      60
a311-1.pep  MTVLKPSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              |||||
m311-1      MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              10      20      30      40      50      60

              70      80      90      100     110     120
a311-1.pep  LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              |||||
m311-1      LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              70      80      90      100     110     120

```

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGEC	LMFSGFWV	FDRPQYELGSLSPVAAVACRRALSRLGLKTQIKWPN			
m311-1	130	140	150	160	170	180
	GRGRQGRKWSHRLGEC	LMFSGFWV	FDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPN			
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGIL	IETVRTGGKT	VAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA			
m311-1	190	200	210	220	230	240
	DLVVGRDKLGGIL	IETVRTGGKT	VAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA			
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGV	VDG				
m311-1	250	260	270	280	290	300
	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGV	VDG				
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSE	RFLLLDGGNSRLKWAVV	ENGTF			
m311-1	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSE	RFLLLDGGNSRLKWAVV	ENGTF			
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSP	LGAEWAEKVDGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL				
m311-1	370	380	390	400	410	420
	ATVGSAPYRDLSP	LGAEWAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL				
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHP	EEHGS	DRWFNALGSR	RRFSRNACVVVSCGTAVTVDALTD	DGHYLG	GGTIMPGF
m311-1	430	440	450	460	470	480
	GIRNHYRHP	EEHGS	DRWFNALGSR	RRFSRNACVVVSCGTAVTVDALTD	DGHYLG	GGTIMPGF
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVM	MMHGRLKEKTGAGKP				
m311-1	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVM	MMHGRLKEKTGAGKP				
a311-1.pep	550	560	570	580	590	
	VDVIITGGGA	AKVAEALPPAFLAENTVRVADNLVIHGLLN	LIAAEGGESEHTX			
m311-1	550	560	570	580	590	
	VDVIITGGGA	AKVAEALPPAFLAENTVRVADNLVIYGLLN	MIAAEGREYEHIX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTAccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggctcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCTCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CAAAATCGT CGTGTTCTGC AACGCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTCGCCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGT CGTGGCACC GACCCCGGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCGTC TGCTCCGTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTC GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGTC A CCGGGGCGGC AGGATTCCCC CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMWADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGC AKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCETH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGCGCA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTCGCcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTC AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGTGCGG
551 CTAAAATTGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTWTGGCG
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
651 CCCAGGTGTC GTAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAACTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCGCGCA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTGAC TTGTGCGCGA CCCCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGCGG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCGTTTG TTCGGTCGGC TTGGATATGA TTGCGGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAT GATCAACAGC AAAACCACTG CCGTGCCAT TATTCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CaGGTCGAG TTCGGCGGCT TGTTGGgCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTG GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMWADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCXSIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGC AKIVVFC NAVEDNPFXA
201 GAFHGSGDAV INVGVSGPV VKAALENS DA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCETHGTTA
301 ALALLNDAVK KGGMMASAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLGYAPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/q312

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMVADQNFVDVRTITITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT					
g312	MSIQSGEILETVKMVADRNFDVRTITITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV					
g312	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVLLIRSIPEAMKTTDIVCXSNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	QKGMSPSDEVLLIRSVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKIVVFCNAVEDNPFXXAGAFHGSG--DAVINVGVS GPGVVKAALENSDATTLTEVAE					
g312	FGCAKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVS GPGVVKAALENSDAVSLTEVAE					
	190	200	210	220	230	240
	240	250	260	270	280	290
m312.pep	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
g312	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFNRRGGRI PAPVQSMKNX					
g312	YAPVMPAKEGSCEVFNRRGGRI PAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGCGCA	AATTTTAGAA	ACCGTCAAAA	TGTTTGCCGA
51	CCAGAATTC	GATGTCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAGAGACT	GGTGGCGACA	GCAAAATATC	TGTCTGCCAA
201	ATACGCGGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAAGCT	GGCGCAACT

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```

301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAATCGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCCGCGT
651 ATCCGCGCCG GGTGTCGTAA AAGCCGCGTT GGAAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CGGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGCGCG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCCGGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGCGGACA CACCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATCCCG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGGT AAAAGAAGGC TCATGCGAAG
1301 TGTTGCTCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
1  MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP VVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCETH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

```

m312.pep      10      20      30      40      50      60
MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISSDINVLNQNINIKITTVGKDLVTT
|||||
a312          10      20      30      40      50      60
MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISTDIDVLNQNINIKITTVGKDLVAT
|||||

m312.pep      70      80      90     100     110     120
AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV
|||||
a312          70      80      90     100     110     120
AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV
|||||

m312.pep     130     140     150     160     170     180
QKGMSPSDEVLIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETVKRTAEITPEG
|||||
a312         130     140     150     160     170     180
QKGMSPSDEVLIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
|||||

m312.pep     190     200     210     220     230
FGCAKIVVFCNAVEDNPF XAGAFHGS G--DAVINVGVS GPGVVKAALENS DATTLTEVAE
|||||
a312         190     200     210     220     230     240
FGCAKIVVFCNAVEDNPF MAGAFHGS GEADAVINVGVS GPGVVKAALENS DATTLTEVAE
|||||

m312.pep     240     250     260     270     280     290
VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCETH
|||||
a312         240     250     260     270     280     290
VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCETH
|||||

```

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	250	260	270	280	290	300
m312.pep	300	310	320	330	340	350
	GTAAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTAAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
m312.pep	360	370	380	390	400	410
	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
m312.pep	420	430	440			
	YAPVMPVKEGSCEVFVNRRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

```

g313.seq
1  atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
51  tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcgatg
101 ccgccaaagg tttggttgcc gttttgcttg cagcgtgct tcaagaaccg
151 ctcggtttat ccgacagcgc aatcgccgcc gtcgactcg ccgcgctggt
201 cgggcatatg tggccggtgt ttttcggatt taaggcgccg aaaggcggtg
251 caacggcatt gggcggtgct ctggcactct ctctgcaac tgccttggtc
301 tgcgcgttga tttggcttgt gatggcatte ggcttcaaag taccctccct
351 tgccgcgctg gtcgccacaa ccgcgcgccc ccttgccgca ctgtttttta
401 tgccgcacat ttcttggtat ttcgcaaccc tcgcaatcgc catattggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaag gcaagaaaag
501 caaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

```

g313.pep
1  MDDPRTYSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAIILV
151 LLRHKSNILN LIKGKESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

```

m313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCGCAAC TGCCTTGCTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTC GGCTTCAAGG TGCTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTCCGCCGA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGCGGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

```

m313.pep
1  MDDPRTYSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
151 LFRHKSNIVK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRS GKKKAAALTLLGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
g313	MDDPRTYGSNPGATNVLRS GKKKAAALTLLGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS W V W A T V A I A L L V L F R H K S N I V K L L E G R E S K I G G S R X					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNILNLIKGKESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

```
a313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTGGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCACAAC TGCCTTGTC
301 TGGCGTGA TTTGGCTTGT GATGGCATTC GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCCCC CCTTGCCGCA CTGTTTTTTA
401 TGCCGCATAC TTCTTGATT TTCGCAACCC TCGCAATCGC CATATTGGTG
451 TTGCTCCGCC ATAAGAGCAA CATCCTCAAC CTGATTAAAG GCAAAGAAAG
501 CAAAATCGGC GAAAAACGCT GA
```

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

```
a313.pep
1  MDDPRTYGS NPGATNVLRS GKKKAAALT LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGV LALSPPTALV
101 CALIWLVMF GFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNILN LIKGKESKIG EKR*
```

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRS GKKKAAALTLLGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
a313	MDDPRTYGSNPGATNVLRS GKKKAAALTLLGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPPTALVCALIWLVMF GFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS W V W A T V A I A L L V L F R H K S N I V K L L E G R E S K I G G S R X					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNILNLIKGKESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
1   atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgattgtgtt
51  cacgctgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101 cctttaccaa ggcggcaaca cagccggcgc cgggctgaa gccttacaat
151 gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttaca
201 ctgccactct caaatgattc gtccgttccg tgcggaacc gagcggtacg
251 gtcattactc tgttgccgga ggtcggttt acgaccatcc gttccaatgg
301 gggtccaaac gtaccgggcc tgatttggca cgtgtgggcg gccgctattc
351 cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401 agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451 gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501 cagtgatgag gaaattgca aagcgctga ggctttggca aacaaatccg
551 agctggatgc tgtagtcgcc tatctgcaag gattgggtct ggctttgaaa
601 aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
1   MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVAVA YLQGLGLALK
201 NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
1   ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGGCAACA CAGCCGGCGC CGGGCTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTG GTCCGTTCGG TCGGAAACC GAGCGTTACG
251 GTCATTACTC TGTGCGCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
1   MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVAVA YLQGLGLALK
201 NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

m401/g401

	10	20	30	40	50	60
m401.pep	MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
g401	MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m401.pep	IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW					

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```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWRLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
g401      HRIHLLNPRDVPESNMPAFWRLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGCGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAA
151 GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGGAACCC GAGCGTTACG
251 GTCATTACTC TGTTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAEEK IGVLVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGGRYSDEW HRIHLLNPRD VPESNMPAF WRLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

          10      20      30      40      50      60
m401.pep  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
a401      MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
          10      20      30      40      50      60

          70      80      90      100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          |||||
a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWRLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
a401      HRIHLLNPRDVPESNMPAFWRLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttccttacc ggatTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGttttcgTT CGCagcAcag tccgtgcctc aggCATTTTC atttattcctt
151 gcctGttttc tgACCGgtat cgccgtcggc gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCcctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATT TCCCACTTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttggtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTtCT GCTGctgtcc
551 cTTTGTtTTg tacaCTGtTC CAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTCCTTAC TGCCGGATTc
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTtTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCGCTT TTGcAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTTCGACCT GATTTTGATG AATTGCACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCTGT TGAGTGCgGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCCG
1201 CATgetTTTg CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCcct AATAAAGAAC
1301 TGCTCaagca aCGCCTTTcc cgTTGATT TGGCCGAAAG CGGCAGgcac
1351 gtATTTGACA GCAGACCGT GGATGCTGCA GCACAAAAGG TTGtctctCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNL SVINMLSFLT GLLSLGIEVL WRMFSFAAQ SVPQAFSFL
51  ACFLTGLIAGV AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IPITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGYANT DIFNSVNGIE RAYLLPSLKS GIRRI FVVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRL
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSSTVDA AOKVVSRLI RMTEPSAGAE VITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGChTTC
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACCCTT
151 GCCTGTTTTc TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTcAsa sGGTTGATT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAmCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTtTTG TACACTGTTC CAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcYtAC TGCCGGATTc

```

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651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAgGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTATTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAACTCT GGCATACGCC
851 GCATTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTTGCTT
901 GCCATTCGGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAAT CGCCCCGCTT TGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCCT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL
51 ACFLTGIAGV AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICKIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAynt DVFNSVNGIE RAYLLPSLKS GIRRIFFVVL STGSWARVLS
301 AIPQMISMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYARYRGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSVTDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPOAFSFTLACFLTGIAGV
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVPOAFSFTLACFLTGIAGV
	10 20 30 40 50 60
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVX
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVR
	70 80 90 100 110 120
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQIYLLICKIS
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQIYLLICKIS
	130 140 150 160 170 180
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDRDRLIENKHGIVAVY
	190 200 210 220 230 240
m402.pep	HRDGDKVYGANVYDGAyntDVFNSVNGIERAYLLPSLKS GIRRIFFVVLSTGSWARVLS
	250 260 270 280 290 300

726

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1 ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCTTTC
51 TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGCTCTG TGGGTAAAGGA
101 TGTTCCTCGT GCGACGATCA TCCGTGCCTC AGGCATTTTT ATTTACTCTT
151 GCCTGTTTTT TGACCCGGTAT CGCCGTCGGC GCGTATTTTG GCAAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGCACTT TTAGTTTGTG GTGCTGCGTG GTTGTTGACG
301 GGTTCCTCCG GCTTCGTCCA CCACGCCGGT ATCTTTCATTA CCGTGTCTGC
351 CGTCGTCAGA GGGTGTGATT TCCCCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCACTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTTCCT GCTGCTGTCC
551 CTGTGTTTTG TACTACTGTC CAAAAAAGTC TCCGACTGAA TGCAGTGTCC
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTCTAC TGCCGGATTG
651 TGTCCTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATATT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACACGCGCGC ATACATAACC GTGATTCTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCCT CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGCGATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAA TCGCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATACGGGTA GCGAATGGCT CGCTGCCCAT
1051 CCTGATGAAA AATTGACCTT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCATATCC ACCAACCTGT TGAGTGCGGA ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGTT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CATCGCCCGT ACACAGTATT CCGTATGCAT ACCGTATAGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAAG CGGCAGGCAC
1351 GTATTTGACA CGACGACCGT GGATGCTGCA GCACAAAAGG TTGCTCTCTG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTCGGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

1 MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSAQAQ SVPQAFSFTL

51 ACFLTGIavg AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSGWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQORLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

m402/a402 99.0% identity in 497 aa overlap

m402.pep	10	20	30	40	50	60
	MDIVNTKPN	SLIYMXSFL	SGLLSLGIE	VLWVRMFSA	AQSVPAQAF	SFTLACFLT
a402	MDIVNTKPN	SLIYMLSFL	SGLLSLGIE	VLWVRMFSA	AQSVPAQAF	SFTLACFLT
	10	20	30	40	50	60
m402.pep	70	80	90	100	110	120
	AYFGKRICRS	RFVDIPFIGQ	CFLWAGIADF	LILGAAWLLT	GFSGFVHHAG	IFITLSAVVX
a402	AYFGKRICRS	RFVDIPFIGQ	CFLWAGIADF	LILGAAWLLT	GFSGFVHHAG	IFITLSAVVR
	70	80	90	100	110	120
m402.pep	130	140	150	160	170	180
	XLIFPLVHHV	GTGDNKSGRQ	VSNVYFAXV	AGSALGPVL	IGFVILDFL	STQIYLLICK
a402	GLIFPLVHHV	GTGDNKSGRQ	VSNVYFANV	AGSALGPVL	IGFVILDFL	STQIYLLICL
	130	140	150	160	170	180
m402.pep	190	200	210	220	230	240
	AAVPLFCTLF	QKSLRLNAVS	VAVSLMFGIL	MFLLPDSVFQ	NIADRPDRLI	ENKHGIVAVY
a402	AAVPLFCTLF	QKSLRLNAVS	VAVSLMFGIL	MFLLPDSVFQ	NIADRPDRLI	ENKHGIVAVY
	190	200	210	220	230	240
m402.pep	250	260	270	280	290	300
	HRDGDKVYVG	ANVYDGAYNT	DFNSVNGIER	AYLLPSLKS	GIRRIFFVGL	STGSGWARVLS
a402	HRDGDKVYVG	ANVYDGAYNT	DFNSVNGIER	AYLLPSLKS	GIRRIFFVGL	STGSGWARVLS
	250	260	270	280	290	300
m402.pep	310	320	330	340	350	360
	AIPMQSMIVAE	INPAYRSLIA	DEPQIAPLLQ	DKRVEIVLDD	GRKWLRRHP	DEKFDLILM
a402	AIPMQSMIVAE	INPAYRSLIA	DEPQIAPLLQ	DKRVEIVLDD	GRKWLRRHP	DEKFDLILM
	310	320	330	340	350	360
m402.pep	370	380	390	400	410	420
	NTTWYWRAYS	TNLLSAEFLK	QVQSHLTPDG	IVMNTTHSP	HAFATAVHSI	PYAYRYGHMV
a402	NTTWYWRAYS	TNLLSAEFLK	QVQSHLTPDG	IVMNTTHSP	HAFATAVHSI	PYAYRYGHMV
	370	380	390	400	410	420
m402.pep	430	440	450	460	470	480
	VGSATPVVFP	NKELLQORLS	RLIWPESGRH	VFDSSTVDAA	AQKVSRMLI	QMTEPSAGAE
a402	VGSATPVVFP	NKELLQORLS	RLIWPESGRH	VFDSSTVDAA	AQKVSRMLI	QMTEPSAGAE
	430	440	450	460	470	480
m402.pep	490					
	VITDDNMIVE	YKYGRGIX				
a402	VITDDNMIVE	YKYGRGIX				
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGCGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTCTCTC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAGC AACATAGACA
951 AGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGRSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGQP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAATGGT CGATTCTCTC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAGC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK

```

```

51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYETT AETTSGLTGT LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGPX *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406 . pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAQVMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAQVMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRIYETTAETTSGLTGT					
m406	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRIYETTAETTSGLTGT					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406 . pep	LTSLSTLNAPALSRQSDGSGSRSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	:					
m406	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406 . pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDPSDIQPYGNHTGNSAPSVEADN					
	:					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDPSDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGPX					
	:					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACCGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

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501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
1  MQARLLIPIIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAANK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTGG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
301 SHEGYGYSDE AVRRHRQGPX *

m406/a406 98.8% identity in 320 aa overlap

m406.pep      10      20      30      40      50      60
MQARLLIPIILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKDMDLQALHGR
|||||
a406          10      20      30      40      50      60
MQARLLIPIILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKDMDLQALHGR

m406.pep      70      80      90      100     110     120
KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGG
|||||
a406          70      80      90      100     110     120
KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGG

m406.pep     130     140     150     160     170     180
LTSLSTLNAAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF
|||||
a406         130     140     150     160     170     180
LTSLSTLNAAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF

m406.pep     190     200     210     220     230     240
FLRGIDVVSFANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
|||||
a406         190     200     210     220     230     240
FLRGIDVVSFANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL

m406.pep     250     260     270     280     290     300
IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN
|||||
a406         250     260     270     280     290     300
IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIQPYGNHMGNSAPSVEADN

m406.pep     310     320
SHEGYGYSDEVVRHRQGPX
|||||
a406         310     320
SHEGYGYSDEAVRRHRQGPX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
1  atgggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc agggttgcgt

```

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101  tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgagggg
151  cagctgggtc atgtcggtcg agccgatgga gaagccgctg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggt cagaccattc tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgtgcccgc
501  cgaccagggt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcy gataaacgca tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacy tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651  taattttccgc tttcagttcg tcgtcttgtt tgtcaaatc caacaaggct
701  ttcgggtgga tgcgatttgc gcggttgatg ataaattcca tacgcgccaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  ttcgcgacgt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccggt
901  atcgccctcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaataccacg ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgcgc cggttgggtc cgatggcgga
1051 agcacggttc atcacgggtt cccaatccgg atcggtcgat tcggtaacca
1101 gtacgtcgcc ggcttcgacy gaatccatct cggaagcatt ttaatacagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgacaaa
1201 gacgggtttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttgagg tttgacggtt tcggggcggg cttgcaggat gttaggtttg
1301 ccgtccagcg cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgctg agtggtccaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgagg tcttcttcgg ggaacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcgggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLTA DT DIFVLLAAGG DGKMQHHFDG RFAVFKRFHG QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFFQAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAADQV GVFGVFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVFKF QQGFVRDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDFFDGCFWH IVQGDIGNLY VQQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHALALD FLTDGTTFAQ
401 DGEFFAVDGV AQAFAAFLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVQC LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFVRVDRALY DVFAQTVRGG NKDDL VVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggtcggac sggccttgac cgcagatgcc gacatatttg tctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgagggg
151 cagttgggtc atgtcggtcg agccgatgga gaagccgctg aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacggttgy caaccattc tcattcgagg cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgcgcg
501 cgaccagggt ggcgtattcg ttggatttga agtcggacat acggacgatg
551 gttttacgcy gataaacgca tgcggccaat gtcgccacgc cttcggcgat
601 tttatcgacy tagaagtcga caggggacgc gtaaccggcg atacggcggg
651 taatttcgcg ttttaattcg tcgtcttgtt tgtcaaatc caacaargct

```

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttgcgaa gctgaatgcg agtcgggat
801 tgccgacgtt catcatgact tttacagggt ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttg gcacaggata cggtaacttc ttgaccgttt ttcagcaatt
951 cggttgcatt gccgcagcgg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcagg acggccgcgg cggttggtaa cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcgggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc ttaatacagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaagcg gcgcagggtg cggttgcctt
1251 cttcttggga ttttacggtt tcgggacggg cttgcaggat gtagagtttg
1301 cgtccaagc cgctcgctcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgcaa ctcagtaatt tcttcgctcg
1401 taatggagaa gcggttgagg tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgttttga
1501 acccatggtt ttacgcagga tggcgggctt gcccggtttg agcgtgggtt
1551 tgaacacatr aaattcgctc gggttgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

m501.pep

```

1  MVGXALTADA DIFVLLAAGG DGKVQHFDG RFAVVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFVEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QXFGVDTDL AVDDKFHTRQ
251 ADAFAQQVGE AECEFGIADV HHDFYRCFRH IVXGDIENLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351 STFHHGFPIR IGHVGNFYVA GFDGIHLGSI FNQAHLLALD FLTDGAFAFX
401 YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVAVAVAS PFDIHRAAVV
451 FFDGQCVMRQ LSNFFVGNGE AVAVFLGDDI VGYGFTGFCF VGKNHFDVFX
501 THGFTQDGLL ARFERGFEXH KFRVRDRTLY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRFAVVKRFGYQAAVAVETEGQLGHVVRADG					
g501	MVGRTLTADTDIFVLLAAGGDGKMQHFDGRFAVVKRFGHQAAVSVAEAGQLGHVVRADG					
	10	20	30	40	50	60
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
g501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQCLNHCFCGFAQSADERNHDFDVG					
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
g501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQCLNHCFCGFAQSADERNHDFDVG					
	70	80	90	100	110	120
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFVEVGH					
g501	QTHFVTNAFQGFQGETVFEALGNITRRTTEAQHRVFFMRVYVAADQVGVFVGFVEVGH					
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFVEVGH					
g501	QTHFVTNAFQGFQGETVFEALGNITRRTTEAQHRVFFMRVYVAADQVGVFVGFVEVGH					
	130	140	150	160	170	180
m501.pep	TDDGFTRINRCQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL					
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL					

733

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAAADNFRFQFVVLFVKFQQGFVRVDADL
	190 200 210 220 230 240
	250 260 270 280 290 300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHDFYRCFRHIVXGDIIGNLYVQQTGIDKAG
	: : : : :
g501	AVDDKFHTRQADAFAGQIGEAECFEGIADVHDFDGCFWHIVQGDIGNLYVQQAIDKAG
	250 260 270 280 290 300
	310 320 330 340 350 360
m501.pep	IAFGTGYGNFLTTFVQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPPIR
	: : : : :
g501	IAFGTGYGNFLTTFVQEFGRIAAADGRNTQFARDDGGVAGASAAVGHGSGSTFHHGFPPIR
	310 320 330 340 350 360
	370 380 390 400 410 420
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLT DGA AFAXYGFVAVDGEAAQVAVALFLG
	: : : : :
g501	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLT DGT TFAQD GFFAVDGVAAQVAAFFLG
	370 380 390 400 410 420
	430 440 450 460 470 480
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGGCVMRQLSNFFVGNGEAVAVFLGDDID
	: : : : :
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVRVCQLGDFVGNGEAVAVFFGDFD
	430 440 450 460 470 480
	490 500 510 520 530 540
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFEXKFFVRVDRDLYDVFAQTVRGG
	: : : : :
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGFEXIKFFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
	550
m501.pep	NKDDLIVXGFGVEGEHHT
	:
g501	NKDDLIVVAGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

1	ATGGTTCGAC	GGGCCTTGAC	CGCAGATGCC	GACATATTTG	TTCTGCTTGC
51	GGCAGGCGGA	GATGGCAAGG	TGCAGCATCA	CTTTGACGGC	AGGGTTGCGT
101	TCGTCAAACG	ATTTCGGATAC	CAAGCCGCTG	TCGCGGTCTGA	GACCGAGGGT
151	CAGTTGGGTC	ATGTCGTTTCG	AGCCGATGGA	GAAGCCGTCG	AAGTATTGCA
201	GGAATTGTTC	CGCCAATACC	GCGTTGCTCG	GCAGCTCGCA	CATCATAATC
251	AGGCGCAGGC	CGTTTTTGCC	GCGTTCCAAG	CCGTTTTCTT	TCAGGGCTTT
301	GACAACGGCT	TCGGCTTCGC	CCAAAGTGCG	GACGAACGGA	ATCATGATTT
351	CAACGTGGT	CAACCCCAT	TCATCGCGGA	CGCGTTTCAA	GGCTTTGCAT
401	TCCAAGCGA	AACAGTCTT	GAAGTTGTCG	GCGACATAAC	GCGCCGCACC
451	ACGGAAGCCC	AACATCGGGT	TTTCTTCATG	CGGTTCGTAT	ACGTTGCCGC
501	CGACCAGGTT	GGCGTATTCG	TTGGATTTGA	AGTCGGACAT	ACGGACGATG
551	GTTTTACGCG	GATAAACCAG	TGCGGCCAAT	GTCGCCACGC	CTTCGGCGAT
601	TTTATCGACG	TAGAAGTCGA	CAGGGGACGC	GTAACCGCG	ATACGGCGGG
651	TAATTTCCGC	TTTTAATTCG	TCGTCTTGTT	TGTCAAATTC	CAACAAGGCT
701	TTGGGGTGGA	TACCGATTG	GCGGTTGATG	ATAAATTCCA	TACGCGCCAA
751	GCCGATGCCT	TCGCTGGGCA	GGTTGGCGAA	GCTGAATGCG	AGTTCGGGAT
801	TGCCGACGTT	CATCATGACT	TTTACAGGTG	CTTTAGGCAT	GTTGTCCAAA
851	GCAACATCGG	TAATTTGTAC	GTCCAGCAGG	CCGGAGTAGA	TGAAGCCGGT
901	ATCGCCTTCG	GCACAGGATA	CGGTAACCTC	TTGACCGTTT	TTCAGCAATT
951	CGGTTGCATT	GCCGCAGCCG	ACAACGGCAG	GAATACCCAG	TTCCGCGCGC

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1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGGT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTCGCACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT
1251 CTTCTCTGGG TTTGACGGTT TCGGGACGGG CTTCGAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTTCGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGCCT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGATC GACGTTTTTC
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGTCGT AACCAGATTG
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```

1 MVGRALTADA DIFVLLAAGG DGKVQHFFDG RFAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVFKF QQGFVVDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAAFAQ
401 DGFFAVDRKA AQVAAFFLG FDGFGTGLQD VEFVAVAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTVTG
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFFDG	RFAFVKRFGYQAAVAVETEG	QLGHVVRADG			
a501	MVGRALTADADIFVLLAAGGDGKVQHFFDG	RFAFVKRFGYQAAVAVETEG	QLGHVVRADG			
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGF	DNGFGFAQSADERNHDFNVG				
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGF	DNGFGFAQSADERNHDFNVG				
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMR	RFVYVAADQVGVFVGFEVGH				
a501	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMR	RFVYVAADQVGVFVGFEVGH				
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFR	FXFVVLVFKFQQXFGVDTDL				
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFR	FXFVVLVFKFQQXFGVDTDL				
	190	200	210	220	230	240
	250	260	270	280	290	300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRH	IVXGDIIGNLYVQQTGIDKAG				
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRH	IVXGDIIGNLYVQQTGIDKAG				
	250	260	270	280	290	300
	310	320	330	340	350	360
m501.pep	IAFGTGYGNF LTVFQQFGCIAAADNGRNTQFARDDGGVAGT	AAAVGNDGRSTFHHGFPIR				
a501	IAFGTGYGNF LTVFQQFGCIAAADNGRNTQFARDDGGVAGT	AAAVGNDGRSTFHHGFPIR				
	310	320	330	340	350	360

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	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLT DGAAFA XYGFVA VDGEAAQVA VALFLG					
a501	VGHVGNQYVAGFDGIHLGSI FNQAYLALTDFLT DGAAFAQDGF FAVDRKAAQVAAFFLG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m501.pep	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCVMRQLSNFFVGNGEAVAVFLGDID					
a501	FDGFGTGLQDVEFAVQAVASPFDVHRAAVVFFDGGQCVMRQLGDDFFVGNGEAVAVFFGDID					
	430	440	450	460	470	480
	490	500	510	520	530	540
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFEXXKFVRVDRTLYDVFAQTVRGG					
a501	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFIEFVGIDCALYDVFAQTVGXS					
	490	500	510	520	530	540
	550	559				
m501.pep	NKDDLIVXGFGVEGEHHTX					
a501	DKDDLVTGFGIEGEHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

g502.seq

```

1 atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcacctgac
51 cgtcgccgtc gcttccgcac aggcgggcgc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca aaccgtccaa
151 agcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 ggcacggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgggcgc agccccgcgc ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgccgc
451 ctaccaatac atccgcacgc gcttcaaagg cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

g502.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTLRYRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RNAQTQRRR
151 LPIHPHRLQR RQPRRHAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

m502.seq

```

1 atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcacctgac
51 cgtcgccgtc gcttccgcac aggcgggcgc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca amccgtccaa
151 wgcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgacc
201 gggccttttc aaatgggaat acaccaaact t.acaggcaa accatcgteg
251 ggcacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgcgc ccatcctgtc
351 gaacaaarcc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgcccgtca
451 ccaatacatc cgcacggtc tcaaaggcgc caacctcgcc gccatgcagc
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

m502.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51 XXXKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQRRRL
151 PIHPHRLQRR QPRRHAA

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLTPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATTC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTGC
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCCG	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

1	MMKPHNLFQF	LAVCSLT	SVS	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKTQTAHG	TFKILRPGLF	KWEYTS	SPYKQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL	
151	PIHPHRLQRR	QPRRHAA*				

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSYKQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```

1 ATGatGAAAc cgcaCaacct gttccaaATtc CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGGCG GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACCTTCAAAA TCCTGCGCCC
201 GGGCCTCTTC AAATGGGAAT ACACTTTGCC CTACAGACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATTTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATCGGCGGC AGCCCCGCGC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CGGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
601 GCGGTGGACG TGTTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPGLF KWEYTLPIRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```

1 ATGATGAAAC CGCACAACTT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGGCG GGTAGACGCG CTTAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACCTTCAAAA TCCTGCGACC
201 GGGCCTTTTC AAATGGGAAT ACACCAAACC TTACAGGCAA ACCATCGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATCTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCGC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
601 GCGGTGGACG TGTTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPGLF KWEYTKPIRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	LKQFNNDADGISGSFTQTVQSKKKTQTAHG				
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	LKQFNNDADGISGSFTQTVQSKKKTQTAHG				
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPIRQTIVGDGQTVW	LYDVDLAQVTKSSQDQAIGGSPAAILSNKT				
g502-1	TFKILRPGLFKWEYTLPIRQTIVGDGQTVW	LYDVDLAQVTKSSQDQAIGGSPAAILSNKT				
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPIRQTIVGDGQTVW	LYDVDLAQVTKSSQDQAIGGSPAAILSNKT				
g502-1	TFKILRPGLFKWEYTLPIRQTIVGDGQTVW	LYDVDLAQVTKSSQDQAIGGSPAAILSNKT				
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSISF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSISF				
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSISF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSISF				
	130	140	150	160	170	180

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```

                190      200
m502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
               |||||
g502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
               190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATC CTCGCCGTTT GTCCTCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGCGGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCTCTTTT AAATGGGAAT AACTTCGCC TTACAAACAG ACTATTGTCTG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCTG
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGCGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPLGF KWEYTSPLYQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTISIF GGLNTNPQLS RGAFTFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep    MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
m502-1        MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep    TFKILRPLGFKWEYTSPLYQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
m502-1        TFKILRPLGFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep    ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
m502-1        ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                130     140     150     160     170     180

                190     200
a502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
m502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgctcgcatc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaaggcggt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

m503.seq

```

1 atgtccgcac cgccggcatc ggcaaccatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaaaggcgt atccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
151 gccagtgcgg cggaaatgcg ttcgctcaga ccgttgtgtg cgaggaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

m503.pep

```

1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNNF
51 ASAAEMRSLR PLCARNAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

m503/g503

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWIRISLPTRASSATSSTSNNFASAAEMRSLR					
	::					
g503	MSAPASVILFHAASISASSCSGKGVSKIHWIRISLPTRASSETSTSNNFARAAEMRSFR					
	10	20	30	40	50	60
	69					
m503.pep	PLCARNAR					
g503	PLCARNAR					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

a503.seq

```

1 ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT
51 TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
101 TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
151 GCCAGTGCGG CGGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC
201 GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

a503.pep

```

1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNNF
51 ASAAEMRSLR PLCARNAR*

```

m503/a503 100.0% identity in 68 aa overlap

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWIRISLPTRASSATSSTSNNFASAAEMRSLR					
a503	MSAPPASATILFHAASISASSCSGKGVSKIHWIRISLPTRASSATSSTSNNFASAAEMRSLR					
	10	20	30	40	50	60
	69					
m503.pep	PLCARNARX					
a503	PLCARNARX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

g503-1.seq

```

1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT
51 AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGGCAGGTCT TCGGCGGTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTGTTC ATGCCGCTTC
201 GATTTCCGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
251 GGATTCTTT GCCGACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
301 TTTGCCAGAG CGGCGGAAAT GCGTTCGTTG AGACCGTTGT GTGCGAGAAA
351 TGCGCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep
 1 MARSLYREAK TWRIAFITLS KPLIFRKVSC WPANDASGRS SAVAERTAT
 51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
 101 FARAAEMRSF RPLCARNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq
 1 ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
 51 AACGTTATCC AAGCCGTTGA TGTCAAGAA GGTTTCCTGT TGTCAGCGA
 101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
 151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTGTTC ATGCCGCTTC
 201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
 251 GGATTTCCTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
 301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
 351 TGCGCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep
 1 MARSLYREAN TWCIALTSL KPLMFKKVSC CPANDASGRS SAVAERTAT
 51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
 101 FASAAEMRSL RPLCARNAR*

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRIAFITLSKPLIFRKVSCWPANDASGRSSAVAERTATEMSAPSASVI					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFARAAEMRSFRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq
 1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
 51 AACGTTTTC AAGCCGTTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA
 101 ATGATGCGTC GGCAGGTCT TCGCGGTTG CGGAAGAGCG TACGGCAACG
 151 GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTGTTC ATGCCGCTTC
 201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
 251 GGATTTCCTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
 301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
 351 TGCGCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep
 1 MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAERTAT
 51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
 101 FASAAEMRSL RPLCARNAR*

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAERTATEMSAPPASAT					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

g504.seq

```

1   atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacgag catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccatcgtgta ccgcatccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattattttt
551 ggctgaccgg cacgcgcagc ggcttgagc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgcgggtgc gcttttggtc tatctcggct cggatttggt
1101 ggttttgggt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
1151 tattgttttc aaacdcaaaa atccgttttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttcaaaaa cagtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

g504.pep

```

1   MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQPPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKQYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLHS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPPK RAWVLSNKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

m504.seq..

```

1   atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacgag catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccggtttt gcaggaaacag gattattttt
551 ggattaccgg cacgcgcagc ggcttgagc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgtc gggtttgag

```

1051 atgacccgtt ccccggtg cgttttggtc tatctcggct cgggtgctgtt
 1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
 1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgacagc
 1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
 1251 gctcggcaag gacttgaatc atga

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..
 1 ILVQDLPFEEV KLKFFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPFEEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	:					
g504	MLVQDLPFEEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGSDLTFKAWNLGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
g504	YQASFADGGSDLTFKAWNLRDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
g504	MSEGAREKSLKSTLNDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPILQDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI					
g504	DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQQDKMQGYFYEMLYGVMNAALDETIR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
g504	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m504.pep	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK					

743

g504 YLGSVLLVLGTVFMFYVPPKKRAWVLSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq

1	ATATTGGTTC	AGGACTTGCC	TTTTGAAGTC	AAACTGAAAA	AATTCCATAT
51	CGATTTTAC	AATACGGGTA	TGCCGCGCGA	TTTTGCCAGT	GATATTGAAG
101	TAACGGATAA	GGCAACCGGT	GAGAACTCG	AGCGCACCAT	CCGCGTGAAC
151	CATCCTTTGA	CCTTGACGG	CATCACGATT	TATCAGGCGA	GTTTTGCCGA
201	CGGCGGTTTCG	GATTTGACAT	TCAAGGCGTG	GAATTGGGT	GATGCTTCGC
251	GCGAGCCTGT	CGTGTGAAG	GCAACATCCA	TACACCAGTT	TCCGTGGAA
301	ATTGGCAAAC	ACAAATATCG	TCTTGAGTTC	GATCAGTTTA	CTTCTATGAA
351	TGTGGAGGAC	ATGAGCGAGG	GCGCGGAACG	GGAAAAAGC	CTGAAATCCA
401	CGCTGAACGA	TGTCCGCGCC	GTTACTCAGG	AAGGTAAAAA	ATACACCAAT
451	ATCGGCCCTT	CCATTGTTTA	CCGTATCCGT	GATGCGGCAG	GGCAGGCGGT
501	CGAATATAAA	AACTATATGC	TGCCGTTTT	GCAGGAACAG	GATTATTTTT
551	GGATTACCGG	CACGCGCAGC	GGCTTGCAGC	AGCAATACCG	CTGGCTGCGT
601	ATCCCTTGG	ACAAGCAGTT	GAAAGCGGAC	ACCTTTATGG	CATTGCGTGA
651	GTTTTTGAAA	GATGGGGAAG	GGCGCAAACG	TCTGGTTGCC	GACGCAACCA
701	AAGGCGCACC	TGCCGAAATC	CGCGAACAAT	TCATGCTGGC	TGCGGAAAAAC
751	ACGCTGAACA	TCTTTGCACA	AAAAGGCTAT	TTGGGATTGG	ACGAATTTAT
801	TACGTCCAAT	ATCCCGAAAG	AGCAGCAGGA	TAAGATGCAG	GGCTATTTCT
851	ACGAAATGCT	TTACGGCGTG	ATGAACGCTG	CTTTGGATGA	AACCATACGC
901	CGGTACGGCT	TGCCCGAATG	GCAGCAGGAT	GAAGCGCGGA	ATCGTTTCCT
951	GCTGCACAGT	ATGGATGCGT	ACACGGGTTT	GACCGAATAT	CCCGCGCCTA
1001	TGCTGCTGCA	ACTTGATGGG	TTTCCGAGG	TGCGTTCGTC	GGGTTTGCAG
1051	ATGACCCGTT	CCCCGGGTGC	GCTTTTGGTC	TATCTCGGCT	CGGTGCTGTT
1101	GGTATTGGGT	ACGGTATTGA	TGTTTATGT	GCGCGAAAAA	CGGCGGTGGG
1151	TATTGTTTTC	AGACGGCAAA	ATCCGTTTTG	CCATGTCTTC	GGCCGCGAGC
1201	GAACGGGATT	TGCAGAAGGA	ATTTCCAAAA	CACGTCGAGA	GTCTGCAACG
1251	GCTCGGCAAG	GACTTGAATC	ATGACTGA		

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep

1	ILVQDLPF	EVKLKKFH	IDFYNTGM	PRDFASD	IEVTDKATG	EKLERTIRVN
51	HPLTLHG	ITIQASFA	DGGSDLT	FKAWNLD	ASREPVLK	ATSIHQFPLE
101	IGKHKYR	LEFDQFT	SMNVED	MSEGAERE	KS	TLNDVRA
151	IGPSIVY	RIRDAAG	QAVEYK	NYMLPVL	QEQDYFW	ITGTRS
201	IPLDKQL	KADTFMA	LREFLK	DGEGRKRL	VADATKG	APAEI
251	TLNIFAQ	KGYLGL	DEFITSN	IPKEQQDK	MGYFYEM	LYGV
301	RYGLPEW	QQDEARN	RFLLSH	MDAYTGL	TEYPAPML	LQLDG
351	MTRSPGAL	LVYLGS	VLLVLG	TVLMFYV	REKRAWV	LFS
401	ERDLQKE	FPKHVES	LQRLGK	DLNHD*		

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPF	EVKLKKFH	IDFYNTGM	PRDFASD	IEVTDKATG	EKLERTIRVN
a504	ILVQDLPF	EVKLKKFH	IDFYNTGM	PRDFASD	IEVTDKATG	EKLERTIRVN
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADG	GSDDLTFK	AWNLDAS	REPVLKAT	SIHQFPLE	IGKHKYR
a504	YQASFADG	GSDDLTFK	AWNLDAS	REPVLKAT	SIHQFPLE	IGKHKYR
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAERE	KS	TLNDVRA	VTQEGK	KYTNIGP	SIVYRIR
	130	140	150	160	170	180
	DAAGQAVE	YK	NYMLPVL	QEQDYFW	ITGTRS	

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|||||
a504 MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPVLQEQ
      130      140      150      160      170      180
      190      200      210      220      230      240
m504.ppep DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
|||||
a504 DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
      190      200      210      220      230      240
      250      260      270      280      290      300
m504.ppep REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
|||||
a504 REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
      250      260      270      280      290      300
      310      320      330      340      350      360
m504.ppep RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
|||||
a504 RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
      310      320      330      340      350      360
      370      380      390      400      410      420
m504.ppep YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
|||||
a504 YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
      370      380      390      400      410      420

m504.ppep DLNHDX
          |||||
a504      DLNHDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.beq
1 atgtttcgtt tacaattcag gctgtttccc cctttgcgaa ccgccatgca
51 catcctgttg accgccctgc tcaaatgcct ctccctgctg tcgctttcct
101 gtctgcacac gctgggaaac cggctcggac atctggcggt ttacctttta
151 aaggaagacc gcgcgcgcat cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacgggtca aagccgtttt tgcggaaaac gcaaaatgcg
251 gtttggaact tgcccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaag cgttacacgg ctgggaacac gtgcagcagg ctttgacaa
351 gggcgaaggg ctgctgttca tcacgccgca catcggcagg tacgatttgg
401 gcggacgcta catcagccag cagcttcctg tccacctgac cgccatgtac
451 aagccgcca aaatcaaaag gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cggccaccgg catacaaggg gtcaaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaccac
601 gtcccttctc cgcaggaagg cggcggcgtg tggcgcgatt ttttcggcaa
651 acctgcatac accatgacac tggcggcaaa attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcccgacgg acaaggcttc
751 gtgttgacac tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1 MFRLQFRLFP PLRTAMHILL TALLKCLSL SLSCLHTLGN RLGHAFYLL
51 KEDRARIIVAN MRQAGLNPD TQVKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAVHGWHEH VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTGIQG VKQIIKALRA GEATIILPDH
201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDQGQF
251 VLHIRPVQGE LNGNKAHDAA VFNRNTEYWI RRFPTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

m505.seq (partial)

```

1  GGCATGTTTC GTTACAATT CAGGCTGTTT CCCCCTTTC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCGAC CCAAAACGG TCAAAGCCGT TTTGCGGAA ACGGCAAAAG
251 GCGGTTTGA ACTTGCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTTGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTCGCGGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCCTC CCCTCAAGAA GGCGGGGAAG GCGTATGGGT GGATTTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAATATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAA
751 GTTTCGATT GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTTCCGACG CatATC...

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI D KIMQAGRVGRK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGG EG VVWDFFGKPA YTMTLAAXLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKAHDA AVFNRNAEYW IRRFPTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHlafYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLSLSCSLHTLGNRLGHlafYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPD PKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGW EHVQQALDKHEG					
	: : : : :					
g505	MRQAGLNPD TQTVKAVFAETAKGGLLELAPAFFKKPEDIETMFKAVHGW EHVQQALDKGEG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPKIKAI DKIMQAGRVGRKGKTAPTSIQG					
	: : : : :					
g505	LLFITPHIGSYDLGGYISQQLPFHLTAMYPKPKIKAI DKIMQAGRVGRKGKTAPTGIQG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVVWDFFGKPAYTMTLAAXLAHVKGVKTLFF					
	: : : : :					
g505	VKQIIKALRAGEATIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	
	250	260	270	280	289	
m505.pep	CCERLPGGQGF DLHIRPVQGE LNKGDKAHDA AVFNRNAEYW IRRFPTHI					
	: : : :					
g505	CCERLPGGQGFV LHIRPVQGE LNKGDKAHDA AVFNRNTEY WIRRFPTQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1 ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51 CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGCGG
251 GTTTGGAACT TGCCCCGCG TTTTTCAGAA AACCAGGAAGA CATAGAAACA
301 ATGTTCAAAG CCGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATAACAAGG GTCAAAACAAA
551 TCATCAAAGC CCTGCGTTCG GGCGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1 MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHAFYLL
51 KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
101 MFKAVHGEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPFAFFRKPEDIETMFKAVHGEHVQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPFAFFRKPEDIETMFKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAKLAHVKGKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	240
	250	260	270	280		
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAVFNRAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAVFNRAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CTTTGGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCACCCC AAAACGGTCA AAGCCGTTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGTGAC CGCCATGTAC
451 AAACCGCCA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGCAAAA GGAACACCG CGCTACCAG CATACAAGG GTCAACAAA
551 TCATCAAAGC CTGCGTTTCG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GPCCTCTCCC CTCAAGAAGG CCGGAAGGC GTATGGGTGG ATTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAGAC CCTGTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTCG ACATCCGCC CGTCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCGGTGTTCA ACCGCAATGC CGAATATTGG ATACGCGGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD PKTVKAVFAET AKGGLLELAPA FFRKPEDIE
101 MFKAVHGW EHVQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRVRGK GKTAPTSIOG VKQIIKALRS GEATIVLPDH
201 VPSPQEGG EGWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ GELNGDKAHD AAVFNRAEYW IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTL	GNRLGHAFYLL	KEDRARIVAN
g505	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	SLSCSLHTL	GNRLGHAFYLL	KEDRARIVAN
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPD	PKTVKAVFAET	AKGGLLELAP	FAFRKPEDIE	TMFKAVHGW	EHVQALDKHEG
g505	MRQAGLNPD	TQTVKAVFAET	AKGGLLELAP	FAFRKPEDIE	TMFKAVHGW	EHVQALDKGEG
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAI	DKIMQAGRVR	GKGTAPTSIOG
g505	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAI	DKIMQAGRVR	GKGTAPTSIOG
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRS	GEATIVLPDH	VPSPQEGG	EGWVDFFGK	PAYTMTLA	AKLAHVKG
g505	VKQIIKALRS	GEATIVLPDH	VPSPQEGG	EGWVDFFGK	PAYTMTLA	AKLAHVKG
	190	200	210	220	230	240
m505-1.pep	CCERLPGGQ	GFDLHIRPV	QGELNGDKA	HDAAVFNRA	EYWIRRFPT	QYLFMYNRY
g505	CCERLPGGQ	GFDLHIRPV	QGELNGDKA	HDAAVFNRA	EYWIRRFPT	QYLFMYNRY
	250	260	270	280	290	299
m505-1.pep	CCERLPGGQ	GFDLHIRPV	QGELNGDKA	HDAAVFNRA	EYWIRRFPT	QYLFMYNRY
g505	CCERLPGGQ	GFDLHIRPV	QGELNGDKA	HDAAVFNRA	EYWIRRFPT	QYLFMYNRY

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTL	GNRLGHAFYLL	KEDRARIVAN
a505	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTL	GNRLGHAFYLL	KEDRARIVAN
	10	20	30	40	50	60
	70	80	90	100	110	120

748

```

m505-1.pep  MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAHVHGWVQALDKHEG
a505          MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAHVHGWVQALDKHEG
              70      80      90      100     110     120

              130     140     150     160     170     180
m505-1.pep  LLFITPHIGSYDLGGYISQQLPPLTAMYKPPKIKAIQAGRVRGKGTAPTSTIQG
a505          LLFITPHIGSYDLGGYISQQLPPLTAMYKPPKIKAIQAGRVRGKGTAPTSTIQG
              130     140     150     160     170     180

              190     200     210     220     230     240
m505-1.pep  VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLLFF
a505          VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLLFF
              190     200     210     220     230     240

              250     260     270     280     290     299
m505-1.pep  CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX
a505          CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAAACAA AGCCTGTTTC TGC CGCTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCGC TTGATTTTCA AAGGCGGTTT GCGGAAGTCG GGTGTGTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGCGCG GGCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GCGGGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGGC GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTTCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATAAGGCA CTTTTCGCGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTGCGCGT
651 GATGGCTTTC GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAAATTCA CCAAAAACG
751 TTCGCCCCTC TCCTTCCAGA AGCTGTAGGT ATGCGAACC GAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGACGGG CTTGCGGCGC CAGCGTCCAG AAGTCCAGT TGTGTTGGC
901 GGAACGCATA TTGGTGCGCG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCTTCTTTC GGTATAGAAT TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTGTT TGATGTCGTG TGTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGCGCGCG CGTTGTTTAT
1351 GGTCAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTGCGG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

```

1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHVQ EQGARLAEEV VIVLAVVPVC
51  RYAVDFQRRF GEVGLLLPLA EAVGFVVVQA AVVAVGAALS VALVAVNRAT
101 RTIDGDIAEV HTQAVTLRVG VIEQTGLQHF IRARADTONE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGRHDLVDH

```

201 RPFRELAALD GFVQVALMAF AVVGDDFCFS FVGQVFNPLL AAEMEFHPKT
 251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVCG
 301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQRKTAD
 351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNGRAVVH
 451 GQMGYGAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFAKTM DAIIRQDFRY *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
 51 TGCCGAACAA TGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
 101 CGCGGTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
 151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GGCGAAATCG GGTGTGTGCT
 201 GCCATTGCCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG
 251 CCGTCGGCGC GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
 301 CGGACGATTG ACGGGAATTT GCGGAAGTT TACGCCCCAA CGGTAGCGTT
 351 GTGCGTCGCG GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG
 401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATGTGTTCCAC
 451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CTCAAACGGA TGATAAGGTA
 501 CTTTTTCGCG GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC
 551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
 601 CGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC AGGTTTTTAA
 651 TGCCTTGTG GGTGCGGAAA TGGAATTTCA CCAAAAACG CTCGCCTGCT
 701 TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
 751 GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGCACTG
 801 CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGC AGAGCGCATA
 851 TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG GGAACCTACG
 901 CGGGTCGCGC AGGAAGAACA CGGGCGTGT GTTGCCGACC ACATCCCAGT
 951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCGCGGAT GTCGCGTTCT
 1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
 1051 CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC
 1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT
 1151 CTTGTTCTCT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC
 1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
 1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT
 1301 ACGCCAAGAT TTTCGCTATT AA

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHGV EQGARLAEIV VIVLAVVPVC
 51 RVAVDFQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
 101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTGENE VARCEGLLPH
 151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHDLDVH
 201 RPFRKLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
 251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFQ QRPEVPVVCG
 301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQKGTAD
 351 VAFICIGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQOR AARTGGQAVL IVGNRRRAVVH
 451 GQMGYRAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFVKTM DATIRQDFRY *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHGV EQGARLAEIVVIVLAVVPVCRAVDFQRRF					
	: : : : : : : : :					
g506	MAVFDEVGRVAHCGGGVVKQSLFLRVVHGV EQGARLAEVVIVLAVVPVCRAVDFQRRF					
	10	20	30	40	50	60

750

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAAXVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
m506.pep	VIEQTRLQHFIKAGADTGNVARCEGGLPHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIKARADTGNVARCEGGLPHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIKAGADTGNVARCEGGLPHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIKARADTGNVARCEGGLPHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	VKRMIRYFFRVCFRDLVDVHRPFRKLAADFDFXVALMAFAVVGDDFGGFFVVGQVFNALL					
g506	VKRMIRHFFGIGFRDLVDVHRPFRELAALDGFVQVALMAFAVVGDDFCSFFVVGQVFNPLL					
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRDLVDVHRPFRKLAADFDFXVALMAFAVVGDDFGGFFVVGQVFNALL					
g506	VKRMIRHFFGIGFRDLVDVHRPFRELAALDGFVQVALMAFAVVGDDFCSFFVVGQVFNPLL					
	190	200	210	220	230	240
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQORPEVPVVCG					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQCFGQORPEVPVVCG					
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQORPEVPVVCG					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQCFGQORPEVPVVCG					
	250	260	270	280	290	300
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFGKTADVAFICGCAAF					
g506	GTHIGARIAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIEFQKTADVAFRIGCAAL					
	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFGKTADVAFICGCAAF					
g506	GTHIGARIAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIEFQKTADVAFRIGCAAL					
	310	320	330	340	350	360
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
m506.pep	IQPQILRQQAARTGGQAVLIVGNRRVAVHGMGYRAFGGSHRSCSFSQVGQMGKRLTV					
g506	IQPQILRQQAARTGGQAVLIVGNRRVAVHGMGYRAFGGSHRSCSFSQVGQMGKRLTV					
	430	440	450	460	470	480
m506.pep	IQPQILRQQAARTGGQAVLIVGNRRVAVHGMGYRAFGGSHRSCSFSQVGQMGKRLTV					
g506	IQPQILRQQAARTGGQAVLIVGNRRVAVHGMGYRAFGGSHRSCSFSQVGQMGKRLTV					
	430	440	450	460	470	480
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
51  TGCCGAACAA TGCCTGTTTC TCGCGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGC GC
151 CGCGTCGCCG TTGATTTC AAGGCGGTTT GCGGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGCGC GTCCTTGTC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGGTTG ACAGGGATT GCGGGAAGTT CACGCCCAAG CGGTAGCGTT
351 GCGGTCGGC GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATACGGCA CTTTTTCCGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTTCGCGT

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651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTGGGTC
701 AGGTTTTTAA TGCCTTGTG GGTGCGGAAA TGGAAATTTCA CCCAAAAACG
751 CTCGCCTGCT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGCGGGG ATGCGCGCGT CGCTCATCAC GATGGTAAC
851 TGGTGCAGTG CTTGCGGCAG CAGCGTCCAG AAGTCCAGT TGTGTGGG
901 AGAGCGCATA TTGGTGCAGC GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CCGGTCGCGC AGGAAGAACA CCGGCGGTGT GTTGCCGACC
1001 ACATCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTCTT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGTTTTTT TTGCGGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCCCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCCTGCG CCAGCAGAGG GCCCGAGGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTCAT
1351 GGTGAGATGG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCCTT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTGGCGG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHVQ EQGARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGN EVARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRKTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVH
451 GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQEQGARLAEIVVIVLAVVPVCRVAVDFQRRF
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQEQGARLAEIVVIVLAVVPVRRVAVDFQRRF
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG
a506	GEVGLLLPLAEAVGFVVRQA AVVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG
m506.pep	VIEQTRLQHFIWAGADTGN EVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
a506	VIEQTRLQHFIWAGADTGN EVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
m506.pep	VKRMIRYFFRVCFRHLVDVHRPFRKLAALDGFXXVALMAFAVVGDDFGGFFVGQVFNALL
a506	VKRMIRHFFRIGFRHLVDVHRPFRKLAALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL
m506.pep	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHH DGNLVQCFGQQRPEVPVVC
a506	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHH DGNLVQCFGQQRPEVPVVC

752

	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVQVQELTRVAQEEHGRVVADHIPVAFFGIKFGGKTADVAFICIGCAAF					
a506	RAHIGARVAFDGFVQVQVQELTRVAQEEHGRVVADHIPVAFFGIKFGGKTADVAFICIGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEGHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEGHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFQVQGMGGKRLTV					
a506	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFQVQGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKMTDATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKMTDATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTTCAGACGG
101 CCTTTGCGCT CTTCTGTGCTT GGCAACGGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGACTTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAGCTGCG ACGCGGATTT
351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGTTGGTG CAGGTTTTCG CCGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTTC CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNLFGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFFDLQLVF LKLHADLLL LPPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTAAAGGCTT GGTTCCTCTG TTTCAGACGA
101 CCTTTGCGCT CTTCTGTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTAATC GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGTTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTTC CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLLQGG CFLRGGGFGF VGQVXGLVFL FQTTFALFVL GNRLFGMGKL

```

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLVFG NLHRPFRQLG
 101 LFFFDLQLVF FKLHADLLLL LMNALXLRRL CLLVAFDALV QVLLMADLFF
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng)
 from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQGGCFLRGGGFGVGVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	: : : : :					
g507	MLLPALQGGGFLSGGGFGLVGQVGLVFLQLTAFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
	: : : : :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXLRRLCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG					
	: : : : :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAALVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq
 1 ATGCTCTTGC TGGCTTTGCA ACAAGGCGGC AGCTTCCTGC GCGGCGGCGG
 51 TTTCGGCTTC GTCAGGCAGA TTCAGGGCTT GGTTTTCCTG TTTCAGACGA
 101 CCTTTGCGCT CTTGCTGCTT GGCAACGGTT TGTTCCGCAT GGGCAAGCTG
 151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT
 201 GGGTTTGGAA GCGGCATTG AGTGTGGCTT GGGTTTCTTC CAATTCGGGC
 251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCG CCAATTCGGT
 301 TTGCTTTTCT TCCGCCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
 351 GCTGCTGCTC CTGATGGATG CGCTGCATCT GCGCCTGCGC CGCTGCTTG
 401 TCGCGTTCGA TCGTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
 451 CAAACGGGCA ATCTGTTTCG GCAACACGCC GCGTTTGTG CCAATTCGT
 501 GCACCGCTG CTGCTGCGAC TGTTCCGCAG TCTGCAAGGC GTGTACTTCG
 551 TCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep
 1 MLLLALQGG SFLRGGGFGF VRQIQGLVFL FQTTFALFVL GNLFMGKGL
 51 LLLQRQFAAD AVCLVLLGLE GGIECGLGFF QFGQTLFVFG NLHRPFRQFG
 101 LFFERLQLVF FKLHADLLLL LMDALHLRL RLLVAFDALV QVLLMADLFF
 151 QTGNLFAQHA AFVAQFVHRL LLRLFGSLQG VYFVV*

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQGGCFLRGGGFGVGVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD					
	: : : : : : :					
a507	MLLLALQGGSFRLRGGGFGFVRQIQGLVFLFQTTFALFVLGNLFGMGKLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
a507	AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
	70 80 90 100 110 120
m507.pep	LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
a507	LMDALHLRLRRLLVAFDALVQVLLMADLFFQTGNLFAQHAAFVAQFVHRLLLRLFGSLQG
	130 140 150 160 170 180
m507.pep	VYFVVX
a507	VYFVVX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
  1  ATGGTAGCGT  TTGGCGTTGA  TCAGGGCCTC  CTGCTGCTGC  AACAGGGCGG
51  TTTGGGTGGC  GGCCTGAAGC  TGCGGCAGCT  TGGTTTGACG  GGTTTGTACG
101 CGGGCGTATT  GCTCCCTGCC  CTGTTCTCTG  ATCTGCGCGA  GTTTTTCTCT
151 CACGGCGATG  TATTCTTCGT  CCAGCGTGTG  TACGGTTTCG  ATCAACTCGT
201 CGAGCTTGAT  GTGCTGCTCG  TCGTTTTGGA  ACTCGGTTTC  GTACGAGGAG
251 GCAAGCTCTT  GCCGGCGTTC  CTGCCAGTCC  AGGGTTTGCT  GTTCGAGCCG
301 GGCGATTTCG  TGCCGGTAGT  TTTGTTTTTG  CGGGTTGAGT  TTGTGGACGG
351 CGACTTCGGC  AAGCCCGTAT  TGGCGGTTGG  CTTCAAACAG  GGCAAGCTGC
401 GCCTGTTTCA  GACGGCCTTG  CTGCTCTTGG  CGGCTGTGCG  CGGTGGTTTG
451 CTGCTGGTGT  TCGAGTTCGG  CGGCGGCTTC  CTGCAAAGTA  GCGATGTCTG
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

g508.pep

1	MVAFGVDQGL	LLLQQGGLGG	GLKLRQLGLQ	GLYAGVLLPA	LFLNLREFFL
51	HGDVFFVQRV	YFGGQLVELD	VLLVVLELGF	IGEGKLLPAF	LPVQGLLFEP
101	GDLLPVVFL	RVEFVDGDFG	KPVLAVGFQQ	GKLRLFQTAL	LLLAARVGG
151	LVVFEEGGGF	LQSSDVF			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```
m508.seq
1  ATGGTAGCGT  TTGGCGTTGA  TCAGGGCTTC  CTGCTGCTGC  AACAAAGCGG
51  TTTGGGTGGC  GGCCTGAAGC  TGCGGCAGCT  TGGTTTGACG  GGTTTGCACT
101  TTAGCGTATT  GCTCCCTGCC  CTGTTCTCGA  ATCTGCGCGA  GTTTCTCTTG
151  CACAACAATA  TATTCTTCGT  CCAAGGTCGT  TACGGCTTCG  CTTAATCTCT
201  CAAGCTTGAT  GTGCTGCTCG  TCGTTTGGGA  ACTCGGTTTC  ATAGGCGAGG
251  GCAAGCTCTT  GCTGGCGTTC  CTGCCAGTCG  AGGGTTTGCT  GTTCAAGCTG
301  GGCGATTTCG  TGCCGGTAGT  TTTGTTTTTG  CTGGTTGAGT  TTGTGGACGG
351  CGACTTCGGC  AAGCCCGTAT  TGGCGGTTGG  CTTCCAACAG  GGCAAGCTGC
401  GCCTGTTTCA  GACGGCCTTG  CTGCTCTTGG  CGGCTGTGCG  CGGTGGTTTG
451  CTGCTGGTGT  TCGAGTTCGG  CGGCGGCTTC  CTGCAAGGTA  ACGATGTCGT
501  CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

m508.pep

1	MVAFGVDQGF	LLLQQGGLGG	GLKLRQLGLQ	GLHFSVLLPA	LFLNLRFLLL
51	HNNIFFVQGL	YGFAFFKLD	VLLLVLELGF	IGEGKLLAF	LPVEGLLFKL
101	GDLLPVVFLF	LVFVDGDFG	KPVLAVGFQQ	GKLRLFQAL	LLLAAVRGG
151	LLVFEFGGFF	LOGNDVV*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

755

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLLLQQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
g508	MVAFGVDQGLLLLLQQGGGLGGGLKLRQLGLQGLYAGVLLPALFLNLREFFLHGDVFFVQVRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVLELGFIGEGKLLLAFLPVEGLLFLKGLDLPVVLFLLVFVDGDFG					
g508	YGFQQLVELDVLLVLELGFIGEGKLLPAFLPVQGLLFEFGDLPVVLFLRVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQGNDDV					
g508	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQSSD VV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGGCGCAGCT TGGTTGCAG GGTGTGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCCTG
151 TACGACAATA TATTCTTCGT CCAAACCTCG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGG ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGT GTTCAAGCTG
301 GGCAATTTGC TGTGGTAGT TTTGTTTTTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508.pep
1  MVAFGVDQGF LLLQQGGGLG GLKLRQLGLQ GLYAGVLFPT LLLNLREFLL
51  YDNIFFVQTL YGFAQLFELD VLLVLELGF IGEGKLLLAFL LPIEGLLFLK
101 GNLLLVLEFL LVELVDGDFG KPVLA VG FQ QG KLR L FQTLL LLLAAVRGGL
151 LLVFEFGGGF LQNGD VV*

```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLLLQQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
a508	MVAFGVDQGFLLLLQQGGGLGGGLKLRQLGLQGLYAGVLFPTLLNLREFLLYDNIFFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVLELGFIGEGKLLLAFLPVEGLLFLKGLDLPVVLFLLVFVDGDFG					
a508	YGFAQLFELD VLLVLELGFIGEGKLLLAFLPIEGLLFLKGNLLLVVFLLVLDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQGNDDV V X					
a508	KPVLA VG FQ QG KLR L FQTLLLLAAVRGGLLVFEFGGGFLQNGD V V X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

756

```

1  atggtcgctg tatgtgatga acgggctgta cagcggacgt tggtagccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtgttag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggctt gccaaacggc cttcggcaag caggcggctg
251 ccgttgctga taagggaacg ttgcaatttt ttcaaatcat cgagaaattt
301 ttgggccgaa gcataaggct cgagaaagcc gaatttgcag cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggg aagggtcttc ggtgcggcgg atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttagcgcgg cggatggaaa
501 gcggcagttc gcggtaaaagt ttgtcgagtt cgtcgggta aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaa cgcagggttt cgccagaaac
601 aaacggattg ccgtcgcggt cgccgccgat ccagccgccg attttaagga
651 tattcggaac gcggacatcg gtagaggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cagcgcgttg ttgatttcgt cgttgacgct gaggttgttg cggcgcgttt
801 cgtggtctg ccacaagccc agaagcacgg tgtcgatttc gcgcgcgagc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttgcg gcagcagcgc
901 gcggatgcgg cgttgaaat tcaaaacggt ttggcgttgc acttcggtcg
951 ggtgcgcggg caaaacggcg gtaacggacg tattgtccaa ctgcgcgtgc
1001 accgatttgc cgtcggcttt ccccgcttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atctctcgtg atttgccggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtc ggaagtggac aagagtttga
1251 ccgttttcga aaccaacggc gaggtctctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgcgcgc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctattgccc taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagtga acgcgcgccg acggcggcgt
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcttc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgcgcgccct gccctatctc
1701 gccgcctcgg ggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAAFALRQQR
301 ADAAVEIQNG LALHFGRVRG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVAG I FVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLRI
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPKCR LKLNAARRRR
501 YNRPQLFFSE HHHRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLRRIGR RRPCISPPIR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTTCGTTTCTAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTGT
151 GCCTGCGTGT TGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTGTA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCTATACCCA
351 AACCAGCGCG GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGGCGGT AGGGTTCTTC GCGCGGGCGG ATTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCGCGATA GAAGCGGAAC

```

```

551  ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601  AAACGGATTG CCGTCGCGGT CGCCGCGCAT CCAGCCGCCG ATTTTGAGGA
651  TGTCCGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701  TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751  CACGCCGTTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801  CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTGATTtC GCgGCGCAGC
851  CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCgCGTTGCG GCAACAGTGC
901  GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTGC
951  GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCGGCTTT CCCCGCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GGCgtTCGTG GTGCACGTCT TCGGCGATGT TCAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCTGTTCA ATTCGGGCAA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGCG GTCCGCGGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCTT CTCTCGTCTG CCGTAAATAT
1401 TGTAAATGTA CCCCAAATGC CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCGGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTtTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCTTGC TCGGTACAG CCGCCACATC
1601 CTCTTGGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTCGG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

```

m509.pep
1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVKAHEGYGT DEVCQTAFGK QTAADVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQDQSVDF AAQPCQRVGI GAAFALRQOC
301 ADAAVEAXDG LALHFGRVRG QNGNGRIVQ LPLHRFVAVG PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRVVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIIVN PQMPHPCQTV HTLTARVPKC RLKLNAAARRQ
501 RYNRPQLFFS EHHHDHRTTR QRCIPAAVQ PPHPLGRNRH RRAAETFRRA
551 YFGRRLRRFG CRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

m509/g509

```

              10      20      30      40      50      60
m509.pep      MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509           MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH
              10      20      30      40      50      60

              70      80      90      100     110     120
m509.pep      HVKAHEGYGTDEVCQTAFGKQTAADVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER
              ||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509           HVEAEHGHGTDEVCQTAFGKQAAADVVDKGTLQFFQIIKFLGRSIRLEKAEFAAHAQTER
              70      80      90      100     110     120

              130     140     150     160     170     180
m509.pep      ARFAHSARHNVDGAAGVFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509           ARFAHSARHNVGAAVRFFGAGDFFVRREGCQCHYVVVDFDAADGKRQFAVKFVEFAAV
              130     140     150     160     170     180

```

	190	200	210	220	230	240
m509 . pep	EAEHGIGVAAEGKAQGFGRNKR	IAVAVAADPAADFEDVRNADAG	IGRLKVVFHLAVELGQ			
g509	KTEHGIGVAAEGKAQGFARNKR	IAVAVAADPAADFKDIRNADIG	IGRLKVVFHLAVEFGQ			
	190	200	210	220	230	240
	250	260	270	280	290	300
m509 . pep	GFPEKAHREDGHAVVDFVVD	AEFVAARFAGLPQAQQDSVD	FAAQPCQRVGIGAAAFALRQ	QC		
g509	GFKKAHREDGHAVVDFVVD	AEFVAARFAGLPQAQKHGVD	FAAQPCQRVGIGAAAFALRQ	QR		
	250	260	270	280	290	300
	310	320	330	340	350	360
m509 . pep	ADAAVEAXDGLALHFGRV	RQNGNGRIVQLPLHRFAVG	FPRFEPADGFRQAAAFRAA	ASG		
g509	ADAAVEIQNGLALHFGRV	RQNGNGRIVQLPLHRFAVG	FPRFEPADGFRQAAAFCCV	VAG		
	310	320	330	340	350	360
	370	380	390	400	410	420
m509 . pep	FFVDLAAAFVHVFGDVQNL	GEQAAGQGXIVGLLFVQLR	QYFFNQCRVVSGQEFDCFD			
g509	IFVDLAAAFVHVFGDIQNL	GEQPAKQIVGLPFVQLRQY	FFNQCRVVSGQEFDRFD			
	370	380	390	400	410	420
	430	440	450	460	470	480
m509 . pep	NQRRGFFVQVEVEQGLFQK	FRVRRQSRVLWIVQNMQLH	DFSLSSAVNIVNVPQMPHC	QTV		
g509	NQRRGFFVQVEVEQGLFQK	FRVRRQSRVLWIVQNMQLH	DFPLI-AVNTVNVNVPQMPH	CQTV		
	430	440	450	460	470	
	490	500	510	520	530	540
m509 . pep	HTLTARVPKCRLKLNAARR	QRYNRPLFFSEHHHDH	DRTRQRRCPAAVQPPHPLGR	NRH		
g509	HTLTTHVPKCRLKLNAARR	RYNRPLFFSEHHHDDR	TRTRQRRTPAAVQPPHPLGR	NRH		
	480	490	500	510	520	530
	550	560	570			
m509 . pep	RRAAETFRRAYFGRRLRR	FGCRRTCPTLPLRV	SAR			
g509	RRAAEAFRRAYFGRRLRR	IGRRRPCISP	PPRSAR			
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509 . seq
1  ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGCGGCT TGTTTTGCT CTCGTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTGTT
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAACGGC CTTGCGCAAG CAGGCGGCTG
251 CCGTTGTCTG TAAGGGAATG TTGCAATTTT TCAAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTGCGAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTTCTTC GCGCGGGCG GTTCTTCGT CGGGCGATTG
451 GTCGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGAGAG
501 GCGGCAAGTT CCGGTAGAGT TTGTGAGTT CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCGCGGT CGCCGCGAT CCAGCCGCGG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTCGT CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTTC GCGGCGCAGC
851 CGTGCCAGCG CGTCGCATT GGTACAGCGT TCGCTTGCG GCAGCAGCGC

```



```

901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTGC
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCGGCTTT CCCCGCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTGGCGGC
1101 GCGGTTCTGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTCGTCCA ATTGCGGCAA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACTTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GCCCTATCTC
1701 GCCGCTTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

a509.pep

```

1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVFAQCVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VNGATVGGF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKAHRKDG
251 HAVVDFVVD AEFVAARFAGL PQAQQDSVDF AAQPCQRVGI GTAFALRQQR
301 ADAAVEIQDG LALHFGVRVG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRVAV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNPV QMPHPCQTVH TLTARVPKCR LKLNAAARRQR
501 YNRPQLFXSE HHHDHDRTRQ RRCIPAAVQP PHPLGRNWHR RAAETFRRAY
551 FGRRLLRRFGC RXPCPISPLP ASAR*

```

m509/a509 93.0% identity in 575 aa overlap

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFAQCVLEKLGNHIGVFACVLAQVERH					
a509	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVFAQCVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
m509.pep	70	80	90	100	110	120
	HVKAHEHGYGTDEVCQTAFGKQTAADVVDKGTQLQFFQIIQKLLCRSIRLEKAEFAAHTQTER					
a509	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGMQLQFFQIIIEKFLCRSIRLEKAEFAAHTQTER					
	70	80	90	100	110	120
m509.pep	130	140	150	160	170	180
	ARFAHSARHNVDGGAAGVFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
a509	ARFAHSARHNVDGATVGGFAGAGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV					
	130	140	150	160	170	180
m509.pep	190	200	210	220	230	240
	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
a509	KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ					
	190	200	210	220	230	240
m509.pep	250	260	270	280	290	300
	GFKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGTAFALRQQR					
a509	GFKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGTAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360

760

```

m509.pep  ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRFEPADGFRQAAFRAAASG
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      ADAAVEIQDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRFEPADGFRQAAFRAAASG
          310      320      330      340      350      360

          370      380      390      400      410      420
m509.pep  FFVDLAAAFVVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRAVVSGSQEFDCFD
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      FFVDLAAAFVVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRAVVSGSQEFDRFD
          370      380      390      400      410      420

          430      440      450      460      470      480
m509.pep  NQRRGFFVQVEVEQGLFQKFRVRQRQSRVLWIVQNMQLHDFSLSSAVNIVNVQMPHPCQTV
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      NQRRGFFVQVEVEQGLFQKFRVRQRQSRVLWIVQNMQLHDFSLI-AVNTVNVVQMPHPCQTV
          430      440      450      460      470

          490      500      510      520      530      540
m509.pep  HTLTARVPKCRKLNAARRQRYNRPQLFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      HTLTARVPKCRKLNAARRQRYNRPQLFXSEHHHDHRTQRRCIPAAVQPPHPLGRNWH
          480      490      500      510      520      530

          550      560      570
m509.pep  RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      RRAAETFRRAYFGRRLRRFGCRXPCPISPLPASARX
          540      550      560      570

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg gggtattcct gccccaaagcg
51  ggatagtgcc ttttggcagg cggtgtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggaggtttt caataggtcg
151 tggacgacgt tgagcgcggc cataatgacg attttttcgc tgtccgcgac
201 gcggccgcct tcgcggatgg ctccggtttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttggtc gatgttcacg ctttaatcct
351 tattgctgcg tttcctgccg ttgggggagg cgcgctgcca gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTISR
101 GVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTCTCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 GGCGTGCAWG ACTTCSatGT GGAATTGTTT GATGTTTCAT CTTTAATCCT
351 TATTGCTGCG TTTCTGCGCA TTGGGGGAGG CCGCTGCGCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTISR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

```

              10      20      30      40      50      60
m510.pep    MPSRTPQGKRGYSCAKRDSA FQWALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT
              |||:|||||
g510         MPSRTPQGKRGYSCPKRDSA FQWALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT
              10      20      30      40      50      60

              70      80      90     100     110     120
m510.pep    IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA
              |||:|||||
g510         IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA
              70      80      90     100     110     120

              130
m510.pep    FPAIGGGALPVRX
              |||:|||||
g510         FPAVGGGALPVRX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

```

a510.seq
1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTATTCTCT GCGCCAAGCG
51 GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTTCGC TGTCGCCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC  GGTCAGCCGG
301 G. CGTGCATG ACTTCGATGT GGACTTGTTT GATGTTTCATC CTTTAATCCT
351 TATTGCTGCG TTTCTGCCG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

```

a510.pep
1  MPSRTPQGKR GYSCAKRDSA FQWALSISAI LRAKSPIAKS PPFREVFNR
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 XVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

```

              10      20      30      40      50      60
m510.pep    MPSRTPQGKRGYSCAKRDSA FQWALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT
              |||:|||||
a510         MPSRTPQGKRGYSCAKRDSA FQWALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT
              10      20      30      40      50      60

              70      80      90     100     110     120
m510.pep    IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA
              |||:|||||
a510         IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA
              70      80      90     100     110     120

              130
m510.pep    FPAIGGGALPVRX
              |||:|||||
a510         FPAVGGGALPVRX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

```

g512.seq
1  atgaaagtgc ttgttttagg tgcgggtggt gccggcgat cctccgtgtg

```

```

51  gtatctggca gaggccggac atgaagtaac ggtcatcgac cgcaccgagg
101  gtgtggcgat ggaaaccagt tttgccaatg caggccagct ttcttacggc
151  tataccacgc cttgggctgc acccggattt ccgaccaaaag cactgaaacg
201  gctgtttaaa agccatccgc ctttactgtt ccgccctgac ggcggcctgt
251  atcaaatcga atggctgtgg cggatgctgc aaaactgcac ggcaacgcgc
301  tatcaaatca ataaagagcg catggtcagg atttccgaat acagccgtga
351  aatgttccgc cgttttgaag cgcaaaccga catgaatttt gagggacgca
401  aaaaaggagc gttgcagatt ttccgccaaa ccgaagaagt cgaagcggca
451  aaacaagaca ttgccgtttt ggaacgctac ggcggtgccg accgcgctct
501  gaagcccgaa gaatgcgcag aattcgagcc tgcgtggca cgcgttaccg
551  ccaaaattgt cggcggctcg cacctgcctg cggatgcgac cggcgactgc
601  cgctcttcca ccgaaaacct gtacaaattg tgtcaagaga agggggtaacg
651  gttctacttc aaccaaacca tcagccgcat cgaccacaac gggctgcgca
701  tcaaagccgt tgaacgaaa cagggcggtt tgaacagat gccgttgtct
751  gcgcgctcgg ctgcttcagc aggactgtgt tggcgagtt ggatctcaat
801  ctgccattt atcccgtaaa aggcatttcc ttga

```

This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:

```

g512.pep
1  MKVLVLGAGV AGVSSVWYLA EAGHEVTVID RTEGVAMETS FANAGQLSYG
51  YTPWAAPGI PTKALKRLFK SHPPLLFRPD GGLYQIEWLW RMLQNCTATR
101 YQINKERMVR ISEYSREMF RFEAQTDMNF EGRKKGTLQI FRQTEVEEAA
151 KQDIAVLERY GVPYRLKPE ECAEFEPALA RVTAKIVGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFYF NQTISRIDHN GLRIKAVETK QGGLKQMPLS
251 ARSAASAGLC WRSWISICPF IPSKAIP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

```

m512.seq (partial)
1  ..GTTTGGAAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51  TGCAGAATTT GAGCCTGCGC TGGCAGCGT TACCGCCAAA ATTGCCGGCG
101 GCCTGCACCT GCCTGCAGAT GCGACGGCG ACTggCGCCT CTTCACTGAA
151 AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTTCAACCA
201 AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAA ACCGTTGAAA
251 CCAAACAGGG CGGTTTGAAG CAGATGCCGT TGTCTGCGC CTCGGTTGCT
301 TCAGCAGGAC GGTTTTGGCG CAGTTGGATC TCAATCTGCC CATTATCCC
351 GTCAAAGGCT ATTCCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:

```

m512.pep (partial)
1  ..VLERYGVPYR RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQEK VRFHFQNIS RIDHNLRIK TVETKQGGK QMPLSARSA
101 SAGRFWRWI SICPFIPSKA IP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

m512/g512

```

m512.pep                                10      20      30
                                         VLERYGVPYRLKPEECAEFEPALARVTAK
g512      TDMNFEGRKKGTLQIFRQTEVEEAAKQDIAVLERYGVPYRLKPEECAEFEPALARVTAK
           130      140      150      160      170      180

m512.pep                                40      50      60      70      80      90
IAGGLHLPADATGDWRLFTEENLYKLCQEKGVRFHFQNISRIDHNLRIKTVETKQGGK
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g512      IVGGLHLPADATGDCRLFTENLYKLCQEKGVRFYFNQTISRIDHNLRIKAVETKQGGK
           190      200      210      220      230      240

m512.pep                                100      110      120
QMPLSARSVASAGRFWRWSISICPFIPSKAIP
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g512      QMPLSARSAASAGLCWRWSISICPFIPSKAIP

```

250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTG GCCGGCGTAT CTTCCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAAACCAAG TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GCGGTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTCGAGCC TCGCGTGGCA CGCGTTACCG
551 CCAAAATTGC CGGCGGCCTG CACCTGCCCC CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAAGAAA AGGGCGTACG
651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTPWAPGI PTKALKWLFK SHPPLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMFR RFEAQTMNF EGRKKGLQI FRQTKEVEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

m512.pep				10	20	30
				VLERYGV	PYRRLK	PEECAEFEPALARVTAK
a512	TGMNFEGRKKGTLQIFRQTKEVEAAKQDIAVLERYGV	PYRRLK	PEECAEFEPALARVTAK			
	130	140	150	160	170	180
m512.pep		40	50	60	70	80
	IAGGLHLPADATGDWRLFTENLYKL	CQEKGVRFHF	NQNISRIDHNG	GLRIKTVETK	QGGLK	
a512	IAGGLHLPADATGDCRLFTENLYKL	CQEKGVRFHF	NQTISRIDHNG	GLRIKTVETK	QGGLK	
	190	200	210	220	230	240
m512.pep		100	110	120		
	QMPLSARSVASAGRFWR	SWISICPF	IPSKAIPX			
a512	QMPLSARSAASAGRFWR	KWISICRF	IPSKAIPX			
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCGG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
51  TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgCAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGGTTTCC TCGCCGTGAT CCTGTTTATG TTTGCCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTT GCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATCAAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTT GCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
	10	20	30	40	50	60
m513.pep	AIVSQVGQWGAGFLAVILEMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILEMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILEMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILEMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLXRDTAKLMGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDTAKLMGKDPEFKLSEHP					
	130	140	150	160	170	180
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

```

1  ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51  CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCACGGGC TTTGTCCAAT TCCGCTGTG CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTG TAACCGGCCT TGCCAGCCGC GTGGCGGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAA CCGCTTAATC GGTATGAGT CCGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CCGCCCTGCC TACTACATCA CTCAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTGTTTCGC CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CCGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCAATCATT
701 TGACCAATAT TCGGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 GCGTTCAAAT TCACGCGGCG AGCAGGCGGC TTAGTCGGCG GTCTGATTTT
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTC CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTG ATACCATCAT
951 CGTTTGTCTT TGCACCGCCT TCATCATCTT GATTACCAA CAGCCTTACG
1001 GCGATTGAG CGGTGCGGCG CTGACGCAGG CCGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCCGTC ATCCTGTTTA TGTTCGCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1  MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLEFTVTTG FVQFRLFGRS
51  IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGGPGA
101 VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGFVFEA VQNTNIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPI PDVFGQIFSG
251 AFKFDAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VFVDTIIVCS CTAFIILIYQ QPYGDLGAA LTQAAIVSQV
351 GQWGAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVFYFAGVAN PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||
a513
260 270 280 290 300 310
DAAAGLLGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
TIIVCSCTAFIILIYQ QPYGDLGAA LTQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY
|||||
a513
320 330 340 350 360 370
TIIVCSCTAFIILIYQ QPYGDLGAA LTQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY

100 110 120 130 140 150
m513.pep
AYAESNVQFIKSHWLI TAVFRMLVLAWVFYFAGVANV PLVWDMADMA MGIMAWINLVAILL
|||||
a513
380 390 400 410 420 430
AYAESNVQFIKSHWLI TAVFRMLVLAWVFYFAGVANV PLVWDMADMA MGIMAWINLVAILL

160 170 180 190
m513.pep
LSPLAFMLLRDYTAKL KMGKDPEFKL SEHPGLKRRI KSDVW
|||||

```

a513 LSPLAFMLLRDYTA KLKMGKDPEFKLSEHPGLKRRIKSDVWX
440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq
1 atggttcaaa tacaggttgt gcgcgcgcgc gccgttgccc gtggtctgca
51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttgcacaatg
101 ccgttttgaa tcacgaagcg cggcgcgcgc gcaacacctt ccgcatcaaa
151 atagctgctg cggaaagagc gggggatgtg cgttcttcgc cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccga acggtggtat cgaagaggac ggggtagctg cctgtcggga
351 tgctgcgcgc gccgagtcgc cgcaaagtgc ggcgggcgcg ggtttgaccg
401 atggtttcgc gctgtccat atccgatgg cggcagcgcg aatcgtacca
451 gtatgcgcgc tgcattccgt tttcgtcgcg ggcgacgacg ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgtgtgcgcg caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgctgcctg ttgcattgt tttgccaagc
651 cgacggcgcg ttccgtatcc aaatcccatt cgtggtaaaag gtcggggtcg
701 ccgatgtggt gcgccatcaa ctcggggtcg gcaagtcgcg cgcaaccgct
751 ttcggcgcgc tggcgggcga tgcggcgcg ggcgcggcgc gtgtcgcgca
801 gggcttgctc ggagaagtgc gcggtgccgc cgcggccttt gcgtttgccg
851 acgtaaacgc taatgtccag cgatttgcgc tgctggaact cgatttgttc
901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggcttcgcg gcggtgcgcg ccgctgctt ttgccaagtc gacggtgcgc
1001 cggcagaggt cgaggagtgc ggaagcgcgc tggttgaaca gcataacaat
1051 ctttcttggg ggagcgttgt ggcattttaa

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep
1 MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RRGNTFRIK
51 IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADDEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFQCV ERAAAEEVEF GSGVVEQHNN
351 LSWWSVFAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)
1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC
151 GGTGGTATCG AAGAGGACCG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGC CGGGCGGCGG TTTGACCGAT GGTTCGGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCCGTA AACGTATTGG
401 TAATGGCCCG TTTGCACCGC CGCGCTTCG GAGTTTCGA TGCGCTCATC
451 CTCGTTACAG GCGGCTTGT TCGATTGTTT TGCCAAGCCG ACGGCGGCTk
501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CCGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGCAGG GCTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTGC GTTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTTGTCTG CTGGAACGCG ATTTGTTsGA TTTsGCCCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
801 CGGTGCGGCC CGTCGCTTTT GCCAAGTCGA GCGTGC GGCG GCAGAGGTG
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)


```

1      ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51     GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFHAVHIRMA AGGIVPVVAL
101    HAVFVGNDAA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151    LVQGGGLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201    AGDVDGGFDG VLQGFPGFVG STGAAFAPAD VNGNVQRLVL LELDLXDAQ
251    PHADALSQXF AEIGFGGGCA RRFQVERAA AEVEEFGSGV VEQHRNLSXX
301    CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

m515.pep      10      20      30
               GKSGGCAFFAQVEEIGQDFSADAVDQETALA
               ::| | | | | | | | | | | | | | | | | |
g515          AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
               30      40      50      60      70      80

               40      50      60      70      80      90
m515.pep      VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
               | | | | | | | | | | : | | | | | | | | | | | | | | | | | | |
g515          VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
               90      100     110     120     130     140

               100     110     120     130     140     150
m515.pep      GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVVLVMAGLHRRRAFGVFDALIL
               | | | | | | | : | | | | | | | | | | | | | | | | : | | | | | | | :
g515          GGIVPVVALHSVFVGDDAAAGNAVVRALPVCCKTVGVAVNVVLVLSGLHRRRAFGVFDAAVR
               150     160     170     180     190     200

               160     170     180     190     200     210
m515.pep      VQGGFLFALFCQADGGXRIQIPFVVKVGVDVFCQHTGIGKSGATVFGGVAGDVDDGGFDGV
               || | | | | | | | | | | | | | | | | : || : | | | | | | | | | | | | | |
g515          VQRCLFALFCQADGGFRIQIPFVVKVGVDVLRHQLGVGKSGATVFGGVAGDVGGGADGV
               210     220     230     240     250     260

               220     230     240     250     260     270
m515.pep      LQGFFGVEVGSTGAFAFADVNGNVQRLVLLLELDLXDQAQPHADALSQXFAEIGFGGGCAR
               || : | | | | : : | | | | | | | | | | : | | | | | | : | | : | | | | |
g515          AQGLFGEVGGAGAAFAFADVNGNVQRFVLLLELDLFDFAQAHADALSERFAEVGFGGGRAR
               270     280     290     300     310     320

               280     290     300
m515.pep      RFCQVERAAAEEVEFGSGVVEQHRNLSXXCFAAF
               | | | | | | | | | | | | | | | | : | |
g515          CFCQVERAAAEEVEFGSGVVEQHNNLSWSVVAF
               330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

1	ATGGTTCAAA	TAAAGTTGT	GCGCGCCGC	GGCGTTGCC	GTGGTCTGCA
51	TTCCAGTTT	GCGCGCGCT	TAAGTCTGA	GGAAATAGCC	TTGCACAATG
101	CCGTTTTGAA	TCACGAAGC	CGGTGCGGT	GCAACGCCT	CCGCATCAAA
151	ATAGTCTGCT	CGGAAGAAG	GGGGATATG	CGGTTCTTCG	CGCAGGTTGA
201	GGAAATCGGG	CAGGACTTTT	TGGCCGATG	TGTGCATCAG	GAAACTGCTT
251	TGGCGGTAGA	GCGCTCCGC	GGAGAGTGC	CCGACGAGT	GTCCGATTAAG
301	ACCGCCCGAA	ACGGTGTAT	CGAAGAGGAC	GGGGTAGTTG	CCTGTCGGGA
351	TGCTGCGGCT	GCCGAGTCGG	CGCAAAGTGC	GGCGGGCCGC	GGTTTGACCG
401	ATGGTTTCGG	TGCTGTCCAT	ATCCGGATGC	CGGCAGGCGG	AATCGTACCA
451	TGATGCGCGC	GGCATGCCGT	TTTCGTCCGC	GGCAACGACG	CTGCAGGAAA
501	TGCTGTGGTG	CGTGCTTTGC	CGGTGTGCGG	CAAAACCGTA	GGTGTTGCCG

```
a515.pep
  1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEIIA  FDNAVLNHEA  RCGGNAFRIK
51  IAAARAGADV  RFFAQVEEIG  QDFFDADAVD  ETALAVERSA  GECADDEVSDK
101  TARNNGTIED  GVVACRDAAA  AESAQSAAAG  GLTDGFGAVH  IRMAAGGIVP
151  VVALHAVFVG  GNDAAAGNAV  RALPVCCKTV  GVAVNVLVMA  GLHRRAFGVF
201  DALILVQGGL  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251  FGGVAGDVXX  GADGVAQGLF  GEIGAGAAAF  AFADVNGNVQ  RLVLKLDLF
301  DFAQPHADAL  SQ*FAEIGFG  GGCARRFCQV  ERAAAEVEEF  GSGVVEQHRN
351  LS**CFAAF*
```

```

m515.pep                                     10          20          30
                                         GKSGGCAFFAQVEEIGQDFSADAVDQETALA
a515    AEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
          30          40          50          60          70          80

          40          50          60          70          80          90
m515.pep    VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
          |||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a515    VERSAGECADEVSDKTARNGGIEEDGVVACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
          90          100         110         120         130         140

          100         110         120         130         140         150
m515.pep    GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRRAFGVFDALIL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a515    GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRRAFGVFDALIL
          150         160         170         180         190         200

          160         170         180         190         200         210
m515.pep    VQGGFLFALFCQADGGXRIQIPFVVKVGVDVFCCHQTGIGKSGATVFGGVAGDVGDFGFDGV
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a515    VQGGFLFALFCQADGGFRIQIPFVVKVGVDVLRHQLGVGKSGATVFGGVAGDVXXGADGV
          210         220         230         240         250         260

          220         230         240         250         260         270
m515.pep    LQGFFGEVVGSTGAFAFADVNGNVQRLVLLLELDLXDQAQPHADALSQXFAEIGFGGGCAR
          |||::|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a515    AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLDFDAQPHADALSQXFAEIGFGGGCAR
          270         280         290         300         310         320

          280         290         300
m515.pep    RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a515    RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
          330         340         350         360

```

g515-1.seq
1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GGC GTTGCCC GTGGTCTGCA

```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGGGGGCGGC GGTGTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGG
551 TAAACGTATT GGTAGTGTCC GGTGTGACG GCCGCGCCTT CGGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGTGCCTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GGCAGGACG GTGTGCGCA
801 GGGCTTTGTT GGAGAAGTCG GCGGTGCGCG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTGTGTC TGCTGGAACG CGATTGTGTC
901 GATTTCGCCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAGT
951 CGGCTTCGGC GCGGTGCGG CCCGCTGCTT TTGCCAAGTC GAGCGTCGGG
1001 CCGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGGT GGAGCGTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RRGNTFRK
51  IAAERAGDV RFFAQVEEIG QDFADAVDQ ETALAVERAA GECADEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHVSFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVK VGVADVLRHQ LGVKGSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RVLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAVEVEF GSGVVEQHNN
351 LSWWSVVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCG GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCAGGCGGC GGTGTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGG
551 TAAACGTATT GGTAAAGGCC GGTGTGACG GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGCTTGCA
801 GGGCTTTTTC GGAGAAGTCG GCAGTACTGG CGCGGCCTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGGAACG CGATTGTGTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEEIA FDNVNLNHEA RCGNNAFRK
51  IAAERAGDV RFFAQVEEIG QDFADAVDQ ETALAVERAA GECADEVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHVSFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGLL FALFCQADGG FRIQIPFVK VGVADVFCQV TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGFF GEVGSTGAAF AFADVNGNVQ RVLLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep MVQIQVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARRGNTFRIKIAAERAGDV
          |||
m515-1      MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGNNAFRIKIAAERAGDV
          10      20      30      40      50      60

```

770

	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVADVLRHQ					
m515-1	GVAVNVLVVSGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLELDF					
m515-1	TGIGKSGATVFGGVAGDVGGGDFGVQGLFGEVGGAGAAFAFADVNGNVQRFVLELDF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVGFGGGRARCFQVERAAAEVEEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAA  TAAAGGTTGT  GCGCGCCGCC  GCGGTTGCC  GTGGTCTGCA
51  TTCCGAGTT  GCGCGCGCTG  TAACGTCTGA  GGAATAGCC  TTCGACAATG
101 CCGTTTTGA  TCACGAAGCG  CGGTGCGGTG  GCAACGCCT  CCGCATCAAA
151 ATAGCTGCTG  CGGAAAGAGC  GGGGGATGTG  CGGTTCTTCG  CGCAGGTTGA
201 GGAATCGGG  CAGGACTTTT  TTCCGATGTC  TGTCGATCAG  GAAACTGCTT
251 TGGCGGTAGA  GCGCTCCGCC  GGAGAGTTCG  CCGACGAGGT  GTCCGATAAG
301 ACCGCCCGAA  ACGGTGGTAT  CGAAGAGGAC  GGGGTAGTTG  CCTGTCCGGA
351 TGTCGCGGCT  GCCGAGTCGG  CGCAAAGTGC  GCGGGGCGGC  GGTTTGACCG
401 ATGTTTTCGG  GGCTGTCCAT  ATCCGGATGG  CGGCAGGCGG  AATCGTACCA
451 GTAGTCGCGC  TGCATGCCGT  TTTCGTCCGG  GGCAACGACG  CTGCAGGAAA
501 TGCTGTGGTG  CGTGCTTTGC  CGGTGTGCGG  CAAAACCGTA  GGTGTGTCCG
551 TAAACGTATT  GGTAATGGCC  GGTTTGCACC  GCCGCGCCTT  CGGAGTTTTC
601 GATGCGCTCA  TCCTCGTTCA  GGGCGGCTTG  TTCGATTGTT  TTTGCCAAGC
651 CGACGGCGGC  TTCCGTATCC  AAATCCCAT  CGTGGTAAAG  GTCGGGGTCG
701 CCGATGTGTT  GCGCCATCAA  CTCGGGGTCG  GCAAGTCCGG  CGCAACCGTC
751 TTCGGCGGTG  TGGCGGGCGA  TGTCGGCGGC  GGCGCGGACG  GTGTCGCGCA
801 GGGCTTTGTT  GGAGAAATCG  GCGGTGCCGG  CGCGGCCCTT  GCGTTTGCCG
851 ACGTAAACGG  TAATGTCCAG  CGACTTGTC  TGCTGAAACT  CGATTGTGTC
901 GATTTCGCC  AGCCGCACGC  TGACGCTTG  TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEEIA  FDNVNLNHEA  RCGGNAFRIK
51  IAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVERSA  GECADDEVSDK
101 TARNGGIEED  GVVACRDAAA  AESAQAAGG  GLTDGFGAVH  IRMAAGGIVP
151 VVALHAFVVG  GNDAAAGNAV  RALPVCCKTV  GVAVNVLVMA  GLHRRAFGVF
201 DALILVQGG  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251 FGGVAGDVGG  GADGVAQGLF  GEIGGAGAAF  AFADVNGNVQ  RLVLLKLDLF
301 DFAQPHADAL  SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNNGGIEEDGVVACRDAAA					

m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
	70 80 90 100 110 120
a515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
	130 140 150 160 170 180
a515-1.pep	GVAVNVLMAGLHRRAFGVFDALILVQGLFALFCQADGGFRIQIPFVVKVGADVLRHQ
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGLFALFCQADGGFRIQIPFVVKVGADVLRHQ
	190 200 210 220 230 240
a515-1.pep	LGVGKSGATVFGGVAGDVGAGDGAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLF
m515-1	TGIGKSGATVFGGVAGDVGDFGLQGFGEVSGTGAFAFADVNGNVQRLVLLKDLF
	250 260 270 280 290 300
a515-1.pep	DFAQPHADALSQX
m515-1	DFAQPHADALSQX
	310

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

g516.seq

```

1 atgttggtcc gtaaaacgac cgccgccgtt ttggcggcaa ccttgatact
51 gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacgtt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccga agattcggcg aagctgacgg
251 gccttttgaa ggcggggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccc gtcaaattcg aagcgcccgg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaaa
451 ctcgacaatc ggaccattta cacgcgctgc gtatccgcca aaggcaaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagtg
551 tgcccgcgca tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctggttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggccggccgc gtgctggtct tgccatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

g516.pep

```

1 MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51 VAEDNAQLEK GSVLMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNIIYTP PLLILDAAA VLVLPMAIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

m516.seq

```

1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51 GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGC GC CTTCCGTTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCCGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

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501 CTACGCCACA CCGCAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
 551 TGCCTGCCGA TATTATTAC ACGTTACTG AAGAACATAC CGACAAATCC
 601 AAGCTGTTTG CAAATATCTT ATATACGCC CCCTTTTGA TACTGGATGC
 651 GCGGGCGCG GTACTGGCCT TGCCTGCGC GGCTCTGGT GCGGTCGTGG
 701 ATGCCGCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep
 1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
 51 VAEDNAQLEK GSLVMMGGKY WFVVPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSQN FSTEGCLRLY DTDKPADIAP LKQLGFPAVK
 151 LDNRTIYTRC VSAKGKYYAT POKLNADYHF EQSVPADIYY TVTEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMMLWGMNPNVSETITRKHVDKQIRAFGVVAEDNAQLEK					
g516	MLFRKTTAAVLAATLILNGCTMLRGMNPNVSTITRKHVDKQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
m516.pep	70	80	90	100	110	120
	GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN					
g516	GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN					
	70	80	90	100	110	120
m516.pep	130	140	150	160	170	180
	FSTEGCLRLYDTDKPADIAPLKQLGFPAVKLDNRTIYTRCVSAKGKYYATPOKLNADYHF					
g516	FSTGGLCLRYDTGRPDDIAPLKQLEFKAVKLDNRTIYTRCVSAKGKYYATPOKLNADYHF					
	130	140	150	160	170	180
m516.pep	190	200	210	220	230	239
	EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq
 1 ATGTTGTTC GTAAACGAC CGCGCCGTT TTGGCGGCAA CCTTGATGTT
 51 GAACGGCTGT ACGGTAATGA TGTGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTCGGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAGG GGCAGCCTGG TGATGATGGG
 201 CGGGAATAC TGGTTCGTG TCAATCCTGA AGATTCGGCG AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTG CCTACCAAGC CCTGCCGTC AACTCGAAT CGCCCGCCAG
 351 CCAGAATTTC AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTT AGTTTGAAG GGTGGAATCT
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCGCCAAAG GCAAATACTA
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACAG GTTACGAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAT ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCGGT
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

773

```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFFVNPEDSA KLTGILKAGL DKQFQMVPEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

m516.pep      10      20      30      40      50      60
MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVVDKDQIRAFGVVAEDNAQLEK
|||||
a516          10      20      30      40      50      60
MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVVDKDQIRAFGVVAEDNAQLEK
|||||

m516.pep      70      80      90      100     110     120
GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSON
|||||
a516          70      80      90      100     110
GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKQFQMVPEPNPRFA-YQALPVKLESPASQN
|||||

m516.pep     130     140     150     160     170     180
FSTEGLCLRYDTPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
|||||
a516         120     130     140     150     160     170
FSTEGLCLRYDTPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
|||||

m516.pep     190     200     210     220     230     239
EQSVADIYYTVTEHTDKSKLFANILYTPFFLILDAAGAVLALPAAALGAVVDAARKX
|||||
a516         180     190     200     210     220     230
EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatcccgatt tgatgttttt gggcagggtcg atttggtcgg
201 tgtcgccggg aatgacggct ttcgcgccga agccgatgag ggtcaggaaac
251 attttcattt gttcgggctt ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgccgttg agcgtcctgc cgcgcataata ggcgagcggg gcgatttcaa
351 tcaggccctt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag ggtcgcactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQRMPE NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRPFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIBGIIKR TEVGVDLFGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCTG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTGAGGAAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCTGA GGATGATGTA
301 TCGCCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCGATTTCAG
351 TCAGGCCCTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep

1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : : :					
g517	MHRVSDGIGVSVVFCRFVGFDDFLHQMPDNVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDCAVERPAAHIGERGDFNQAF					
	: : : : : :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : : :					
g517	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq

1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCAGC
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGCAGGTCG ATTTGGCTGG
201 TGTCGCGCGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTGAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TCGCGCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCGAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep

1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : : :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDCAVERPAAHIGERGDFNQAF					
	: : : : : :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDCAVERPAAHIGERGNLQTF					

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	70	80	90	100	110	120
m517.pep	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	130	140	150	160		
	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1  atgacgtttt  cggcggcaaa  gctcaacatt  tcggcactga  tgttggtgtct
51  ttcggcagga  atgaccgttt  tactttccgc  ttttttactg  ctccgaccgg
101 aaggcagcat  cttattcaac  cattttttca  gcataaatat  tctgaccgga
151 agagcggcat  ctccacgggc  aaccgtgttc  agactgcata  aggcggtacg
201 attccacaag  atgccgaaaa  ccataagcaa  aatgcgtaga  aactacgccg
251 tccgaatcac  gccgcctect  cggcgggcaa  cgcttcatta  taacagattg
301 ccccttaaaa  aatcacagacc  tgcttttgtg  gcggagtctg  aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1  MTFSAAKLNI  SALMLCLSAG  MTVLLSAFLL  LRPEGSILFN  HFFSINILTR
51  RAASPRATVF  RLHQAVRFHK  MPKTISKMR  NYAVRITPPP  RAATLHYNRL
101 PLKKSDFAFV  AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1  ATGACGTTTT  CGGCGGCAAA  GCTCAACATT  TCGGCACGGA  TGTGTGTGCT
51  TTCGGCAGGA  ATGACCGTTT  TACTTTCCGC  TTTTACTGCT  CTCCGACCGG
101 AAGGCAGCAT  CTTATTCAAC  CATTTTTCAT  GCATAAATAT  TCTGACCCGA
151 AGAGCGGCAT  CTCCACAGGC  AACCCTGTTC  AGACGGCATC  AGGCGCGGTT
201 TGCAAGATGC  CGTACCATAA  ACAAAGGCG  TAGAACTAC  GCCGTCGGAA
251 TCACGCCGCC  CTCGCG.GCG  GCAACGCGTC  ATTATAACAG  ATTGCCCTCC
301 GCGGCAGGCT  TAGTGCGGCG  GGAGCGCCGC  CGTTGCGCAG  TAATATTGTC
351 TAACGGGAGG  AAAAAATCAG  ACCCTGCTTT  TGTGGCAGAG  TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1  MTFSAAKLNI  SARMLCLSAG  MTVLLSAFLL  LRPEGSILFN  HFFSINILTR
51  RAASPOATVF  RRHQARFARC  RTINKRRRNY  AVRITPPSXA  ATRHYNRLPS
101 AAGLVRRERR  RCAVILSNGR  KKSDPAFVAE  SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep  MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
g518      MTFSAAKLNI SALMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
          10      20      30      40      50      60

          70      80      90      100     110
m518.pep  RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSN
g518      RLHQAVRFHKMPKTISKMRNRYAVRITPPPRATLHYNRLPL-----
          70      80      90      100

m518.pep  120      130
g518      GRKKSDFAFVAESEI
          110
g518      --KKSDPAFVAESEI
          110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCGACCCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTTCa GCATAAATAT TCTAACCCTGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCAGGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....AAAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*

m518/a518 79.9% identity in 134 aa overlap

              10      20      30      40      50      60
m518.pep  MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
          |||
a518      MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
              10      20      30      40      50      60

              70      80      90      100     110     119
m518.pep  RRHQA-RFARCTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSNG
          ||| : |||
a518      RRHQAVRFRKMPTINKRRRNYAVRITPSSXAATRHYNRLPS-----
              70      80      90      100

m518.pep  120      130
          RKKSDPAFVAESEIX
          |||
a518      -KKSDPAFVAESEIX
              110
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgcccgtt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcggy ggcttggggt
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccgcct tcaaaaccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggaattaag cccgccaagg ttgccgaaat cgggaaccct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaataa
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

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101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGAEQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAAN
 251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
 301 NFRRHEKFSP EAKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

m519.seq (partial)
 1 ..TCCGTTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
 51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
 101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
 151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
 201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
 251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
 301 GCGGTCAATG CGTCAAATGC CGAGAAAAATC GCCCGCATCA ACCGCGCCAA
 351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
 401 TCCGTCAAAT TGCCGCGGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
 451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
 501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGGAC ATCGGCAGCC
 551 TGATTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

m519.pep (partial)
 1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIROIAAA LQTGGADAV
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGLISAGMK IIDSSKTAK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE				
g519	GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE					
	150	160	170	180	190	200
m519.pep		100	110	120	130	140
		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA EAIROIAAALQTGGADAV				
g519	IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA EANRQIAAALQTQSGADAV					
	210	220	230	240	250	260
m519.pep		160	170	180	190	200
		NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL- ISAGMKIIDSSKTAK				
g519	NLKIAGQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK					
	270	280	290	300	310	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

a519.seq
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT

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201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGTTGCCG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGRKSFV VIPQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GOREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAELI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519/a519 99.5% identity in 199 aa overlap

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
a519 YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
a519 GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAVNASNAEKIARINRAKGEAESLRLVAEANAELIRQIAAALQTQGGADAV
a519 IQQSEGEAQAVNASNAEKIARINRAKGEAESLRLVAEANAELIRQIAAALQTQGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSTAKX
a519 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC GAACGCGGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGT AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGGGGCGG ATGCGGTCAA

```

801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPOQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVA YRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
 101 SNYIMAITQL AQTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.aeq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAAGT CCACGTTGTC GAAAGGCTGG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCGTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTTGCG GCTTTGGACG AGCGCGCCGG GGCTTGGGGT
 451 GTGAAGGTTT TGCATTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAAGCGGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTACGCGCG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAG
 701 GTGAAGCGGA ATCCTTGCGC CTGTTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAAAATG CGCGCCCTT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPOQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVA YRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
 101 SNYIMAITQL AQTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep						
m519-1						

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```
m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240
              250      260      270      280      290      300
g519-1.pep   LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep   ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

a519-1.seq

```
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCTC ATACGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAC GTTTGAAGAA CGGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCGCGCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTGAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTGTTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

a519-1.pep.

```
1  MEFFIILLAA VVVFQKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPP
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 GQREAEIQQS EGEAAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*
```

m519-1/a519-1 99.0% identity in 315 aa overlap

```
              10      20      30      40      50      60
a519-1.pep   MEFFIILLAAVVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPPIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPPIDRVAYRHSL
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep   KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep   RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep   KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              |||||
```

m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR	190	200	210	220	230	240
		250	260	270	280	290	300
a519-1.pep	LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL						
m519-1	LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL						
		250	260	270	280	290	300
		310					
a519-1.pep	ISAGMKIIDSSKTAKX						
m519-1	ISAGMKIIDSSKTAKX						
		310					

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaacct gtttgcgcgc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgcgcg ttc aaattgg acgatgacgt tttgttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgcccga caattcgacc aagacatcga cgtctttacg
351 cggaacagt tcgaacggat cttttgacaa gggcgggcga cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccaa gggcggggaa atttcctctg cgttgtcccg caacacggca
501 gccgcaccgc cgccgaccgt acctaagcct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDLILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCGGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

```

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```

301 GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCACACAGT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
401 TTGTGCGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCTCCG CGTTGTCCsCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1 MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDLILFAA KPSRRALMIG
  51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
 101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
 151 RAPSDGKFPP RCXATROPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520
      10      20      30      40      50      60
m520.pep MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW
|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g520      MPALLSIRANALPFSRISERMKLLVPLIMPAMDILILFAAKPSRTALMIGIPPATAASNW
      10      20      30      40      50      60

      70      80      90      100     110     120
m520.pep TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g520      TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
      70      80      90      100     110     120

      130     140     150     160     170     180
m520.pep SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPFRCXATROPYRRRPYPNLKDR
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g520      SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFLRCPATRQPHRRRPYLSLKDR
      130     140     150     160     170     180

      190
m520.pep CLLASLCLLVSRKCKY
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g520      CLLASLCLLVSRKCKY
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1 ATGCCTGCGC TTCTTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
  51 CATTTTCGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCAGTGG
 101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
 151 ATACCGCCCG CTAATGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
 201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTGG
 251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
 301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
 351 TGCACACAGT TCGAACGGAT CTTTGACAAA GGCTG.CGG ACGGGCAGGT
 401 TTGTGCGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGATT
 451 CGCGCCCCAA GCGACGGGAA ATTTCTCTCCG CGTTGTCCCG CAACACGGCA
 501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
 551 CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1 MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDLILFAA KPSRRALMIG
  51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
 101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```


151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCTGTTG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSILTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCTGTTG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTC GGGCTTTTTC
351 TTCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```

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101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
 151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRAFSSLK	
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSSLK	
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKR	REISSALSRNTA	APPTVPKPKRPM	FTGFIVSPCKP	TEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTA	AVPPPTVPKPKR	PMFTGFIVSPCK	PTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq
 1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
 51 TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
 101 CTGCCGCTTC AAATTGGACG ATGACGTTT GTTTTCCGC CAGCGGAAG
 151 ATTTCTGTTG CGTATTGGGC GAGCAGTTT TTGTTGGCGG TAACGATGTG
 201 TTGCGCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
 251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACAGTGC GACCAGTTTCG
 301 AACGGATCTT TGACAAGGC TCGGGACGGG CAGGTTTGTG GGGCTTTTTC
 351 TTCACTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCAAGCGAC
 401 GGGAAATTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
 451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
 501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep
 1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTCFCSASGK
 51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
 101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
 151 TVPKPKRPMF TGFIVSPCKP TEM*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSSLK	
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSSLK	
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKR	REISSALSRNTA	AVPPPTVPKPKR	PMFTGFIVSPCK	PTEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTA	AVPPPTVPKPKR	PMFTGFIVSPCK	PTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq
 1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTC AAG
 51 CCATTGGGT GCGAATGCGG CCAAATCTA TACCTGCACA ATCAACGGAG
 101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAAACTCC
201 CGAACCGGCA CCATCACC GT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaag
351 cAatgaacgc aaagccctGa ctGaAGCCCC AAAAATGTGA TCACAagcac
401 gtCtGGCAAA AGGCGgcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451 AGCAATGTTt tggacAGACA GCAAAATaTc Caagcactgc aaaGAGAAAt
501 GGGCGCTATG TAA

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

q521n.pep

```

1  MKSKPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTDL
51 PFIGNYSRR YILPQTPEPA PPSNGGQAV KYKAPVKTVS KPAKSNTPPQ
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGN INHQKINAL*
151 SNVLDRONI QALORELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1473>:

m521.seq

1	ATGAAATCAA	AACCTCTCTT	AATCCTAATC	AACCTTTTCCC	TGATTTCAAG
51	CCCATTGGGT	GCGAATGCGG	CCAAAATCTA	sACCTGCACA	ATCAACGGAG
101	AAACCGTTTA	CACCA _s CAAG	CCGTCCAAAA	GCTGCCACTC	AACCGATTTG
151	CCCCCAATCG	GCAACTACAG	CAGCGAAGCG	TATATCCCGC	CCCCAACGCC
201	CGAACCGGTA	TCATCAACCGT	CAACCGCGCG	ACwGGTTGTG	ACCATATAAG
251	CCCCGGTCAA	AACAGTATCC	AAGCCGGCAA	ATTC _{CA} TATAC	GGCGCCGCGC
301	CAACAAGCAC	CCTCAAACAA	CAGCAGACGC	TCCATTCTCG	AAACAGAATT
351	GAGCAACGAA	CGCAAAGCAT	TGTTTGAAGC	CCAAAAATG	TTATCACAAG
401	CACGTCTGGC	AAAGGGCGGC	AACATCAACC	ATCAAGAAAT	AAATGCATTA
451	CAAAGCAATG	TATTGGACAG	GCAGCAAAAT	ATTCAAGCCC	TGCAAAGGGA
501	ACTGGGCGGT	ATGTAA			

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

m521.pcp

```

1  MKSKLLLLILI NFSLLSSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTDL
51  PPIGNYSSER YIPPQTPEPV SSPSNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROON IOALORELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/q521

```

      10      20      30      40      50      60
m521.pep  MKSKLLILINFLISSPLGANAAKIXTCTINGETVYTXKPSKSCSTDLPPIGNYSSER
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g521      MKSKLPILILINLSLISSPLGANAAKIYTCTINGETVYTTKPSKSCSTDLPPIGNYSSER
          10      20      30      40      50      60

      70      80      90      100     110     120
m521.pep  YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNSRRSILETELSNE
          ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g521      YILPQTPEPAPSPSNGGQAVVKYKAPVKTVSKPAKSNTTP-QQAPVNNSRRSILEAELSNE
          70      80      90      100     110

      130     140     150     160     170
m521.pep  RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g521      RKALTEAQKMLSQARLAKGGNINHQKINALXSNVLDROQNIQALQRELGRMX
      120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

a521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAAG

```

51 CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAAA GCTGCCTCTC AACCGATTTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCAGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AACAGAAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CAGTCTGGC AAAAGGCGG CACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAAGAGA
501 ATGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYCT INGETVYTTK PSKSLSTDL
51  PPIGNYSSER YIPPQTSEPT PPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQON IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFLISSPLGANAAKIXTCTINGETVYTXKPSKXSCHSTDLPPIGNYSSER					
a521	MKSKLPLILINFLISSPLGANAAKIYCTINGETVYTTKPSKSLSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE					
		:		:		
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcaccat ccgcatttgg gcgtgggtca
101 ttttggcggt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatattcc
201 gtttgcgtga aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccg tctcgccgtc gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtg
351 acaagaacag cttgacctgc tcggcggcgc aaacgcgttt gaaactcgag
401 acaacaatg tgtcgcggtt ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
51  KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGGG GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCAATG CCGATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTGCGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAAA ACGATTGCGG GGCCCGCGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```


788

```

                130      140
m522.pep      LDLLGGANAFEARDKQCVADLKSEX
               |||||:|||||
a522          LDLLGGANAFETRDKQCVADLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
  1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51  gacgggaacg gtttatcttt tggtgttcag cgcggctttg gcgggttcgg
101 gcattgccta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gcactgcttt ccgcgctggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga tttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcctcgccc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
  1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
  1  ..GCCGTCCTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCTGCCGCG CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTTnG
151 TTCGTACACG CCAAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCGGACAAT ATGTCGAAAT CCTCCGACAC ACAGCGGGCA
251 ACCGTTACGA AGTTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCATTG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
  1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLG AGQYVEILRH TGGNRYEVFY RgTHWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTXALLSALGIXF
               |||||:|||||
g523          MTVWFVAAVAVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLGAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
               |||||:|

```

g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
1   ATGACTGTAT GGTTTGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51  GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCGCT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GGCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
1   MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDYQDLDA GQYAEILRHA GGNRYEVFVR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
1   atgaagtacg tccggttatt tttcctcggc acggcactcg cccgcactca
51  agcggcggct gccgaaatgg ttcaaatcga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcctgatta agtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaacccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggg taccaatatt tcctggtttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttccgcc acgcagaaaa aacggctcaa acgaacccgg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaagca ccgcccgaac tactgggggtg tttatgatat
551 gcacgggctg a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
1   MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW OKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRTR
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

m525.seq
 1 ATGAAGTATG TCCGGTTATT TTWCCTCGGC GCGGCACTCG cCrCACTCA
 51 ArCGGCGGCT GcCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCrC
 101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
 151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
 201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
 251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGc GCCGAAGgCG
 301 GgCGAATTAA AACAACCGGT AACCAATGTT TCCTGGwTG CCGCCAACgC
 351 CTAtTGC GCCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
 401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
 451 CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
 501 TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
 551 GCACGGGCTG A

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

m525.pep
 1 MKYVRLFXLG AALAXTOXAA AEMVOIEGGS YRPLYLKDDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGRSYAPKA
 101 GELKQPVTNV SWXAANAYCA AQGKRLPTID EWEFAGLASA TQKXRLKRTR
 151 LQPHYSRLVC RRRTERPARC RXKAARTGA FMICTG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

m525/g525

	10	20	30	40	50	60
m525.pep	MKYVRLFXLGAALAXTOXAAEMVOIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF					
	:					
g525	MKYVRLFFLGTALAGTQAAAEMVOIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGRSYAPKAGELKQPVTNVSWXAANAYCA					
g525	AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGRSYAPKAGELKQPVTNISWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525.pep	AQGKRLPTIDWEFAGLASATQKXRLKRTRLQPHYSRLVCRRTTERPARCRXKAARTTGA					
g525	AQGKRLPTIDWEFAGLASATQKRLKRTRLQPHYSRLVCRRTTERPARCQSTARTTGV					
	130	140	150	160	170	180
m525.pep	FMICTGX					
g525	FMICTGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

a525.seq
 1 ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
 51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
 101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
 151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
 201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
 251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
 301 GGCGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTCG CCGCCAACGC
 351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
 401 TTGCCGGACT TGCTTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
 451 CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
 501 TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
 551 GCACGGTCTG A

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
1  MKFTRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          ||::||: | |||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      MKFTRLLFLCAALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          10      20      30      40      50      60

      70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAAANAYCA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
          70      80      90      100     110     120

      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRLRLQPHYSRLVCRRTTERPARCRXKAARTTGA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AQGKRLPTIDWEFAGLASATQXKRLKRLRLQPHYSRLVCGWRPERPARCRQXVARTTGA
          130     140     150     160     170     180

m525.pep  FMICTGX
          ||||
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
1  ATGAAGTACG TCCGGTTATT TTCTCTCGGC ACGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGCAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAA CGAACC CGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAGGCCT
501 GCACGATGTC GGCAAAGACC GCCCGAATA CTGGGGTGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACTATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAACT TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKGLHDV GKDRPNYWG YDMHGLIEW TEDFNSLLS
201 SGNANAQMF C SGASVGASDS SNYAFLRYG IRTSLQSKYV LHNLFRCAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
1  ATGAAGTATG TCCGGTTATT TTCTCTCGGC GCGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

792

```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1 MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGRSRYAPKA
101 GELKQPVTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWG YDMHGLIEWE TEDFNSSLSS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLFRCRCS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLG	AALAGTQAAA	AEMVQIEGGS	YRPLYLKDT	GLIKVKPFKL	DKYPVTNAEF
g525-1	MKYVRLFFLG	TALAGTQAAA	AEMVQIEGGS	YRPLYLKDT	GLIKVKPFKL	DKYPVTNAEF
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQW	QKGRIGSKQA	EPAYLKHWK	MNGRSRYAP	KAGELKQPV	TNVS
g525-1	AEFVNSHPQW	QKGRIGSKQA	EPAYLKHWK	MNGRSRYAP	KAGELKQPV	TNIS
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTID	EWEFAGLASA	TQKNGSNEP	GYNRTILD	WYADGGKRL	HDVGKGRPN
g525-1	AQGKRLPTID	EWEFAGLASA	TQKNGSNEP	GYNRTILD	WYADGGKRL	HDVGKDRPN
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWE	TEDFNSSLSS	SGNANAQMFC	SGASIGSSD	SSNYAAFLR	YGIRTSLSKYV
g525-1	YDMHGLIEWE	TEDFNSSLSS	SGNANAQMFC	SGASVGSAS	SSNYAAFLR	YGIRTSLSKYV
	250					
m525-1.pep	LHNLFRCRCS					
g525-1	LHNLFRCASR					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```

1 ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCG GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGRKDLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSLSS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

```

              10      20      30      40      50      60
m525-1.pep  MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              ||::|||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
a525-1      MKFTRLFLC AALAGTQAAA AEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60

              70      80      90      100     110     120
m525-1.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVNTVSWFAANAYCA
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a525-1      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA
              70      80      90      100     110     120

              130     140     150     160     170     180
m525-1.pep  AQGKRLPTID EWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWGV
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a525-1      AQGKRLPTID EWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYWGV
              130     140     150     160     170     180

              190     200     210     220     230     240
m525-1.pep  YDMHGLIEWE TEDFNSSLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a525-1      YDMHGLIEWE TEDFNSSLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV
              190     200     210     220     230     240

              250
m525-1.pep  LHNLGFRCTSRX
              || | | | | | |
a525-1      LHNLGFRCTSRX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atggttttac cagtctcctt ttttcagcct gtccagttgg cggcggtcgc
51  gcttggtcgg tctgccgtcg ggatgggagg aagtgatgag gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtctctctc
151 atacagaagc cgcgcctcgg gtgccgggag gcggttggtg ttcaaacctt
201 taaccttgat tttatgggga agggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tggttttact gtttttgact ttcgagccgt ttacttgaac
301 cctaccagct tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
351 gtgccgccca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatac gattttgttt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLVPSFFQP VLAAVALGR SAVGMGGS DAELVELFALF PQCCRFRVFF
51  IQKPRLGCR ALVVQTFNLD FMKGIERQV DNIADVYGFT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51  GCTTGGTCCG TCTGCCGTCTG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCCTCTCTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```

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```

201 TAACCKTGAT TTTATAGGGA AGGG.AATTk AgCkTCaGty GrTwATaTCG
251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTGTT GAAATAATTG AATTGTGTTT GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

```

m527.pep
1  MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLf
51  IQKPRXGCRA ALVVQTFNxD FIGKXNXASV XXIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRXRVLf	IQKPRXGCRA
g527	MVLPSVFFQP	VQLAAVALGR	SAVGMGSDA	AELVELFALF	PQCCRFRVFF	IQKPRXGCRA
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNxD	FIGKXNXASV	XXIADVYGFT	VFDLRAVYLN	PTQFDVLLRK	GTGLEKTCRP
g527	ALVVQTFNLD	FMGKIERQVD	NIADVYGFT	VDFRAVYLN	PTQFDMLLRK	GTGLEKTCRP
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
g527	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

```

a527.seq
1  ATGGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG
51  GCTTGCTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TCGCTCTTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
251 CCGATGTCTA TGGTTTTACT GTTTTGTACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTGTT GAAATAATTG AATTGTGTTT GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

```

a527.pep
1  MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLf
51  IQKPRXGCRA ALVVQTFNLD FIGKIERQV DNIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRXRVLf	IQKPRXGCRA
a527	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRFRVLf	IQKPRXGCRA
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.pep	ALVVQTFNDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc gggaataaaa atatacggca acggtgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 ccggttggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggcggcgaga gtccgctgtc ttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatcctt
251 actttttatag gaaaataggg aagtttgaag cctgcgggtt ggattggcgt
301 acgcgtgacg gcaaaccttt gtttgagagg ttcaaacagg aaggtttcga
351 ctgtttggaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLGWCKPR KPAAIDFWDI
51  GGESPLSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQGGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGAA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

```

m528/g528
10      20      30      40      50      60
m528.pep MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||
g528      MEIRVIKYTATAALFAFTVAGCRLAGWYEC LSLGWCKPRKPAAIDFWDIGGESPLSLGD
      10      20      30      40      50      60
m528.pep YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||
g528      YEIPLSDGNSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQGGFDCLE
      70      80      90      100     110     120

```

m528.pep K
|
g528 KQGLRRNGLSERVRW

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

a528.seq
1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

a528.pep
1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

m528/a528 95.0% identity in 121 aa overlap

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
a528	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
a528	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE					
	70	80	90	100	110	120

m528.pep K
|
a528 KQGLRRNGLSERVRW
130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

g528-1.seq
1 ATGGAAATTC GGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCAAT
51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGAA AAGCAGGGGT TCGGCGCAA CGGCTGTCC GAGCGCGTCC
401 GATGGTAA

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

g528-1.pep
1 MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

m528-1.seq
1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT

```

51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGA
351 CTGCTTGAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAIDFWDI
51  GGESPPSLGD YEIPLSDGNR SVRANEYESA QSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

	10	20	30	40	50	60
g528-1.pep	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAIDFWDIGGESPLSLED					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g528-1.pep	YEIPLSDGNRSVRANEYESAOKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE					
m528-1	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE					
	70	80	90	100	110	120
	130					
g528-1.pep	KQGLRRNGLSERVRWX					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

	10	20	30	40	50	60
a528-1.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAIDFWDIGGESPPSLED					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a528-1.pep	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE					
m528-1	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE					
	70	80	90	100	110	120
	130					
a528-1.pep	KQGLRRNGLSERVRWX					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
  1 atgaccata tcaaaccgt cattgccg ctcgcactca tcgggcttgc
 51 cgcctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggtcgcaccg cctgatcaaa ctcgaagtcc cgcctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc ggttcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcgatg
251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgcgt tgacggcaaa tccccgccg aaatctccgc
351 cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
 51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF..
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
  1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
 51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTCGCACCG CCTGATCAAA CTGGAAGTCC CACCTGATTT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GGCAGCGCGG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCACACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCCCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TCGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
 51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAELVLSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPAIGQME TEWAENRAKI
151 PQDSLRLRFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDTTV WQPSPSDPNL EAAFLTRFMQ YLGVDGQOAE NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

```
g529/m529
          10      20      30      40      50      60
g529.pep MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA
```


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```

m529.pep  FWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRLRFDKVLGGIYSTGERDKFIVRI
           |||||
a529       FWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRLRFDTVLGGIYSTGERDKFIVRI
           130      140      150      160      170      180

           190      200      210      220      230      240
m529.pep  EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQFSPSPDNLEAAFLTRFMQYLGVDGQQAE
           |||||
a529       EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQFSPSPDNLEAAFLTRFMQYLGVDGQQAE
           190      200      210      220      230      240

           250      260      270      280      290      300
m529.pep  NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQONTERHAFLVQ
           |||||
a529       NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQONTERHAFLVQ
           250      260      270      280      290      300

           310      320      330      340      350      360
m529.pep  KAPNESNAVTEQKPLFKRLLGKGKAEKPAEQPELIVYAE PVANGSRIVLLNKDGSAYAG
           |||||
a529       KAPNESNAVTEQKPLFKRLLGKGKAEKPAEQPELIVYAE PVANGSRIVLLNKDGSAYAG
           310      320      330      340      350      360

           370
m529.pep  KDASALLGKLHSELRX
           |||||
a529       KDASALLGKLHSELRX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga ggcgcgcaat gacgggtttg atatgggtca tcgtgtcatc
51  ctgtgtgatg gatattaaag tggttgatcat gttatgccgt ccgaacgggt
101 cagacggcat ggctatatatt aaagtgtgcc tgaggctttc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtccgc atccgcccaa ggcggatacc gcccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgctgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCV M DIKVFVMLCR PNGSDGMAIF KVVLRLSGRR
51  GLLPVRLPSA ERAAGARAVR IRPRIPPIS VRRDWVRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  WTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTCA TC
51  sTGTGTGATG GATATTAAAG TGtYtGTTGC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGA CTkTTGC wTGTCGTTT yCCGTCAGCG GAACGAGCGG CAGGCGGACG
201 TGC GGTTCGC ATCTGCCCAg GCGGATAACC GCCCATTTTC GTGCGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCV M DIKVXVAXCR PNGSDGMXIF KVVLRLSGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

```

m530.pep  XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA
           |||||

```

g530	MSASAAMTGLIWVIVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVRI C PGRI P PISVRRGWVRRTWCRKSES V GR	99
	: :	
g530	ERAAGARAVRIRPRRI P PISVRRDWRRTWCRKSESAGR	99

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1529>:

```

a530.seq
1  ATGAGTGCGA GCGCGGCAAT GACGGGTTTG ATATGGGTC TCGTGTCA TC
51  CTGTGTGATG GATATTAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTCG CTGTCCGCCT TCCGTCAGCG GAACAGGCGC CAGGCGGAGC
201 TGCGGTTTCG ATCTGCCCCA GTCGGATAAC GCCCATTTCC GTGCGGCGGG
251 GCTGGGTTTC CAGAACATGG TGTGCTAAAT CGGAATCAGC CGTCGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1530; ORF 530.a>:

a530.pep
1 MSASAAMTGL IWVIVSSCVM DIKVFVALCR PNGSDGMAIF KVLRLSRR
51 GLLPVLRLPSA ERAAGGRAVR ICPGRIPPI S VRRGWVRRTW CRKSESAGR*

m530/a530 93.9% identity in 98 aa overlap

```

          10          20          30          40          50          60
m530.pep  XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA
          |||||
a530       MSASAAMTGLIWVIVSSCVM DIKFVVALCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA
          10          20          30          40          50          60

          70          80          90         100
m530.pep  ERAAGGRAVRICPGRIPPISVRRGWVRRTWCRKSESVGRX
          |||||
a530       ERAAGGRAVRICPGRIPPISVRRGWVRRTWCRKSESAGR
          70          80          90         100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 1531>:

```
g531.seq
  1  ATGACCGCCC  TACTCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCAGGCATC  GTCTATCCCG  CCCTGCCCGG  CTGGGCATTG  ATGTTTGC CG
101 GAACATGGCT  GCTTGCCTAT  GCCGGCGGCT  ATCAAATCTA  CGGCGCAGCG
151 ATCTTTGTGA  CGTCCGGACT  CATCAGCCTT  GCGGCATAC  TGGCGGACTA
201 TATGGCAGGC  ATGTTGGGGG  TAAAAATAC  TGGGGCAGCA  AACTCGCGCG
251 TCCGAGGTGC  ATTGGCCGGC  AGCATCATCG  GCATATTTT  CTCCTTCCC
301 GGAATAATAC  TCGGCCCTT  TATCGGCGCG  GCGGCAGGCG  AACTGATCGA
351 TCGGCGTAAT  CGCTTTCAG  CAGGTAAAG  GGGCTTGGT  ACGCTGTTGG
401 GGTCTGTCT  GTGCACGGCG  TTCAAAATCG  GCTGCGCGGT  ATCCATCTTG
451 TTTATCTGT  TGGTGAATA  CATCGCATAC  CTGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1532; ORF 531.ng>:

g531.pep

1	MTALLVILAL	ALIAVGTAGI	VYPALPGLAL	MFAGTWLLAY	AGGYQIYGAG
51	ILWTVGLISL	GGILADYMG	MLGVKYTAG	KLAVRGALAG	SIIGIFSLP
101	GLILGPFIGA	AAGELIDRRN	MLQAGKAGLG	TLLGLVVGTA	FKIGCAVSIL
151	FILLVKYIAY	LF			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1533>:

m531.seq

```
1  ATGACCGTAC  TGACCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCGGGCATC  GTTTaCCCCG  CCCTGCCCGG  ATTGGCATTG  ATGTTTGCCG
101 GAACATGGCT  GCTTGCCCTAT  GCCGGCGGCT  ACCAAATCTA  CGCGCGCGGC
151 GTTTTGTGGA  CGGTCCGACT  CATCAGCCTT  GCCGGCCTAT  TGGCGGACTA
201 TGTGGCAGG  ATATGGGGGA  CAAAATATAC  CGGAGCAGGC  AAGCTCGCCG
251 TTCGCGCGC  ATTGGCCGGC  AGCATCATCG  GCATATTTT  CTCCTTCCC
301 GGACTAATAC  TCGGTCCCTT  TATCGGCGCG  GCGGCAGGCG  AACTGATCGA
```

m531.ppt

```

1  MTVLTVILAL ALIAVGTAGI VYPALPGLAL MFACTWLLAY AGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTYKTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m531/g531

[illegible]

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCTGATAG	CGGCCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTTGGT	CGTCGCCTAC	TCCGCGCGCT	ACCAATCTA	CGCGCGGGC
151	GTTTTGTGGA	CGGTGGACT	CATCAGCCTT	GCCGGCATA	TGGCGGACTA
201	TGTGGCAGG	ATATGGGGGA	CAAAATATAC	CGGAGCGGGC	AAGCTCGCCG
251	TTCGCGGCGC	ATTGGCCGGC	AGCATCATCG	GCATATTTT	CTCCCTTCCC
301	GGACTAATAC	TCGGTCCCTT	TATCGGCGCG	GCGGCAGGCG	AACTGATCGA
351	ACGGGCAAT	ATGCTTCAG	CAGGTAAAGC	GGGCTTGGGT	ACGCTGTTGG
401	GGCTTATCGT	CGGTACGGCG	TTCAAAATCG	GCTGCGCGGT	ATCCATCTTG
451	TTTATCTCTGT	TGGTGAATA	CATCGCCTAC	CTGTTTTAA	

a531.pep

```

1  MTALLVILAL ALIAAGTAGI VYPALPLAL MFAGTWLLAY SGGYQIYAG
51  VLWTVGLISL AGILADYVAG IWGKYGTAG KLAVRGALAG SIIGIFFSLP
101 GLILPFFIGA AAGELIERN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

```

	10	20	30	40	50	60
m531.pep	MTVLT	VILAL	ALIAV	GTAGI	VYPAL	PGLAL
	MFAGT	WLLAY	AGGYQ	IYGAG	VLWTV	GLISL
	:		:		:	
a531	MTALL	VILAL	ALIAA	GTAGI	VYPAL	PGLAL
	MFAGT	WLLAY	SGGYQ	IYGAG	VLWTV	GLISL
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILAD	YVAGI	WGTYT	KGAGK	LAVRG	ALAGS
	IIGIFF	SLPGL	LILGP	FFIGAA	AGELI	ERRN

803

```

a531      |||||
          AGILADYVAGIWGTYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN
          70      80      90      100      110      120

          130      140      150      160
m531.pep  MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          |||||
a531      MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1 atggctgaaa caatgaaaaa acaggcggat tcgcctgatt tgggtgacgg
51 tttggaagac aggcgcgcgt tcggtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cgcccgcgct gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgtcgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1 MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51 GALELPVEMT AYLVSAMVA SGVGYTLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1 ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51 TTTGGAAGAC AGGCGCCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCgcgctgg AATTGCCGgt GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTGCGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTTC GCGGCGGCTT CGGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTGCGCA TGAGCGGCAT
651 TCGGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG TGTGGCTGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGC GCA AAACAACGGC GTGATTGAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTT GATGTTCCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTG CATTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGT CCAAACCTCT ATTTCGCCC
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1 MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51 GALELPVEMT AYLVSAMVA SGVGYTLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```



201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NPLPLVTLPVP
251 FKYGFAPDWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL
301 RGGVLA DGLV SVIATALGSL PLTTFAQNNG VIQMTGVA SR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA
401 VIATSVGLG LGVAFEPFV KNPVLVFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKPDTH LEH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

q532/m532

	10	20	30	40	50	60
g532.pep	MAETMKKQADSPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	: :	: :	: :	: :	: :	: :
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLSIQRYRHCARRGDERGRFEX					
	: :	: :	: :	: :	: :	: :
m532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532.seq

```
1 ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51 TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGATGCTG GCACATTATT CGAGGTCAAC CGCTTCGGGC
251 CGGTCCGGTTC GGGGATGCTG TCCATCCAGT GCGTGAATTT CTCGTTCTGTT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT TTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGGTACA
501 CGTCGGTATT ACCGATTTCG GCGGCGGCTT CGGCGCAAAG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCGC CTGCTGCGGA TGAGCGGCAT
651 TGCGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCAC TGCAA AACCTGCCGC TGTTTACGCT GCCCGTACCG
751 TTTAAATATG GTTTTGCTTT TGA CTGGCAC GCATTTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATT TG ACGGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGCG AGGAATACAC CAAACGCTTG
901 GCGGCGCGCG TGTTGGCGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGCAGA CCGTTGCACA AACCAACGGC GTGATT CAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGCGC CGATGGTTTT GATGTTCCGC TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GCGAGTCTTG CTGAATTTGG TCTTGCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA
```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pap

1	MSGQLGKGAD	APDLVYGLED	RPPFGNALLS	AVTHLLAIFV	PMITPALIVG
51	<u>GALELPVEMT</u>	AYLVSMAMVA	SGVGTYLQVN	RFGPVGSGML	SIQSVNFSFV

805

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
 151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
 201 VLVFNCKMNP LLRMSGIAVG LIAGYIVALE LGKVDLSALQ NLPLVTLVPV
 251 FKYGFADWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
 301 RGGLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRL VSHGIRREA
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
 451 EAARKFDTDH LEH*

m532/a532 100.0% identity in 463 aa overlap

m532.pep	MSGQLGKGADAPDLVYGLED	RPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532	MSGQLGKGADAPDLVYGLED	RPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
m532.pep	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM	
a532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM	
m532.pep	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK	
a532	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK	
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCKMNP LLRMSGIAVGLIAGYIVALFLGKVDLSALQ	
a532	ADGTFGSMENLGLASLVLLIVLVFNCKMNP LLRMSGIAVGLIAGYIVALFLGKVDLSALQ	
m532.pep	NLPLVTLVPVPFKYGFADWHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL	
a532	NLPLVTLVPVPFKYGFADWHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL	
m532.pep	RGGLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASR HVGKYIAVILVLLGLFPVVG	
a532	RGGLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASR HVGKYIAVILVLLGLFPVVG	
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRLVSHGIRREAVIAATSVGLGLGVAFEPEVF	
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRLVSHGIRREAVIAATSVGLGLGVAFEPEVF	
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX	
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

1 atgccctttc ccgttttcag acaantattt gcttngtcct tgctacggtt
 51 ttttgccgta ggtcggatcc tcgaatccga catttccaac agcgggtttt
 101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
 151 gcctgcattt caaatattaca tcgcttccaa ttctgcaaac ttggtatcca
 201 gttctttcac gccctgtttg ccgaagtgtg ttggtcagtcg ggcggattcg
 251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
 301 gacgttttgt ccgatgcgga agcctgcgta ggtttgccgc tgtttgaagt

806

```

351 catcgatgat tttgtcccgt tgtacggtgg tttggcgcgt gttgccgtag
401 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcgatgcc gaattgggtt tgtccgtgca
501 gcatgcgttg ctgtgccatg gtgatgtaga ggcgtttgcg ggcgcgggtg
551 atggcgacgt acatgagggc gcgttcttct tcgagggcgc cgcgctcggc
601 aaggctcatt tcgctgggga aacgcccctc ttccataccg gtgaggaaga
651 cggcgttgaa ttccaagcct ttggcggcgt ggacggtcac cagttaggacg
701 gcttttttcg ctgcccctgc ttggttttcg ccggaattcga gggcggcgtt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

```

g535.pep
1  MPFPVFRQXF AXSLRFFAV GRILESDISN SGFSETINAS NVFVGYEYP
51  ACISNLHRFQ FRKLGIQFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFVIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

```

m535.seq
1  aTGCCCTTtC CCGTTTTCAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
51  TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTCCAAC AGCGGTGTTT
101 CGGAAACAAT AGACCGGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTTCGAATTT CGCAAATTTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATGATGG TCAGTCGGGC GGATTCCGCT
251 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTTGG CGTGGCGGAC
301 GTTTTGTCGG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGTT GCCGTAACCTG
401 TCGTAGGCAG GCTTTTGGAC GGACAGGTAG TGCAATACTT CGGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
501 TCGTGTGTTG CGCCATGGTG ATGTAGAGGC GTTTCGGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTTCGAGG CGGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

```

m535.pep
1  MPFPVFRPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51  YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEFGVAD
101 VLSDETETCVG LGLFVVVDDF IFGCGGLARV AVTVVGRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEGENGEGGV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/g535

	10	20	30	40	50	59
m535.pep	MPFPVFRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ					
	: : : : :					
g535	MPFPVFRQXFAXSLRFFAVGRILESDISNSGFSETINASNFFVGYEYPACISNLHRFQ					
	10	20	30	40	50	60
	60	70	80	90	100	110
m535.pep	FRKLGVLQFHALFAEIDGQSGGFVFCGIDNHAGAEFGVADVLSDETETCVGLGLFVVDD					
	: : : : : : : :					
g535	FRKLGIQFFHALFAEVDGQSGGFVFCGIDNHAGAEFGVTDVLSDAEACVGLRLFVIDD					
	70	80	90	100	110	120

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	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRLLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDDVEAFA						
	: : : :						
g535	FVPLYGGLARVAVAVEGGFFDQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFAFGGVDGHLDGLFACAC						
	: : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVVEFQAFGGVDGHQLDGGFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIAXEGENGEGGVV						
	: : : :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

a535.seq (partial)

1	TTCAGACGGC	CTTTGCCTT	GTCCTTGCTA	CAGTTTTTTG	CCATAGGTCG
51	GATTCTCGAA	TCCGACATT	CCAACAGCGG	TTTTTCGGAA	ACGATAGACG
101	CGTCAAAATAT	TTTTGTCGGA	TACGAGTATC	CAGCCTGCAT	TTCAAATTTA
151	CATCGCTTCC	AATTCGCAA	ACTTGGTGTC	CAACTCTTTC	ACGCCCTGTT
201	TGCCGAAATT	GATGGTCAGT	CGGGCGGATT	CGCCTTTATC	TGCGGCATCG
251	ATAATCACGC	CGGTGCCGAA	TTGGCGTGG	CGGACGTTT	GTCCGATACG
301	GAAACCTGCG	TAGGTTTGGG	GCTGTTTGTA	GTGTCGATG	ATTTGTCTT
351	TGGGCGCGGC	GGTTTGGCGC	GTGTTGCCAT	AGCGGTCGTA	GGCGGGTTTT
401	TTGACGGACA	GGTAGTGCAA	TACTTCGGGC	GGGATTTCTT	CGACGAAGCG
451	GGAGACGATG	CCGAATTGGG	TTGTCCGTG	CAGCATGCGT	TGTTGCGCCA
501	TGGTGATGTA	GAGGCGTTT	CGGGCGCGG	TGATGGCGAC	GTACATCAGG
551	CGGCGTTCTT	CTTCGAGGCC	GCCGCGTTCG	GCAAGGCTCA	TTTCGCTGGG
601	GAAGCGGCCT	TCTTCCATGC	CGGTGAGGAA	TACGGCGTTA	AATCCAAGC
651	CTTTGGCGGC	GTGCACGGTC	ATGAGTTGTA	CGGCTTTTTC	GCCCGCGCCT
701	GCTTGGTTTT	CGCCGGATTC	GAGAGCAGCA	TTGCTTAGGA	AAGCGAGGAT
751	GGGGAAGGCG	GGGTCGTCTG	A		

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

1	FRRPFALSLL	QFFAIGRILE	SDISNSGFSE	TIDASNIFVG	YEYPACISNL
51	HRFQFRKLG	VLQFHALFAEI	DGQSGGFAFI	CGIDNHAGAE	FGVADVLSDT
101	ETCVGLGLF	VVDVDFVGRG	GLARVAIAVV	GGFFDQVVQ	YFGRDFFDEA
151	GDDAELGLSV	QHALLRHGDV	EAFAAGDGD	VHQAFFFEA	AAFKAHFAG
201	EAFFHAGEE	YGVKFAFGG	VHGHLYGFF	ARACLVFAGF	ESSIA*ESED
251	EGGVV*				

m535/a535 88.7% identity in 256 aa overlap

	10	20	30	40	50	60
m535.pep	MPFPVFRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGVEYPTYISNLHLFQF					
	: : :					
a535	FRRPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGVEYPACISNLHRLFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
a535	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGRLLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	: : : : : : :					
a535	VFGRGGLARVAIAVVGFFDQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIIAXEGENGEGGVVX					
a535	VFAGFESSIAXESEDGEGGVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

```

g537.seq
1  atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51  tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatcagg gacggcgggc atgcgctgca ctacctcaac
151 cgcacccgca caaaaatcgg ttgacgcgcg ctggcacacg cgccggtttt
201 gggaaaattcc gcccgcaggc acgcacgcta tctcacgctc aatcccgaag
251 acggacacgg cgaacacccat cccgacaatc cgcactacac cgcacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgtccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcaggtgcgg catttgtgcg
501 cgaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcagc cggaagcagg acggaatat
601 taccgcaacg cttgccacaa cgggtcggcc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgcgc
701 tgccttattt ttacggggaa cgtcccgaac ccgtgccgga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gaggcggcag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 ggggttttaac cgccggcaac gaccctaacg gcaggtgac cgcgaccaa
901 ttgcgccctt tcccgtctaa acctttggaa tacggcacgc tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatggcagt
1001 ttagaaccgg aaaaccgat tacccttatt ttgaggtaaa cggcggcgag
1051 acacttgctg ttagaaaagg cgaaaaatat ttcattccact ggcgcggacg
1101 ctggtgtctg gaagcgtgta cccgttatac ctaccggcgg cagttcggca
1151 acagcctgtc catactccgg caggaagcgg gcggcattgt cttcagcgtc
1201 agcggaatgg cgggaagccg catcaggctt actccggaag acagcccgga
1251 acgcggtgta accctttatt tgcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

```

g537.pep
1  MKSLFIWLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DALMSAIYHR
151 LSLDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RRQPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDVPPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAHQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

```

m537.seq (partial)
1  ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCAGGCGT
51  TTTCTACCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTGCACAAG CTGGCACACG CGCCGGTTTT
201 GGAAACTCC GCCCGCAGGC ACGCAAGCTA CCTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

```

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)
 1 MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
g537	MKSLFIWLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRITQIGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
g537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq
 1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCCG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTGTCTATC
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
 151 CGCATCCGCG CCCAAATCGG TTGACACAAG CTGGCACACG CGCCGGTTTT
 201 GGAAAATTCG GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCGG
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
 651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
 751 ACGGGCAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATTAC
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCCGTCA
 851 GGGTTTAAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
 951 GGTATTGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
 1001 TTAGAACCCG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG
 1051 ACACTTGCGG TTAGAAAAGG CGAAAATAT TTCATCCACT GGCGCGGACG
 1101 CTGGTGTGTT GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

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1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTACAGCGTT
 1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPPEYEI
 251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAYQ
 301 FALFPLKPLE YGTLTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPGSRLSIGR HKAGGIVFSV
 401 DGMAGSRITL APEGETERGV TLYLQD*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
a537	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQK LTERTRLAGYLYNGVHENIS					
a537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQK LTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
a537	GRFERHCAQGRNQPEAGRKYRYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq
 1 atgtcaggtga gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
 51 cgtcatgctg gtggcgctaa tgttgataa agatgatacg ggcagcaatg
 101 ccgcccgtct gaacggtttt cagacggcat tggcggaagc cgtcgagctg
 151 gtcaaagcgg cggcgggcga ttccgtacgc gtggagactg ccaaaccgca
 201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
 251 cggaaagcagt tgccgcagac ggcattgatt tggctgatt caaccacgaa
 301 ctactccca cgcaggaacg caatttgaa aaaatcctcc aatgccgcgt
 351 attggacaga gtggggctga ttctggcgat tttcgccgc cgcgccgca
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttgcg
 451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
 501 cggcatgaaa gggccgggcg aaaccaaact ggaaccgac cgccgattaa
 551 ccgcccacg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
 601 cagcgcgccc tgcgcccga gtcccgcgag tggggcagaa tcaaaacgtt
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
 701 tgaccaagtc ggcatatat gcgaaagacc agcttttcgc cactctcgac
 751 acgacggcgc ggcggtgta catcagtcgc gcacaaactg atttccgct
 801 cgataccgct ggattcgtca gcgatctgcc gcacaaactg atttccgct
 851 tttccgccc cttggaagaa accgtgcaag ccgatgtgct gctgcacgtc
 901 gtcgatgctg ccgcccggaa cagcgggcag cagattgaag acgtggaaaa
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcatc aaggtgtaca
 1001 acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc
 1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaaaac

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

g538.pep

```

1  MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLTVFNHE
101 LTPPTQERNLE KILQCRVLDL VGLILAI FAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLTAHRINA LKKQLANLKK
201 QRALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
251 TTARLYISP ACSIIITDTV GFVSDLPKHL ISAFSATLEE TVQADVLLHV
301 VDAAARNSGQ QIEDVENVLQ EIIAHDI PCI KVINKTDL LP SEEQNTGIWR
351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

```

1  ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGTAGTG
101 CCGCCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTGCGCAC GGGCAAGGCG GCGGAGCTGT
251 CAGAAGCAGT TGCCGAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsA AATGCCGCGT
351 ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCGCTCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTCnCGCGAA TCGGGCAGAA TCAAAACGTT
651 TGCGCTGGTC GGCTATACAA ATGTCGGAAA ATCCAGCCTG TTCAACCGGC
701 TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751 ATTATCCTGA CCGATACCGT CGGATTCTGn AGCGATCTGC CGCACAACCT
801 GATTTCGCC TTTTCgCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
851 TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901 GACGTGAAA ACGTACTGCA AGAAATCCAT GCCGGCGATA TTCCGTGCAT
951 cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATGGCG CGACGCTGCG GGAAAAATTG CCGCGCTCCG CATTTCCGTT
1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCcATTG CCGAGTCTTG
1101 TGCCCGCCGA CCAACACAG ACGAAACCGA AATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538.pep

```

1  MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLTVFNHE
101 LTPPTQERNLE KELKCRVLDL VGLILAI FAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LIKQLANLKK
201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
251 IILTDTVGFV SLDLPHKLISA FSXTLEETAQ ADVLLHVDA AAPNSGQIE
301 DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
351 AENTGIDALR EAIAESCAAA PNTDETEMP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQALAEAVELVKAAGGDSVR					
	: : : : : :					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAELSEAVAADGIDLTVFNHELTPTQERNLEKELKCRVLDL					
	:					
g538	VETAKRDRPHTALFVGTGKAELSEAVAADGIDLTVFNHELTPTQERNLEKILQCRVLDL					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSORGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSORGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQALRRKSRESGRIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLP HKLISAFSXTLEETAQADVLLHV					
g538	AKDQLFATLDTTARRLYISPACSIILTDTVGFVSDLP HKLISAFSATLEETVQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
g538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1  ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTT CAGACGGCAT TGGCGGAAGC TGTGAGCTG
151 GTCAAAGCGG CGGCGGCGA TTCCGTGCGC GTGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTGCGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCGCCCCG CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGCG AAACCAAAC GGAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCCGCAA GTCCCGCGAA TCGGGCACAA TCAAAACGTT
651 TCGCGTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAACTG ATTTCCGCTC
851 TTTCGCGCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CGTACTGCAA GAAATCCATG CCGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CCTGCTGCCG TCTGAAGAAC AAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1  MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEVAAD GIDLTVFNHE
101 LTPTQERNLE KILQCRVLDL VGLILAI FAR RTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKQLANLKK

```

813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDV GFVSDLPKHL ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLEKDKGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
a538	MTGRTGRNGSTQAQPERVMLVGVMLEKDKGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLNVFNHELTPTQERNLEKELKCRVLDR					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLNVFNHELTPTQERNLEKILQCRVLDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLSQRGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALKKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDVGFVSDLPKHLISAFSXTLEETAQADVLLHV					
a538	AKDQLFATLDTTARRLYISPECSIILTDVGFVSDLPKHLISAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccagatcc ggcaacggca
101 aggcggacga tgtattgttt gcgttctttt tgggtggcgg cttcgatttt
151 ttgcgcgtca taggtgacgg cgggtgtagc tgtctgccgg atttcaaca
201 gaatgtcggg gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggattgg
401 acttcgggca ggtcgtagag gcggatttgg tcgaggattt cttggggcgg
451 cagttcgggt ttttgcggt cggcggtgcg tcgtttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggt cttcgcttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtgga aacaggtttt tttcatggca tttcggtttc

```

```

651 gtctgtgttt ggtgcgccgg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccgtgttt tgttcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgct gttccggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
951 ggtgcgcgaa aaggcggaat tcagtttgtg cggcagatcg ctgacgaatc
1001 cgacggatc ggtcaggata atgctgcacg cgggactgat gtacagccgc
1051 cgcgcgcgtc tgcgcagagt ggcgaaaagc tggctcttcg catatatgcc
1101 cgacttggtc agccggttga acaggctgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

g539.pep

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVQ ADLVEDFLGR
151 QFGFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPLFRA
301 AASTCSSTS ACTVSSKVAE KAEISLCGRS LTNPVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

m539.seq (partial)

```

1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCTTTT TGGTTGGCGG CTTTCGATTTT
151 TTGCGCGTCA TAGGGTGCAG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCaGcGg
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAACCAGC CTGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTTGCCTG CGGCGGTGCG TTGTTTGTA TAACTGCCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaAgG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACA GTCAGGTGGA GGTGTTTCGGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTTCATGGA TTTTCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTTT
751 CCCGCGCGT CCGCCATAT GCCCCTGTTT TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGAGCGG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCAGCG TTTCTCCAG
951 CGTGCGAA AAGCGGAAA TCAGTTgTG CCGCAGATCG CTnACGAATC
1001 CGACCGTATC GGTcAGGATA ATGCTGCATT CCGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

m539.pep (partial)

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFRLVGGA LfVITAQARV NNALCDRLTA GAQGFVAVFV VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA
301 AASTCSSTS ACAVSSSVAX KAEISLCGRS LTNPVSVRI MLHSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

m539/g539

```

          10      20      30      40      50      60
m539.pep  MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          |||||
g539      MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```


815

	10	20	30	40	50	60
m539.pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	70	80	90	100	110	120
	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
m539.pep	130	140	150	160	170	180
	LARAAGVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	130	140	150	160	170	180
	FVRAIMGFHKVGLDFGQVVQADLVEDFLGRQFGFFRVGGASFVITAQAGIDDALCDCLTA					
m539.pep	190	200	210	220	230	240
	GAQGFVAFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
g539	190	200	210	220	230	240
	DAAGFAVFAFVADGQMQVFGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
m539.pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSTFSTSSICCPLEFA					
g539	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSTFSTSSICCPLEFA					
m539.pep	310	320	330	340		
	AASTTCSSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	310	320	330	340	350	360
	AASTTCSSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVVSRAKS					
g539	370	380				
	WSFAYMPDLVSRLNRLDLPTLV					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTTCGATTTT
151 TTGCGCGTCA TAGGTTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCCTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTCTG TACGCAAAAG
301 CTGCTGTTCT ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTGCGCGCTG CCGCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTTGCCTG CCGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCGCGGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGA AACAGGTTTT TTTCATGGCA TTTTCGGTTT
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAT TGCGGACGGC GGCAATTTT
751 CCCGACGCGT CGCGCCATAT GCCCGTGTTC TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGACGATC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCCTGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CGGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GCGGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGTTTGA ACAGACTGGA TTTGCCGACA TTGTTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

```

816

51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAAVRAVIEV DADDAVCTQK
 101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
 151 QLGFRLVGGG LFFVITAQARV NNALCDCLTT GAAGFAVVFV VTDGQMVFVG
 201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
 251 PAASRHPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
 301 AASTTCSSTS ACAVSSVAE KAEISLCGRS LTNPTVSVRI MLHSGLMYSR
 351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

m539/a539 97.1% identity in 345 aa overlap

	10	20	30	40	50	60
m539.pep	MEDLQEIGFDVA	AAVKVGRQREHRLHHPQPGNGEADDVLF	FAFFLVGGFD	FLRVIGCGGVA		
a539	MEDLQEIGFDVA	AAVKVGRQREHRLHHPQPGNGEADDVLF	FAFFLVGGFD	FLRVIGCGGVA		
	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
a539	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGFRLVGGGALFVITAQARVNNALCDRLTA					
a539	LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGFRLVGGGALFVITAQARVNNALCDCLTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFVAVFVFTDSQVEVFNGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
a539	GAQGFVAVFVFTDSQVEVFNGNIQTAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA					
a539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
a539	AASTTCSSTSACAVSSVAEAEISLCGRSLTNPTVSVRIMLHSGMLYSRRRAVVSSVAKS					
	310	320	330	340	350	360
a539	WSFAYMPDLVSRLNRLDLPTLVX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

1 atgccgccct ccgacgcgg caacgggggtg ttttatcaaa acggcaaaact
 51 tgccaatgcg gtttcgcgtt gccgattgcc aaaccggcaa acctttcccg
 101 tgccggtgcc gaaccgatg ccgtctgaac cttcagacgg catcggtgtg
 151 ttatttgtcc actcggacgg gtgcaggttc gtattgtgtc gattcgtcgc
 201 cgtaatacag cacgccgagt ttgacgggga tgcgtccctg cgatttgagg
 251 tgggcgttgg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg
 301 gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgccgccgc
 351 ctttgcgcca gttgaagtc caataggcca catcatcgta aggcgcggcg
 401 gcacggtgtc cgcagtcgtt gatttgcgcc atattttcc agcgtga

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

g540.pep

1 MPPSRRGNGV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP PSEPSDGIGC

51 LFVHSDGCRF VLRCRFVAVIQ HAEFDGDASL RFAVGVGIAQ GIRAAAVFLL
 101 VEVFADFNF HTRAAAFAP VEVPIGHIIV RRGTVSAVV DLRHIFPA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1569>:

m540.seq (partial)
 1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTTGT
 51 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCGTC GCCGTAATAC
 101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTGC GGTGGGCATT
 151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
 201 TTTCACGTTT GCTGATTTC AATCATGCGC CGCTGCCGCC GCCTTTGCGC
 251 CAGTTGAAAT CCAATACAC CACATCATC TAAGCGCGG CGGCGCGGTG
 301 TCCGAGTCG TTGATTGCG CCATATTTT CCAGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1570; ORF 540>:

m540.pep (partial)
 1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
 51 GIPQGIGTTA IFLLVEVFTF ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
 101 SAVVDLRHIF PA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 540 shows 85.7% identity over a 112 aa overlap with a predicted ORF (ORF 540.ng) from *N. gonorrhoeae*:

m540/g540

m540.pep				10	20	30
				PNMPSEPSD	GIGCLFVHPD	GGRFVLCRFV
g540	GNGV	FYQNG	KLANAV	SACRLPN	RQTFFV	PNMPSEPSD
	10	20	30	40	50	60
m540.pep		40	50	60	70	80
		AVIQHAEFDG	DSALXFAV	GIGIPQ	GIGTTAIF	LLVEVFTF
g540		AVIQHAEFDG	DASLRF	AVGVGIAQ	GIRAAVFL	LEVFAFAD
	70	80	90	100	110	120
m540.pep		100	110			
		HIIVRRGG	AVSAVVD	LRHIFPAX		
g540		HIIVRRGG	TVSAVVD	LRHIFPAX		
		130	140			

L' estremita' N-terminale di meningococco e' assente perche' interviene la fine del contig

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1571>:

a540.seq
 1 ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAAC
 51 TGCCAATGCG GTTTCCGATT GCAGATTGCC AAACCGGCAA ACCTTTCCCG
 101 TGCCGATGCC GAACCCGATG CCGTCTGAAC CTTAGACGCG CATCGGGTGT
 151 TTATTTGTCC ACCCGGATGG GTGCAGGTTT GTATTGTGTC GATTCTGCG
 201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTGCGG
 251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG
 301 GTAGAAGTTT TCACGTTTGC TGATTCAAT CATACGCGCG CTGCCGCCGC
 351 CTTGCGGCCA GTTGAAATCC CAATACACCA CATCATCGTA AGGCGCGGCG
 401 GCGCGGCGGC CGCAGTCGTT AATCTGGTTC ATGTTTTTCC A

This corresponds to the amino acid sequence <SEQ ID 1572; ORF 540.a>:

a540.pep (partial)
 1 MPSSRRNGV FYQNGKLANA VSDCLPNRQ TFPVPMNPM PSEPSDGIGC
 51 LFVHPDGRF VLRCRFVAVIQ HAEFDGDASL *FAVGVGIPQ GIGTTAIFLL
 101 VEFTFADFN HTRAAAFAP VEIPIHHIIV RRGAAAAVV NLVHVFP

818

m540/a540 92.8% identity in 111 aa overlap

				10	20	30
m540.pep				PNMPMPSEPSD	GIGCLFVHPD	GGRFVLCRFV
a540	GNGVFYQNGKLANAVSD	CRLPNRQTFFV	PMNMPSEPSD	GIGCLFVHPD	GCRFVLCRFV	
	10	20	30	40	50	60
	40	50	60	70	80	90
m540.pep	AVIQHAEFDGDSALXFA	VGIGIPQIGITTAIF	LLVEVFTFADFNHAR	AAAAFAPVEIPIH		
a540	AVIQHAEFDGDSALXFA	VGIGIPQIGITTAIF	LLVEVFTFADFNHTR	AAAAFAPVEIPIH		
	70	80	90	100	110	120
	100	110				
m540.pep	HIIVRRGGAVSAVVDL	RHIFPAX				
a540	HIIVRRGGAAAVVNLV	HVFP				
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

g542.seq
 1 atgccgaaat ggtcgcgcac acggcggtgc agcgctcctt cgctgatgtt
 51 cagcgccggt gtcagccggt tgacttggtg tgcgccgcgc tcgaacgcgc
 101 cattcaggtt gcggctgaag tcttcagacg gcatagcgtc tgcttccgcc
 151 gtttgccccc ccgcccggct gatgccgtct gaaaccgtgt cccacaaatc
 201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatgtt tcgcccacaa
 251 gcccttttgg gacggtttgc aggcaggatg ccgccaagcc gcgcagggtt
 301 gggggcaaat cccatatact gaccggttcg cggttaa

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

g542.pep
 1 MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFVRRLK SSDGIASASA
 51 VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
 101 GKGSHILTGS R*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

m542.seq
 1 ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
 51 CAGCGCGTCT GTCAGCCGGT TGAATGGTG TCGCCGTCG GCAAACGCGG
 101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
 151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
 201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
 251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTT
 301 GGGGGCAAAAT CCCATATCCT GACCGGTTTC CGGTAA

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

m542.pep
 1 MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFVRRLK SSDGIASASA
 51 VCPAAGSMPS ETVSHKSDSS RNTSASRAMF RPNAPLGRNV SPKCPFGTAF
 101 RQDAAKPRRF GKGSHILTGS R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

m542/g542

		10	20	30	40	50	60
m542.pep		MPKWSRIRRC	SVLSLMFSAS	VSRLTWCAPS	ANAAFVRRLK	SSDGIASAS	AVCPAAGPMPS
g542		MPKWSRIRRC	SVLSLMFSA	VSRLTWCAPP	SNAAFVRRLK	SSDGIASAS	AVCPAAGSMPS
		10	20	30	40	50	60
		70	80	90	100	110	
m542.pep		ETVSHKSDSS	RNTSASXRN	VSPKCPFGT	AFRQDAAKP	RRFEGKGSH	ILTGSRX

g542 ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```
a542.seq
1  ATGCCGAAAT  GGTGCGCAT  ACGGCGTTGC  AGCGTCCTTT  CGCTGATGTT
51  CAGCTGTCT  GCCAGCCGGT  TGACTTGAT  TGCGCCGCCG  GCAAACGCGG
101 CATTCAGGAT  GCGGCTGAAG  TCTTCAGACG  GCATAGCGTC  TGCCTTCGCG
151 GTTTGCCCGC  CCGCCGGCCC  GATGCCGTCT  GAAACCGTGT  CCCACAAGTC
201 CGACAGCAGC  CGAACACCTG  CCGCCTCGCG  GCGCAATGTT  TCGCCCAAAT
251 GCCCCATTAG  GACGGCTTTC  AGGCAGGATG  CCGCCAAGCC  GCGCAGGTTC
301 GGGGGCAATT  CCCATATCCT  GACCGGTTGC  CGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

a542.pep

1	MPKWSRIRRC	SVLSLMFSVS	ASRLT*CAPP	ANAAFRMRLK	SSDGIASASA
51	VCPAAGPMPS	ETVSHKSDSS	RNTSASRRNV	SPKCPFGTAF	RQDAAGKPRRF
101	GGKSHILTS	R*			

m542/a542 94.6% identity in 111 aa overlap

	10	20	30	40	50	60
m542.pep	MPKWSRI RR CSVL S LMFSASVSRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS					
a542	MPKWSRI RR CSVL S LMFSVSASRLTXCAPPANAAFRMR L KSSDGIASASAVCPAAGPMPS					
	10	20	30	40	50	60
	70	80	90	100	110	
m542.pep	ETVSHKSDSSRN T SASXRN V SPKCPFGTA FR QDAAKPRRFGGKSHIL T GSRX					
a542	ETVSHKSDSSRN T SASRRN V SPKCPFGTA FR QDAAKPRRFGGKSHIL T GSRX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

9543..seq
1   atggttttgc ggttatttgc cgccgttttt ggctttcaac tcggcaatca
51  gcccgctgat gccctttggct ttgatgattt cgccgaattg gttgcggtac
101 acggtacaaca ggcctgtgcc ttcgatggcg acgttgtagg tacggtattc
151 gccgcgcgtt ggttaggtgg taaagtccat atgtacggcg tctcgaccgg
201 ggatgccgac ttcggcacgg acgacgattt ccttgccgcc cttattgacg
251 atgggatgtg ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcgggatc gcagggtttt aaattctttg gccaacgcgtt
351 gttttttcgc gtcggacgcg gtacggcaag ggttgccgac cgccaatgcg
401 gtcatacgtt ggaatacgaa ataggaacc  gcataggctt cgttcatttg
451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggtcaaa acctgtgtgg
501 cgttttggcg gattttgtcc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgtca  aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 ccgatgtct  ttcctgaaaa tttgtgtgt  tgattattct cgcgcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagtcggt catgaattta
701 ccgatcaggt ttccagAAC  cattgcagaa ctggttacgg agatggtgtc
751 gccggcagca aggtttttcg tatcgccgcc ctgctgcagc ccgatgtact
801 gttcgcccaa aagtcctcga gtcaggattt gcgcggaacc gtcactgctg
851 aactgatact tgcgtccaa  atcaaggcgc accctgcctt cataggattt
901 cgggtcaagc ccgatagcgc cgacgcgcc  gaccaatacg ctgcggattt
951 tgacgggggc attgaccttc aaaccgcgca tgtcgcgcaa atcggcataa
1001 acggcgtaag ttttgcctga accgcgaagc gccgcgcgcg ccgccacgcg
1051 gaaagcgaag aaggcaaccg ccgcgcgcac gatcaagacg aacagtcgca
1101 cccaaaattc caatatgttc tttttcatta a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

g543.ppe
1 MVCRLFAAVF GFQLGNQPVDF AFGFDDFAEL VAVHGNQARA FDGDVVGTVF

51	AAALVGKKVH	IDGLLTGDAD	FGTDDDFLAA	LIDDGIVFDV	DGRVFEFQHR
101	AGIGADQQGL	KFFGQRLFLR	VGRGTPRVAD	RQCCHTLEIE	IGNRIGFGFW
151	ACRSRVAAFE	DQNLNCGVLA	DLSHCVGRGG	KCHADAQNTD	AQCADEGGFF
201	HDVFPENGCV	CLFCGFFRIA	ALSFLVGEAG	HEFTDQVFQN	HCRTYGQDGV
251	RGSKVFRIAA	LLQPVDVFAQ	KSRSDQLRGN	VTAEILILVQ	IKAHPRLIGF
301	RVKPDSADAP	DQYACGDFGG	IDLQTADVAE	IGINGVSFVR	TAERRAARHA
351	ESEKGNRRRA	DODEOSDPKF	OYVLFH*		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1581>:

m543.seq

1	ATGTTTGTGTC	GGTTATTTGCG	CGCGGTTTTT	GGCTTTCAC	TCGGCAATCA
51	GTCCGTCCAC	GCCTTTCGCT	TTGATAATT	CGCCGAATTG	GTTGCGGTAC
101	ACGGTGACCA	GGCTCGCGCC	TTCGATGGCG	ACGTTGTAGG	TACGGTATT
151	ACCGCGCGTT	TGGTAGGTGG	TGAAGTCCAT	GTTGACGGGT	TTTGTGCCCG
201	GTACGCCGAC	TTCCGCGCGG	ACGATGATT	CTTTGCCGCC	TTTATTGACG
251	ATGGGATTGT	CTTTGACGTT	GACGTTGGCG	TTTTTTAATT	TCAGCATCGT
301	GCCGGGAATG	GTCCGGATCA	GCAGGGTTTG	AAATCTTTTG	GCCAAACGTT
351	GTTTTTGCGC	GTCGGACGCG	GTGCGCCAAG	GGTTGCCGAC	CGCCAATGCG
401	GTCATACGTT	GGAATCGAA	ATAGGGAATT	GCATAGGCTT	CGCGTTTTTG
451	GCGAGCGGTG	TTGGCATCGC	CGTTTTTTAA	GATGCTCAAT	ACTTGAGTGG
501	CGTTTTGACG	GATTTGGCTT	ACGCGTCGCG	CAGGGGCGGC	AAATGCCATG
551	CCGATGCTCA	AAATACCGAT	GCCCAATGCG	CTGATAGGTT	AGGATTTTTT
601	CATGATTAA	TGTCCTAGTT	TGAATATGAT	GGCATACGTT	TATTCGGCGG
651	CTTTTTCGCG	ATTGCCGCGG	TCGCGATT	TTCTCGGCAA	ACTCGTCATG
701	AATTTGCCGA	TAAGGTTTTT	CAGAACCAT	GCAGAACTGG	TTACGGAGAT
751	GGTGTCGCGG	GCAGCAAGGT	TTTCCGTGTC	GCCGCCCTGC	TGCAGCCCGA
801	TGTACTGCTC	GCCCAAAAGT	CCCCAAGTCA	GGATTTGCGC	GGAACGTCG
851	CTGCTGAACT	GATACTTGCC	TGCCAAATCG	AGGCGCACCC	TGCGCTGATA
901	GGATTTCCGG	TCAAGTCCGA	TAGCCCGGAC	GCGCCCGAC	AATACGCGTG
951	CGGATTTGAC	GGGGGCATTG	ACCTTCAAAC	CGCCGATGTC	GCCGAAATCG
1001	GCATAAACGG	CGTAGTTTTT	GTCCGAACCG	CCGAACCGCG	CACCGCCGGC
1051	CACGCGGAAA	CGGAGAAAGT	CAACCGCCGC	CGCGCCAATC	AGGACGAACA
1101	GTCCGACCCA	AAATTCCAAT	ATGTTCTTCT	TCATTAA	

This corresponds to the amino acid sequence <SEO ID 1582; ORF 543>:

m543 . pep

1	<u>MVCRLFAAVF</u>	<u>GQGLGNQSVH</u>	<u>AFRFDNF AEL</u>	<u>VAVHGNQARA</u>	<u>FDGDVVGTVF</u>
51	TAALVVGGEVH	VDGFLPGYAD	FGADD DFFAA	FIDDGIVFDV	DVGVFVXFQHR
101	ASIGADQVQL	KFFGQRLFLR	VGRGAPRVAD	RQCCHTLEIE	IGNRIGFGFL
151	ASGVGTAVFX	DAQYLGSVLT	DLAYRVGRGG	KCHADAQNTD	ACQADEGGFF
201	HDXVSXFEYD	GIRLFGGFFR	IAAVGIFLKG	TRHEFADKVF	QNHCRGTGYD
251	GVAGSKVFRV	AALLQPDVLL	AQKRSQDLR	GNVA AELILA	VQIEAHPRLI
301	GFRVKSDSAD	APDQYACGFD	GGIDLQTADV	AEINGINGVSF	VRTAERRTAG
351	HAESEKGNRR	RANODEOSDP	KFOYVLLH*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

m543/g543

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAAALVGGEVH					
g543	MVCRLFAAVFGFQLGNQNPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAAALVGKGVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIDDGIVFDVDVGVFXFQHRAGIGADQQGLKFFGQRLFLR					
	: : : :					
g543	IDGLLTGDADFGTDDDFLAALIDDGIVFDVDGRVFEFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180

821

```

m543.pep  VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGCVLADLSHCVGRGG
          130      140      150      160      170      180

          190      200      210      220      230      239
m543.pep  KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIA AVGIFLGKTRHEFADKV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
          190      200      210      220      230

          240      250      260      270      280      290      299
m543.pep  FQNHCRRTGYGDGVAGSKVFRVAALLQPDVLLAQKRSRQDLRGNVAAELILAVQIEAHPRL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       FQNHCRRTGYGDGVAGSKVFRIAALLQPDVLFQKRSRQDLRGNVTAELILAVQIKAHPRRL
          240      250      260      270      280      290

          300      310      320      330      340      350      359
m543.pep  IGFRVKSDSADAPDQYACGFDGGIDLQTDADVAEIGINGVSFVRTAERRTAGHAESEKGNR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       IGFRVKPDSADAPDQYACGFDGGIDLQTDADVAEIGINGVSFVRTAERRAARHAESEKGNR
          300      310      320      330      340      350

          360      370      379
m543.pep  RRANQDEQSDPKFQYVLLHX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       RRADQDEQSDPKFQYVLFHX
          360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTGGCG TTTTAAATT TCAGCATCGT
301 GCCGAATAG GTGCGGATCA GCAGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTCGCG GTCGGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATGCG
401 GTCATACGTT GGAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTCGAC GATTGGTTT ACCGCGTCGG CAGGGCGCGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCGCG ATTGCCGCGG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTGCCGA TAAGGTTTTC CAGAACCAT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCGG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCG
851 CTGCTGAAGT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCGC CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCGC CGCGCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLA VX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRRTGYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSRQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTDV AEIGINGVSF VRTAERRTAG

```

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0% identity in 378 aa overlap

m543.pep	MVCRLFAAVFGFQLGNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
a543	MAYGLLAAVXSLQLXNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
m543.pep	VDGFLPGYADFGADDDFFAAFIDDGIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR
a543	VDGFLPGXADFGADDDFFAAFIDDXIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR
m543.pep	VGRGAPRVADRQCGLTLEIEIGNRIGFGFLASGVGIAXDAQYLSGVLTDLAYRVGRGG
a543	VGRGAPRVADRQCGLTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAGVIFLGKTRHEFADKVF
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAGVIFLGKTRHEFADKVF
m543.pep	QNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAELILAVQIEAHPRLI
a543	QNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAELILAVQIEAHPRLI
m543.pep	GFRVKSADSADPDQYACGFDGGIDLQADVAEIGINGVSFVRTAERTAGHAESEKGNRR
a543	GFRVKSADSADPDQYACGFDGGIDLQADVAEIGINGVSFVRTAERTAGHAESEKGNRR
m543.pep	RANQDEQSDPKFQYVLLHX
a543	RANQDEQSDPKFQYVLFHX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgccgccgctc gcaactgatcg gcatcctcct
51  cgccaccgctc ctcacccccg acagtaaaac cgcgcccgcc ttctccctgc
101 ccgacctgca cggaataaac gtttccaacg ccgacctgca aggcaaatgc
151 accctgatta atttttggtt tcctcctgtt ccgggttggtg tgagcgaaat
201 gcccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tctcgcgcgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gtttaccgctc atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttcc gtccttatcg
401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcggaacc cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544.pep

```

1  MKKILTAADV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```


151 KLYQEIDTAL AQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

m544.seq

1	ATGAwAAAAA	TACTCACCGC	CGCGGTCTGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCCG	ACAGCAAACG	CGCGCCCCGC	TTCCTCmTGC
101	CCGACCTGCA	CGGAAAAAAC	GTTTCCAACG	CCGACCTGCA	AGGCAAAAGTA
151	ACCTTGATTA	ATTmTTGGTT	TCTTCCTGTG	CCGGTTGTG	TGAGCGAwAT
201	GCCCAAAATC	ATTAAACCG	CAAATGACTA	TAAAwCAAA	AACTTCCAAG
251	TACTTGCCGT	CGCCACGCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTG	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	GCGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAAATAGG	CGAAATCTTC	AAAACCTACG	TCCGCGAACG	CGATTTCGGC
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	GCCAATAG	

This corresponds to the amino acid sequence <SEQ ID 1588; ORF 544>:

m544 . pep

```

1  MXKILTAAVV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGVK
51  TLINFWFPSC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIQK*GEIF KTYVGEPDFG
151 KLYQEIDTRV AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60
m544.pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGKVTLINFWFPSC					
	:					
g544	MKKILTAAVALIGILLATVLIPDSKTAPAFSLPDLHGKTVSNADLQGKVTLINFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSXMPKIIKTANDYKKKNFQVLAVAQPIDPIESVRQYVKDYGLPFVTMYDADKAVGQ					
	: : : : :					
g544	PGCVSEMPKVTKTANDYKNKDFQVLAVAQPIDPIESVRQYVKDYGLPFVTIYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
	: : : :					
g544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1589>:

a544.seq

1	ATGAAAAAAA	TACTCACCGC	CGCGCTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCCG	ACAGCAAAAC	CGCGCCCGCT	TTCTCCCTGT
101	CCGANCTGCA	CGGAAAAANC	GTTTNCACG	CCGACCTGCA	AGGCNAAGTT
151	ANCCTGATTA	ANTTTTGGTT	TCCCTCCTGT	CCGGGTTTGT	TGAGCGAAAT
201	GNCCANAATC	ATTAATAACG	CAAAATGACTA	TAAAAACAAA	AACCTTCAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCTCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCCTG	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	GCGTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAAAAGG	CGAAATCCTC	AAAATTTAT	TCGGCGAAC	CGATTTTCGGC
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAAATAG	

This corresponds to the amino acid sequence <SEQ ID 1590; ORF 544.a>:

a544.pcp

1 MKKILTAAVV ALIGILLAIV LIPDSKTAPA FLSXLHGKX VXNADLQGXV
51 XLIXFWFPSC PGCVSEMXXI IKTANDYKKN NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGPEPFG

151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544.pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGKVTLINFWFPSC					
a544	MKKILTAAVVALIGILLAIVLIPDSKTAPAFSLXSLHGKXVXNADLQGXVXLIXFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
a544	PGCVSEMXXIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
a544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547.seq

```

1  atgttcgtag ataacggatt taataaaacg gtagcagatt ttgccccaaat
51  cgtcgaaact ttcgacgtat tcttcttttag gaacgattgc gccttttttta
101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggg atattctcgtt
151 gatataatta caagatgcgg cttcgagatt ccgaaccgct cctttaaaga
201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
251 ccgaagtcga gatggatgcc cattacttcc cttactcag aaaatattta
301 aaattttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaaccgaa
401 aaaagcgggt tgttttttgt tggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVENMDA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNLN PNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq

```

1  ATGTTTCGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTSTA
101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCT CTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTTGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
401 GAAAAAAGCG GTTTGTTTTT TGTGTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVENMDA HYFPLLRKYL
101 KFIMLHIFTN IKVFXVCVKE ELLTILVKNL SPNGKKRFVF CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
g547	ELLTILVKNLSPNGKKRFVFCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

a547.seq

```

1  ATGTTCTAG  ATAACGGATT  TAATAAAACG  GTAGCGAGTT  TTGCCCAAA
51  CGTCGAACT  TTCGACGTAT  TCTTCTTTAG  GAACAATTGC  ACCTTTT
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGT
151 GATATCTTTC  CAAGATGCGG  CTTCGAGATT  CCGAACCGCT  CCTTTAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAAT
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTACTCAG  AAAATATTT
301 AAATTTATAA  TGTTACATAT  ATTTACAAAT  ATTAAAGTT  TTTT.TGTG
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T

```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

a547.pep

```

1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYL
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRLKY
101 KFIMLHIFTN  IKVFXCVCVK  ELLTILV

```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

g548.seq

```

1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  tacttgccgc
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgcggcgcaa  gccgtttctt
101 caagtgcac  cgcgcgggct  gcggaaaatg  cggcaaagcc  gcaaacgcgc
151 ggtacggata  tgcgtaagga  agacatcggc  ggcgatttca  cactgaccga
201 cggcgaaggc  aagcctttca  gcctgagcga  ttgaaaggc  aaggtcgtga
251 ttctgtcttt  cggctttacg  cactgtcccg  atgtctgcc  gacagggctt

```

```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggt ttctgcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acgggcgggc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccgggtg gtatcttata gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFLTLDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVVV FVSIDPERDT PEIIGKYAQ FNPDFIGLTA
151 TGGQNLPIK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTCCG TACCGCGTTC CTTTTGCGG GCGTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CCGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGATTTCa CGCTGACCGA
201 CCGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAATATTTC GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
51 GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVVV FVSIDPERDT PEIIGKYAQ FNPDFIXLTA
151 TGGQNLPIK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
	:					
g548	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTPELLTYSIDLKQLGGQAKDVVV					
	:					
g548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPFIIGKYAQFNPDFIXLTATGGQNLPIKQQYRVVSAKVNQKDDSENYL					
	:					
g548	FVSIDPERDTPFIIGKYAQFNPDFIGLTATGGQNLPIKQQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

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```

                190      200      210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||||
g548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTTGCCG GCGGTTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGCGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CCGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGGTAAGGA AGACATCGGC GCGGATTTC ACGTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTAGCA TCGATCCGGA ACGGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCCG ACTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGCATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACATTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSFLP GVFLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTTEL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

```

                10      20      30      40      50      60
m548.pep      MFSVPRSFLPGVFVLAALAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG
                |||||
a548          MFSVPRSFLPGVFVLAALAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG
                10      20      30      40      50      60

                70      80      90      100     110     120
m548.pep      GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTTELLTYSIDLKQLGGQAKDVKVV
                |||||
a548          GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTTELLTYSIDLKQLGGQAKDVKVV
                70      80      90      100     110     120

                130     140     150     160     170     180
m548.pep      FVSIDPERDTP EIIIGKYAKQFNPDFIXLTATGGQNLPIKQQYRVVSAKV NQKDDSENYL
                |||||
a548          FVSIDPERDTP EIIIGKYAKQFNPDFIGLTATGDQNLPIKQQYRVVSAKV NQKDDSENYL
                130     140     150     160     170     180

                190     200     210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||||
a548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```

g550.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

m550.seq (partial)

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

m550.pep (partial)

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ____% identity over a ____ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1  CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCAGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGCGGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTTAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCG
451 CAGCGGCGGC AGGATTTCCG GATTCGGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTC AGTATTTTCA GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTTCG GTTCAAGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTCGTCGTG GAATACGGGG ATTTTGCAGC GTTTCGCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1  LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNO VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVFVF AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

					10	20	30
m550.pep					DGIGKHALAVVFNGVELFGLVHTVFVFAGL		
a550	EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVFVFAGL						
	170	180	190	200	210	220	
		40	50	60	70	80	90
m550.pep	VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTGXGVQYGGGGNDG						
a550	VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYQSGGGNDG						
	230	240	250	260	270	280	
		100					
m550.pep	RAVLVVVEYGDFAAFAX						
a550	RAVLVVVEYGDFAAFAX						
	290	300					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1  atgaagctga aaaccttgtt attgcccttc gccgcactgg catttgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttgga cgttggtctg
101 atacgcagaa ttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga ttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggta gtcgctcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggatc ttggactgca
```

451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
501 acggcgcatc atctgcggcg gtatagtgga ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIARHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA
201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG
551 CCGGACAGGT TGGGAAAAG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	: : : : : :					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	: : : : :					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	: : : : :					
g552	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
	190					
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA

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201 AGCGAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCGAGTSTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51  NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

```

          10      20      30      40      50      60
m552.pep  IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
          |||
a552      IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
          10      20      30      40      50      60

          70      80      90      100     110     120
m552.pep  ALAEMPEAKKDQAAEAFNRYRENVLKDITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
          |||
a552      ALAEMPEAKKDQAAEAFNRYRENVLKDITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
          70      80      90      100     110     120

          130     140     150     160     170     180
m552.pep  YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
          |||
a552      YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
          130     140     150     160     170     180

          190
m552.pep  CKQAGQVGKRHQKX
          |||
a552      CKQAGQVGKRHQKX
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAA CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLTLL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGVGQSVV VAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

832

```

1   TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGCGGCCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CCGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1   LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEFN RYRENVLDL ITPEVKQAVR
101 NTLLKNAREI YTQEEIDGMI AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
m552-1	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
	10	20	30	40	50	60
a552-1.pep	DKALAEMPEAKKDQAAEFN RYRENVLDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEFN RYRENVLDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEAKKDQAAEFN RYRENVLDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEFN RYRENVLDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGGKNPD					
m552-1	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGGKNPD					
	130	140	150	160	170	180
a552-1.pep	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGGKNPD					
m552-1	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGGKNPD					
	130	140	150	160	170	180
a552-1.pep	AGCKQAGQVG KRHQKX					
m552-1	AGCKQAGQVG KRHQKX					
	190					
a552-1.pep	AGCKQAGQVG KRHQKX					
m552-1	AGCKQAGQVG KRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1   atggattatc tgcaaacct gtctttgggc ttgacaaaaa agctgcccg
51  tatactgcaa acagaagtag cggagtgtg cttggcatgt ctacggcgtg
101 tggccggatt ttatggtttc tatacggatt tgcgcgact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacggcggtt gaggctggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcggatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgcaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtttcgaggc aggggaagaa
451 aagcaggaaa tccgcatcct acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaaagt catgataaat gggcacgaca
701 tttacagctt accgccacct tttattccgc aatttgagtg cgatgggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

```

1 MDYLQNLSLG LTKKLPIVLQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK
51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDLNHF
101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
151 KQEIRILPML RGISILGRTL FQLLALAAAM EVFAFLQNVS FKIGRGESLA
201 LIGRSGCGKS TLLDLSGNL PPESGKVMIN GHDIYSLPPP FIPQFECDDQ
251 LTRMFYSGLN LNR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1621>:

```
m553.seq (partial)
1  ATGGATTATT TATCAAGACT GTCCTTTGGA TTTAACAAAA AGCTACCTGT
51  CATTCTGCAA ACAGAAAGTTG CTGAATGTGG TTATGACATGC CTGACATCCA
101 CTTTGTGCTTA TTATGCGTTT CACACTGATT TAAGAACATTT ACGCAAAAAA
151 TACACCCTGT CATTAAAGGG CGCAAATCTT GCAGACATTT TGAGATTTGG
201 CAATGAAATG AATTTAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
251 TGTCAAATTT ACACTACCC TGCATTCTCC ATTGGAACCTT AAACCATTTT
301 GTTGTACTTT ACTCCATTTC CAAAGACAGT ATCGTCATTA TGGACCTGTG
351 TGTGCGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTCACAG
401 GGATTGCCCT AGAATTATTC CCCAATACCC ATTTTGAAGA GAAAAAAGAA
451 ACAAAGAAAA TCAAAATATT ATCTCTATTA AGGGGGGG. T CAGGCTTAAA
501 ACGCTCTTTA ATTCAAATGC TTATATTAGC TATTTCCTTG GAAGTCTTTG
551 CATTG...
```

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

m553.pep (partial)

1	MDYLSRLSFG	FNKKLPVILQ	TEVAEGLAC	LTSILSYGYF	HTDLRTLQK
51	YTLSLKGAN	ADIMRFGNEM	RLTPRALRL	LDELSNLQLP	CILHWNLNHF
101	VVLCSISKDS	IVIMDPAVGM	NKIKMDEVSG	KFTGIALELF	PNTHFEKKKE
151	TKTIKILSL	RGXSGLKRS	IOMLILAISL	EFVAL...	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNL	SLGLTKKLPVILQTEVAECGLACLA	AAVAGFYGFYTDLRALRSKYCLSLKGEN			
	::	:::	:::	:::	::	
m553	MDYLSRLS	SFGFNKKLPVILQTEVAECGLACLS	SILSYGFHTDLRTL	RQKYTTL	SLKGAN	
	10	20	30	40	50	60
	70	80	90	100	110	120
g553.pep	ADIVRFADD	MGLTGRALRLDLDELGSLRLPCILHWDLNHFV	LVESVSSDGA	AVMDPASGR		
	::	:::	::	:::		::
m553	ADIMRFGNEM	NLTPRALRLELDEL	SNLQLPCILHWNLNHFV	VLCSISKDSIVIMDP	PAVGM	
	70	80	90	100	110	120
	130	140	150	160	170	180
g553.pep	RKVKTEEIS	IRKFTGIALELWPNT	RFEAGEEKQEIRILPMLRGISGLGR	TLFQLLALAAAM		
	::	:::	::	:::		::
m553	RKIKMDEV	SQKFTGIALELFPNTH	FEKKETKKIKILSLLRGXSG	LKRS	LQMLILAI	SL
	130	140	150	160	170	180
	190	200	210	220	230	240
g553.pep	EVFAFLQNV	SFKIGRGESLALIGRSGCGKSTLLDILSGNLP	PPESGKVMINGHDIYSL	PPPP		
m553	EVFAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

```
a553.seq
  1  ATGCCCCATC  TGCAAAACCT  GTCTTTGGGC  TTAAAGAAAA  AGCTGCCTGT
51  TATCCTGCAA  ACAGAAATAT  CAGAAATCGG  CTGGCATGT   CTGGCGGCTG
101 TGGCGGGATT  TCATGGTTTC  CATACGAATT  TACGCGCACT  GCGTTCAAAA
151 TAC
```

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

```
a553.pep
      1  MPHLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
     51  Y
```

m553/a553 62.7% identity in 51 aa overlap

	10	20	30	40	50	60
m553.pep	MDYLSRLSFGFNKKLPVILQTEVAECGLACLSILSYYGFTDLRTLRLQKYTLSLKGANL					
a553	MPHLQNLSLGLKKKLPVILQTEISECGLACLAAVAGFHGFHTNLRALRSKY					
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLTPRALRLEDELNLQLPCILHWNLNHFVVLCSISKDSIVIMDPVGM					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

```
g554.seq..
      1  atgacagcac ataaaatcct gcccgctcctt cttcccatca tcttaggcgt
     51  ttctcagca acggctgcat cgcccgcgcc caacagaccg acggtacacg
    101  ccgccccac gctccaaaca cccgaaaccc tcacggcgcc acacatcggt
    151  atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaataccccc
    201  tgtcgaaccg gcggcactaa cccaactgat gaccgcatat ttgggtttca
    251  aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaataccc
    301  gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccgcgca
    351  tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
    401  acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
    451  aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
    501  caccgtattc aaaaaccgca caggcttggg tagagaagga cagggtttcca
    551  ccgccaaga cctctccctg ctgtctgaag cattgatgcg cgactttccg
    601  gaatattacc cgctgttttc catcaaatcg ttcaagttag aaaacataga
    651  acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
    701  tgaaagccgg gcacacagaa agcggcggtt acaaccttgc cgtgtcatal
    751  tccggcaacg gcaggcacat ccttgtcatc acactaggtt cggaatccgg
    801  ggaaaaccgc gcatcggaca acagcaagct gctgaaccgg gcattgcagg
    851  ccttcgatac gcccaaaata tatccgaaag gcaaaaccgt tgcccaaatc
    901  caaatttccg gaggcagcaa aaaaaccgtc cgcgagggtt tcctcaaaga
    951  agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
   1001  tggaaaccat acagccgatt cccgccccgg taaaaaaagg gcagatttta
   1051  ggaaaaatca aaatcaggca aaacggacat accattgccg aaaaagaaat
   1101  cgtcgactg gaaaacgtag aaaaagaag ccggtggcaa aggccttggg
   1151  cgcgtctgac agggcagtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

```
g554.pep..
      1  MTAHKILPVL LPIILGVSHA TAASPAPNRP TVHAAPTLOT PETLTAAHIV
     51  IDLQSRQTL AKNTNTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
    101  ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LCANDAALTL ADRLNGSIE
    151  NFVQQMKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
    201  EYYPLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
    251  SGNRHLILVI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
    301  QISGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKQIL
    351  GKIIRQNGH TIAEKEIVAL ENVEKRSRWQ RLWTRLTGQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

```
m554.seq..
      1  ATGACAGCAC ATAAATCCT GCCCGTCTG CTTTCCATCA TCTTAGGCGT
     51  TTCTCAGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGTACACG
    101  CCGCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
    151  ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
    201  TGTGTAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTC
    251  AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACCTT AAAAATACCC
```

301	GAATCCGCAT	GGGCTTCAGA	AGGAAGCAGA	ATGTTTGTAC	GTCCCGGCCGA
351	TACGGTGACG	ACCGACAAC	TCTTAAAAGG	CATGATTGCA	CTATCCGCAA
401	ACGATGCCGC	CCTAACCTT	GCCGGCCGGC	TGGGCAACGG	CTCGATTGAA
451	AATTTTGTGC	AACAATGAA	CAAAGAAGCC	CGACGCTTGG	GCATGAAGAA
501	CACGTATTTC	AAAAACCGA	CAGGCTTGAG	TAGAGAAGGA	CAGGTTTCCA
551	CCGCCAAAAG	CCTCGCCTG	CTGTCTGAAG	CATTGATGCG	GCACTTTCCG
601	GAATATTACC	CGCTGTTTTC	CATCAAATCT	TTCAAATTCA	AAAATATAGA
651	ACAAAACAAC	CGCAATATCC	TTTATATAG	GGACAACAAT	GTAACCGGTC
701	TGAAAGCCGG	ACACACAGAA	AGCGGCGGCT	ACAACCTTGC	CGTGTCTATC
751	TCCGGACAAG	GCAGGCACAT	CCTTGTTCAT	ACATTGGGTT	CGGAATCGCG
801	GGAAACACGC	GCATCAGACA	ACAGCAAGCT	GCTGAAGCTG	GCATTTCGAG
851	CCTTCGATAC	GCCCAAAATA	TATCCGAAAG	GCAAAACCGT	TGCCCAATC
901	CAAATTTCGG	GAGGCAGCAA	AAAAACCGTC	CGCGCAGGCT	TCCTCAAAGA
951	AGCCTACATC	ACTCTGCCAC	ATAAGGAAGC	GAAAATGGCA	GAACAAATTC
1001	TAGAAACCAT	ACAGCCGATT	CCCGCCCCAG	TAAAAAAAGG	GCAAAATTTA
1051	GGAAACCATCA	AAATCAGACA	AAACGGATAC	ACCATTGCCG	AAAAAGAAAT
1101	CGTCCGACTG	GAAATGTAA	AAAAAGAAG	CCGGTGGCAA	AGGCTTTGGG
1151	CGTGTCTGAC	AGGGCAGTAA			

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554 . pep . .

1	MTAHKILPVE	LSIILGVSHA	TAASPAPNRP	TVHAAPTFTQ	PETLTAAHIV
51	IDLQSKQILS	AKNINTPVEP	AALTQLMTAY	LVFKNMKSNG	IQSEENLKIP
101	ESAWASEGSR	MFVRPGDTVS	TDKLLKGMIA	LSANDAALTL	AGRLNGSIE
151	NFVQQMNKEA	RRLGMKNTVF	KNPTGLSREG	QVSTAKDLAL	LSEALMRDFP
201	EYYPLFSIKS	KFKKNIEQNN	RNILLYRDNN	VNGLKAGHTE	SGGYNLAVSY
251	SGNGRHILVI	TLGESAEATR	ASDNSKLLNW	ALQAFDTPKI	YPKGKTVAQI
301	QISGGSKKTV	RAGFSLKEAYI	TLPHKEAKMA	EQILETIQPI	PAPVKKQGIL
351	GKIKIRQNGY	TIAEKEIVAL	ENVKKRSRWQ	RLWACLTOQ*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554 . pep	MTAHKILPVLLSIIILGVSHATAASAPAPNRPTVHAAPT	FQTPETLTAAHIVIDLQSKQILS				
g554	MTAHKILPVLLPIILGVSHATAASAPAPNRPTVHAAPT	LQTPETLTAAHIVIDLQSRQTL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m554 . pep	AKNINTPVEPAALTQLM	TAYLVFKNMKS	GNIQSEENLKI	PESAWASEGSRMFVRPGD	TVS	
g554	AKNTNTPVEPAALTQLM	TAYLVFKNMKS	GNIQSEENLKI	PESAWASEGSRMFVRPGD	TVS	
	70	80	90	100	110	120
	130	140	150	160	170	180
m554 . pep	TDKLLKGMIALSANDAAL	TLA	GRNGS	IN	EFVQOMNKEARRLGMKNTV	FKNPTGLSREG
g554	TDKLLKGMIALCANDAAL	TLA	DRNGS	IN	EFVQOMNKEARRLGMKNTV	FKNPTGLGREG
	130	140	150	160	170	180
	190	200	210	220	230	240
m554 . pep	QVSTAKDLALLSEALMR	DFPEYYPLFSIKSFKFKNIEQNNRN	ILLYRDNNV	NGLKAGHTE		
g554	QVSTAKDLSLLSEALMR	DFPEYYPLFSIKSFKFENIEQNNRN	ILLYRDNNV	NGLKAGHTE		
	190	200	210	220	230	240
	250	260	270	280	290	300
m554 . pep	SGGYNLAVSYSGNGRH	ILVITL	GSESAETRAS	DN	SKLLN	WALQAFDTPKIYPKGKTV

836

```
g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554 . pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRQNGY
           |||||||||||||||||||||||||||||||||||||||||||||||||||||:
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRQNGH
           310      320      330      340      350      360

           370      380      390
m554 . pep TIAEKEIVALENVKKRSRWQRLWACL TGQX
           ||||||||||||:|||||||:|||||
g554      TIAEKEIVALENVKRSRWQRLWTRLTGQX
           370      380      390
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```
a554 . seq
1   ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCAGCA  ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCAC  GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAACA  TCAATACCCC
201 TGTCGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTCA
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAACTT  AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTA  GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAGG  CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTGTGTC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCAG CTGTCTGAAG CATTGATGCG CGACTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTC  AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCTATC
751 TCCGGCAACG GCAGGCACAT CCTTGTCATC ACATTGGGTT CGGAATCGGC
801 GGAACACGCG GCATCAGACA ACAGCAAGCT GCTGAAGTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA  TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGGCA  GAACAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG  GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGATAC  ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA  AAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGCTGAC  AGGGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```
a554 . pep
1   MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFQT PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGDTV S TDKLLKGMIA LSANDAALTL AGR LGNGSIE
151 NFVQMNKEA  RRLGMKN TVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SNGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACL TGQ*
```

m554/a554 99.2% identity in 389 aa overlap

```
           10      20      30      40      50      60
m554 . pep MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFFQTPETLTAAHIVIDLQSKQILS
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      MTAHKILPVLLSIILGVSHATAASPAPNRP TAHAAPTFFQTPETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554 . pep AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTV
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSNGIRSEENLKIPESAWASEGSRMFVRPGDTV
```

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	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLGKNTVFKNPTGLSREG					
	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY					
	310	320	330	340	350	360
m554.pep	370	380	390			
a554	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcttgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatcctgct tgcgcgctc atcgctgcgc ccgctgcggg cggtttgtt
151 tggacatccc gccgacagca acgccagttt atcgaacgct tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cagcgtatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPRTR QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC TGCCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTGTG
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAA C TGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTCGCAAA AATGTTCCGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

838

101 LSQKCSVDEA HAMFKKRPT* QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
g556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT*					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT*					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
g556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAA	ACT	GCGCTTGGGC	GGCCTGATT	TACTGACCAC
51	CGCCGTTT	AGCCTCAT	TATGAT	TGTCGATTCC	TGGCCGCTTG	
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCCGG	CGGCTTTGTT	
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT	
201	CGACATCGAT	CCCGAAAAAG	GCAGAAATCAA	CGAGGCAAAC	CTGCGCCGTA	
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC	
301	CTGTGCAAAA	AATGTTTCGGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG	
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC	
401	AGAAACGTCC	GCACCGTTAA				

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKTCLRGLG	GLILLTTAVL	SLIIVLIVDS	WPLAILLA	IVIAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HQKDAITLIC
101	LSQKCSVDEA	HAMFKKRPT*	QEINQMAAKQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
a556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT*					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT*					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
a556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

g557.seq

```

1 atgaacaaaa tattccttac tgccgcagcc ttggtgctgg gcgcgtgcgg
51 tttccacctg aaaggtgcag acggcatttc tccgccgctg acctaccgga
101 gctgggcacat cgaaggcgga caggcattgc aatttccttt ggaaaccgcg
151 ctgtatcagg cttcgggcag ggtggacgat gctgccggcg cgcagatgac
201 cctgcgtata gacagcgttt cccaaaacaa ggaaacctat accgttacct
251 gtgcggcagt catcaacgaa tatcttttga tattgacggt tgaagcgag
301 gtattgaaac gcggcgagcc ggtcggaaca ccgatgaccg tgtccgtccg
351 ccgcattttg gattatgccg acaacgaaat tttgggcaaa caggaagaag
401 aagaaaccct gtgggcggaa atgcggcagg atgttgccga acagattgtc
451 cgccgcctga cctttctgaa ggcggaatga

```

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

```

1 MNKIFLTAA LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
51 LYQASGRVDD AAGQMTLRI DSVSONKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRIL DYADNEILGK QEEBETLWAE MRQDAEQIV
151 RRLTFLKAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

```

1 ATGAACAAAC TGTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGC GG
51 TTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC GGTTCCTTT GGAAACCGCG
151 CTGTATCAGG CTTCCGGCAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCAAAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGCGAGGCC GGTCCGTAAA CCGATGACCG TGTCCGTCCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGCGGGA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCCGCCTGA CCTTCTGAA GGCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pep..

```

1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
51 LYQASGRVDD AAGQMTLRI DSVSONKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTFLKAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA LYQASGRVDD					
	: :					
g557	MNKIFLTAA LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA LYQASGRVDD					
	10	20	30	40	50	60
m557.pep	70	80	90	100	110	120
	AAGQMTLRI DSVSONKETY TVTRAAVINE YLLILTVEAQ VLKRGEFVGK PMTVSVRRVL					
g557	AAGQMTLRI DSVSONKETY TVTRAAVINE YLLILTVEAQ VLKRGEFVGK PMTVSVRRIL					
	70	80	90	100	110	120
m557.pep	130	140	150	160		
	AYADNEILGK QEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
g557	DYADNEILGK QEEETLWAE MRQDAEQIV RRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

a557.seq
 1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
 51 TTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
 151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGCGC CGCAGATGAC
 201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
 301 GTATTGAAAC GCGGCGAGCC GGTCGGCAAA CCGATGACCG TGTCCGTCGG
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
 451 CGCCGCCTGA CCTTCTGAA GGCGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

a557.pep
 1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51 LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRA AVINE YLLILTVEAQ
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
 151 RRLTFLKAE*

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALRFPLE
a557	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALQFPLE
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTR	LIDSVSQNK	ETYTVTRA	AVINEYLL	ILTVEAQV	LKRGE PVGK
a557	AAGAQMTR	LIDSVSQNK	ETYTVTRA	AVINEYLL	ILTVEAQV	LKRGE PVGK
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEIL	GKQEEEAAL	WAE MRQDA	AEQIVRRL	TFLKAEX	
a557	AYADNEIL	GKQEEEAAL	WAE MRQDA	AEQIVRRL	TFLKAEX	
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

g558.seq..
 1 ATGGATGCTT GTTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
 201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

g558.pep..
 1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMMPLYTFS ELYMLQQGTA
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSNQSP
 101 LSDGIV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

m558.seq..
 1 ATGAATGCTT GTTTTTTCGT CATTCCACAA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
 201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

m558.pep..

```

1  MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPYTFSE ELYMFQOQTA
51  HQAPHCVLPE RDYPPIRFYR HKQTGFNRKG MGIKSISDIX RAMPSENQSP
101 LSDGIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/g558

```

              10      20      30      40      50      60
m558.pep  MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPYTFSELYMFQOQTAHQAPHCVLPE
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g558       MDACFFVIPAQAGIRRFIVFKRSGRILAGAGMMPYTFSELYMLQOQTAHQAPHCVLPE
           10      20      30      40      50      60
              70      80      90     100
m558.pep  RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSPLSDGIVX
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g558       RGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSPLSDGIVX
           70      80      90     100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

```

a558.seq
1  ATGAATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT
51  CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
101 TGCCCTTATA TATAGTGGAT TAAATTAAAT TCAGGACAAG GCGACGAAGC
151 CGCAGACAGT ACAAATAGTA CGGCAAGGCG AGGCAACGCC GTACTGGTTT
201 AAATTTAATC CACTATACTT TCTCCGAGCT TTATATGTTT CAACAGAGGA
251 CGGCACATCA AGCACCGCAC TCGGTGTTGC CCGAACGAGA CTGCCCTCCG
301 ATTAGATTCT ATCGCTATAA ACAGACGGGT TTCAACCGAA AAGGAATGGG
351 AATGAAGTCC GTTCCGACA CCTCTCGGGC GATGCCGTCT GAAAACCAAT
401 CTCCACTTTC AGACGCATT GTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

```

a558.pep
1  MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPYIVD *I*IRTRRRS
51  RRQYK*YGKA RQRTGLNLI HYTFSELYMF QQRTAHQAPH CVLPERDCPP
101 IRFYRYKQTG FNRKGMGMKS VSDTSRAMPS ENQSPLSDGI V*

```

m558/a558 70.2% identity in 141 aa overlap

```

              10      20      30
m558.pep  MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPY-----
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a558       MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPYIYDXIXIRTRRRSRQYKXYGKA
           10      20      30      40      50      60
              40      50      60      70      80
m558.pep  -----TFSELYMFQOQTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a558       RQRTGLNLIHYTFSELYMFQOQTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS
           70      80      90     100     110     120
              90     100
m558.pep  ISDIXRAMPSENQSPLSDGIVX
           :|| |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
a558       VSDTSRAMPSENQSPLSDGIVX
           130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1649>:

```

g560.seq
1  atgctcatca tccgcaacct gatttactgg ctgatactct gttccagcct

```

842

```

51  gattttcctc tttcccttta tgctgctcgc ctgcctttc cgggacgggg
101 cgcacaagat ggcgcggtgc tgggtcggca tcctcaactg gtcgctcaaa
151 cacatcgctg ggctcaaata ccgcatcctc ggcgcggaac acattccgga
201 ccgcccctcc gtcatctgcg ccaaacacca aagcggctgg gaaacgctcg
251 cgctccaaga gatttttccg ccgcaggttt acgttgccaa gcgcgagttg
301 ttcaaaatcc cttttttcgg ctggggcttg aaactggtca aaaccatagg
351 catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
401 gtttggcgcg caaaaacgaa ggttattgga ttaccatttt cccgaaggc
451 acgcgccctg cgcccggaaa acgcggcgaa tacaaactcg gcggcgcgcg
501 catggcgaaa atgtttgaga tggacatcgt ccccgctgcc ctcaacagcg
551 gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
601 gtcatcatct gtccgaccat cccgcacgca agcggcagcg aagccgaatt
651 gatggaaaaa tgcgaacacc tcattgaaac gcaacaaccg cttatttccg
701 gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

```

1  MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAEHIPDRPS VICAQHSGW ETLALQEIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQLARKNE GYWITIFPEG
151 TRLAPGKR GK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1  ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101 CGCACAAGAT GGCGCGGGTC TGGGTGCGCA TTCTCAACTG GTCGCTCAAA
151 CACATCGTGC GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCTTTCAGGA CATTTTTCGG CCGCAGGTTT ACCTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AAACGTGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTGCTGCG CAAAAACGAA GGCTATTGGA TTACCATTTC CCGGAAGGC
451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGAAGAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTTCGG
701 GCGCAGGCCG GTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQLVRKNE GYWITIFPEG
151 TRLAPGKR GK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng)

from *N. gonorrhoeae*:

m560/g560

```

              10      20      30      40      50      60
m560.pep  MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g560      MLIIRNLIYWLILCSSLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
              10      20      30      40      50      60

              70      80      90     100     110     120
m560.pep  GAENIPDRPAVICAKHSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g560      GAEHIPDRPSVICAKHSGWETLALQEIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR

```

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVIICTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1   ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGAGACGGGG
101 CGCACAAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTCCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AAACCTGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTGGCGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCGAAGGC
451 ACACGCCTTG CGCCCGGAAA ACGCGGCAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCCTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAA TCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTCCG
701 GCGCAGGCC GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1   MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAKHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAM FEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*

```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMFEMDIVPVA					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMFEMDIVPVA					

844

	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMGKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

m561.seq.

```

1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GCGCGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAC ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCCTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCCTCCA GTCCTACCGG CGACCGACTC
401 AGGTGCTGCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGACGGCA
451 TTGGAATAAT CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCTGC TGTACTGATG CTGTTTGGC
551 ACCAGATTTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTGCGGC GTTGTTCCTA TCAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTG GGAAGTACC ATGAGGAAAT CTTCCCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GGCACAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAC CCGCCTTTGC
1251 CGAAAAACAA CGGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTTCCGT
1351 ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCGGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTGTTCCTT GCCGCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCGCGGCCA CCCATGTAAA
1551 ATTACCCCTT TCCGAACAG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTGACACG GAGAAAATAG GAGAACCAC GGGCAGCCAT
1651 GTCGGACTGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

m561.pep

```

1  MILPARFSDG ISLSRLRLKL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQNQLTL LYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEERKL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFAENK REEAAENISF IKTGVQECYE DVRELLLNFR
451 TKISNKEFFE AVADLFARFT QQTGITVETA WENGSLFPPQ EAQLQMIFIL

```

501 QESLSNIRKH ARATHVKFTL SEHGGRFTMT IQDNGQGFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS	VVLTLLLSRL	LENAASVIEE	EAGNLR	MQAY	
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALS	VVLTLLLSFRLENAASVIEE	EAGNLR	MQAY		
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAE	FEKSLKRIAQSDAIH	PLIPSDTPLAYDLIQS	MLIIDWQA		
g561	RLAYMAGEGSPRAQIDNQIAE	FEKSLKRISQSDAIH	PLIPSDNPLAYDLIQS	MLIIDWQA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYR	FAGNIELFLOALENANE	KNTWWLRRFQWAIM	MLTLVSSVLM		
g561	NILPPLQAYRRPTQIELYR	FAGNIELFLOALENAGE	KNTWWLRRFQWVIM	MLTLVSSVLM		
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGA	ERIGRRCFDIPVPEGGT	PEFKQVGR	CFNQMGGRLKILY	DDDL	
g561	LFWHQIWVIRPLQALREGA	ERIGQRHFDIPVPEDV	RNSNRSGGVSTK	WRSGX		
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNQLT	LLYQTTDLHQSYIPQQA	AEHFLNRILPAVGAD	SGRVC	LDG	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTTACAGCGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCTGGGT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTGCCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCTT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAACA	TCGAACTGTT	TTTGCAGGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTAATGATG	CTGTTTGGCC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTCTGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATCCG	GCAGAGTTT	TTTGGACGGC
901	GGATCCGATG	TTTATGTTT	CATTATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCCGATTTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCAT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCTG	CTTGACGAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCTTTGCG
1251	CGAAAACAAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCGGTTGCCG	ACCTATTCTC

```

1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMIIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQM GRLKILYDDL EGQVAEQTRS
251 LEKQONQLTL LYQTTDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFENK REEAAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFDT ENIGEPSGSH
551 VGLHIMQERA KRIHAVLEIR SQAQQTTS LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

10 20 30 40 50 60
m561.pep MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRLLENAASVIEEAGNLRMQAY
|||||
a561 MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRLLENAASVIEEAGNLRMQAY
10 20 30 40 50 60

70 80 90 100 110 120
m561.pep RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMIIIDWQA
|||||
a561 RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMIIIDWQA
70 80 90 100 110 120

130 140 150 160 170 180
m561.pep HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
|||||
a561 HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
130 140 150 160 170 180

190 200 210 220 230 240
m561.pep LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLKILYDDL
|||||
a561 LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLKILYDDL
190 200 210 220 230 240

250 260 270 280 290 300
m561.pep EGQVAEQTRSLEKQONQLTLLYQTTDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
|||||
a561 EGQVAEQTRSLEKQONQLTLLYQTTDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
250 260 270 280 290 300

310 320 330 340 350 360
m561.pep GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
|||||
a561 GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
310 320 330 340 350 360

370 380 390 400 410 420
m561.pep LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFNLQVQMLETAFENK
|||||
a561 LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFNLQVQMLETAFENK

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847

	370	380	390	400	410	420
m561.pep	430	440	450	460	470	480
a561	430	440	450	460	470	480
m561.pep	490	500	510	520	530	540
a561	490	500	510	520	530	540
m561.pep	550	560	570	580	590	
a561	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1 atggcaagcc cgctcagctct gcctttcaat tcgggcaaga ccaaaccgac
51 ggcttttgcc gcgccggttt tggtcggaat catgttttcc acgccgctgc
101 gggcgcgccg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgcttcc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaaacgac ggtcatgtcg gcggtcagga cgctgtcggt caccgcttac
301 acgacggttg catcgacatc gtcgccgccc ggtgcgaaa tgaggacttt
351 tttcgcgccg ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tgcgggtcga gaagaagggg attttgcgcg cggtgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcggtg
601 acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1 MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51 VSAWMVVIAP LTMP TSLNT LATGERQLVV QEAL ETVMS AVRTLSETPY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTSASKR PCTVSNLVRW ALVSRPLPAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1 ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51 GGCTTTTGCC GCGCCGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC
101 GGGCGCGCGC CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTATGTGCG GCGGTACGGA CGCTGTGCTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCCC GGTGCGGAAA TGAGGACTTT
351 TTTCCGCGCC CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TCGGGGTCGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501 GAGGTGCGCG CCGTCGTGGG ATACGTGCGC TTCAAAGCGT CCGTGCACGG
551 TGTCGAATTT GGTGAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1 MASPSSLPFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51 VSAWMVVIAP LTMP TSLNT LATGERQLVV QEAL ETVMS AVRTLSETPY

```

848

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLPLAL
 201 TATSWWS*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
g562	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPTTVASTSSPPGAEMRTFFAP					
g562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTASAKR					
g562	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTASAKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRPLALTATSWWSX					
g562	PCTVSNLVRWALVSRPLALTATSWWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq
 1 ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC
 51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTTCC ACGCCGCTGC
 101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
 151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
 201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
 251 TGGAAACGAC GGTCATGTCG GCGGTCAGGA TGCTGTCGTT CACGCCGTAC
 301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
 351 TTTGCGCGCG CTTTCCAGAT GAACTTTGGC TTTTCTTTG CTGGTGAACG
 401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTCTTT CCACGGCAGT
 451 TCGGCAGGGT TCGGGGTCNA GAAGAANGG ATTTTGTGCG CGTTGACGAT
 501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
 551 TGTCGAATT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
 601 ACGGCGACGA TTTGGAGTTG GTCTTGA

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep
 1 MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
 51 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRMLSFTPY
 101 TTVASTSSPP GAEMRTFFAP LSR*TLAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVXXKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLPLAL
 201 TATIWSWS*

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
a562	MASPSSLSFN SGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60

849

	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMASVRTLSTFTPYTTVASTSSPPGAEMRTFFAP					
a562	LTMPTLSLNTLATGERQLVVQEALETTVMASVRLSTFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
m562.pep	LSRWILAFSLLVNAPVHSMKSTPSSFHGSSAGLRVEKKGILSPLTMRLLPPSWDTSASKR					
a562	LSRXTLAFSLLVNAPVHSMKSTPSSFHGSSAGLRVKKXGILSPLTMRLLPPSWDTSASKR					
	130	140	150	160	170	180
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
a562	PCTVSNLVRWALVSRLPLALTATIWSWX					
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
a562	PCTVSNLVRWALVSRLPLALTATIWSWX					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

```

1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCAGTTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GCGGTTGGA TTCAAGGCAA TCCTTGGTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTAAAC CAAATCAACA GCAGCCATCC
501 TTCACAATG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACACG
701 GTTTGGATGC CCGTGATACC GATTTCACAC GTATCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTG GTAATCAAGG
801 GCAGTTGTTT GCTTCTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGCACGATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAGTCAA TATCCGAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACATGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTACAG CAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGTGATAA TAACTGGAT ATTGCGTTAC AAGATGATT
1251 TTATGTAGAA CGAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGATTTCGG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CGGTACGACA GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAAACCAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
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1601 TGAATTTAGG CATTGAACAA TTAATAAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
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1851 AGCATTGGA CGACACGAAT TATTGCGAGA AGGCAGGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAACGT CGCCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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2151 AACCTTTGGC GAGAAGAAAG TCTTCAGCGA AAATGGTAAG TTGCACAAC
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA
2251 AATTATACTT TGCCGGAGGA AATCACACGC GACATTTCAC TGGGTTCAAT
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG
2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TCGGAAAAGC
2401 AACGGTATTT CGTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG
2451 CAGCAGCTTA TACATTATCA ATCCTGCCAA TAAAGGCTAT CTTGTTGAAA
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTTGGGTAG TGAATATATG
2551 CTGGGCAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA
2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG
2651 GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC
2701 TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG
2751 CATTGCATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT
2801 GGTGGGTACA AAAAGAAGTT AAACCTCCTG ATGGCGGCAC ACAAACCGTA
2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA
2901 AGGTGCATTG TTGTCAAGCA GCAATACACA AATCAATGTT TCAGGCAGCC
2951 TGAAAAACTC AGGCACGATT GCAGGCGCGA ATGCGCTTAT TATCAATACC
3001 GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA AATCAGCGGT
3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC
3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTATGCA GCGCAGGCAG
3251 GCAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA ATCAGATCAA
3301 GGGCAAACCC GGCTGCAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA
3351 AACCGGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATACCATCC
3401 GAGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT
3451 ACCCtattGT CAGGGAATAA TCTCAATGCC AAAGCTGCCG AAGTCGGCAG
3501 CGCAAAAGGC ACACCTGCGG TGTATGCTAA AAATGACATT ACTATCAGCT
3551 CAGGCATCCA TGCCGGCCAA GTTGATGATG CGTCCAAACA TACAGGCAGA
3601 AGCGGCGGCG GTAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA
3651 CGAAACTGCT CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT GTATTGCAGG
3701 CAGGAAACGA TGCCAACATC CTTGGCAGTA ATGTTATTTT CGATAATGGC
3751 ACCCGGATTG AAGCAGGCAA TCATGTTCGC ATTGGTACAA CCCAAACTCA
3801 AAGCCAAAGC GAAACCTATC ATCAAACCCA AAAATCAGGA TTGATGAGTG
3851 CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA AGAAAACCAA
3901 TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCC TGAAGGCGCA
3951 TACCACCATT GTTGCAAGCA AACACTACGA ACAAACCGGC AGCAACGTTT
4001 CCAGCCCTGA GGGCAACAAC CTTATCAGCA CGCAAAGTAT GGATATTGGC
4051 GCAGCACAAA ACCAATTAAT CAGCAAAACC ACCCAAACCT ACGAACAAAA
4101 AGGCTTAACG GTGGGCATTG AGTTCGCCCC TTACCGATTT GGCACAACAA
4151 GCGATTGCCG TAGCACACAA AGCAGCAAAC AAGTCGGACA AAGCAAAAAC
4201 GACCGCGTTA ATGCCATGGC GGCTGCCAAT GCAGGTTGGC AGGCCTATCA
4251 AACAGGCAAA GGCGCACAAA ACTTAGCCAA TGGTACAACC AATGCCAAAC
4301 AAGTCAGCAT CTCCATAACC TACGGCGAAC AGCAAAACCG ACAAACCACC
4351 CAAGTTCAAG CCAATCAAGC CCAAGCGAGT CAAATTCAAG CAGGCGGCAA
4401 AACTACCCTT TATTGCCGAA GGTGCGGCGA ACAATCCAAT ATCAACATCA
4451 CAGGCTCAGG TGTTTCAGGC AGAGCAGGAA CCGGCCTGAT TGCCGATAAG
4501 CAAATCCATC TGCAATCAGC CGAGCAAAGC AATACCGAAC GCAGCCAAAA
4551 CAAATCAGCA GGCTGGAACG CAGGTGCTGC CGTATCATTC GGACAAGGAG
4601 GCTGGTCATT AGGCGTTGCC GCAGGCGGCA ATGTCGGCAA AGGCTACGGC
4651 TATGGCGATA GCGTAACCCA CCGCCATAGC CATATTGGCG ACAAAGGCAG
4701 CCAAACCTT ATCCAAAGTG GTGGCGATAC CATCATCAAA GCGCGCAAG
4751 TACGCGGCAA AGGCGTACAA GTCAATGCCA AAAACCTAAG CATTCAAAGT
4801 GTACAAGATA GAGAACTTA TCAAAGCAAA CAACAAAACG CCGGTGCACA
4851 AGTTACCGTA GGTATGGCT TCAGTGCCAG TGGCGATTAC AGCCAAAGCA
4901 AAATCCGAGC CGACCATGCT TCGGTAACCG AGCAAAGCGG TATTTATGCC
4951 GGAGAAGACG GCTATCAAAT CAAGGTGCGA AACCATACAG GCCTCAAAGG
5001 CGGCATCATC ACCAGCAGCC AAAGCGCAAA AGACAAGGGT AAAAACCGAT
5051 TCAGCACAGG CACACTCGCC GGCAGTGATA TTCAAATTA CAGCCAATAC
5101 GAAGGAAAAA GTTTTGGATT GGGTGCCAGC GTTGCCGTAA GCGGCAAAAC
5151 ACTGGGACAG GGCGCAAAAA ATAAACCTCA AGACAAACAC CTGACAAGCA

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5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CAAAAACAT
5301 TCAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
5401 CGACATTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
5451 TGAAC TGGAT TTACAAgaa CCGTCAGCCA AGATTTTAGT AAAAATGTTC
5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
5651 CAGATAATTG GCAACAAGGC AAAGTCATT CCAACATGTT AGCCTCAGGT
5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
5751 GCCagaCGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
5801 AAAACGCGAA TGGCAAAC TAACCGCAGTC AagaAACCGC TCACGTCTCT
5851 GCCCAGCGCG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
5901 CCGCGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCAATCA
5951 TCGGCAAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgcggag
6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggt cGgctGCCGG
6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGGT TGTTTTcaaa
6101 cggctTCaga TTTCGCTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

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This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pcp..

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1 MNKTLRVIF NRKRGA VAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
51 SKAFCF SALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTNGNIP
101 QVNIQTPTSA GVSVNQY AQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNGGGFIN
201 ASRATLTGQ PQYQAGDFSG FKIRQGNV AGHGLDARDT DFTRILLYAN
251 KITLISTAEQ AGIRNQQLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
301 TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
351 SLNNQNGEIA TNQQLIHDG QQSTVVIDNT NGTIQSGRDV AIQAKSLSN
401 GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
451 IKANNLDNAV QGNIQSGGTT DIGTQHNL TN RGLIDGQOTK IQAGQMNIG
501 TGRIYGDNIA IAATRLDNQD ENGTGAAIAA RENLNLGIEQ LNNRENSLIY
551 SGNDMAVGG A LDTNDQATGK AQRIHNAGAI IEAGKMR LG ESKLHNTNEH
601 LKTQLVETGR ERIVDYEA FG RHELLREGTQ HELGWFVYNN ESDHLRTPDG
651 VAHENWHKYD YEKVQTETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHN YWRARRK GHDETHREQ
751 NYTLPEEITR DISLGSFAYE SHSKALS RHA PSQGTLPQS NRDNIRTAKS
801 NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQWLGS DYM
851 LGS LKLD PNN LHKRLGD GYY EQRLINEQIA ELTGHRRLDG YONDEEQFKA
901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVVLVQKEV KLPDGGTQTV
951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
1001 DTLDNIGGRI HAQKSAVTAT QDINNIGGIL SAEQTL LLLNA GNNINNQSTA
1051 KSSQNAQGS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AGQISNQSDQ
1101 QTRLQAGRD INLDTVQTGK YQEIHFADN HTIRGSTNEV GSSIQT KGDV
1151 TLLSGNNLNA KAAEVGSAK TLAVYAKNDI TISSGIHAG VDDASKHTGR
1201 SGGGNKL VIT DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG
1251 TRIQAGNHVR IGTQTQSQS ETYHQTQKSG LMSAGIGFTI GSKTNTQENQ
1301 SQSNEHTGST VGS LKGD TTI VASKHYEQTG SNVSSPEGNN LISTQSM DIG
1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYR GTTSDCRSTQ SSKQVQGSKN
1401 DRVNAMAAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQQNRQT
1451 QVQANQAQAS QIQAGGKTTL YCRRCEQSN INITGSGVSG RAGTGLIADK
1501 QIHLQSAEQS NTERSQNKSA GWNAGAAVSF GQGGWSLGVA AGGNVKG YG
1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTI IK GAQVRGKG VQ VNAKNLSIQS
1601 VQDRETYQSK QONAGA QVTV GYGFSASGDY SQSKIRADHA SVTEQSGIYA
1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFTGT LA GSDIQNYSQY
1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LTSIADKN GA SSSVGYGSDS
1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTIDTAE
1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDPS KNVQQTNT EI NQHLDKL KAD
1851 KEAETA AAE ALANGDMETA KRKAHEAQDA AAKADNWQQG KVILNMLASG
1901 LAEPTQSGAG IAAATASPDV SYAIGQHFKD LAGQANANGKL TASQETAHVL
1951 AHAVLGA A VA AAXGNNAPAG ALGAGGSEAA APIGKWLYG KGDGGS LNAE
2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM*

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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

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1  ATGAATAAAA CTCTCTATCG TGTAATTTTC AACC GCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATTCAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTTCTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGGCATT A
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAACA
301 GGTAAACGGCA TACC GCAAGT CAATATTC AA ACCCTACTT CGGCAGGGGT
351 TTTCTGTTAAT CAATACGCC CAGTTTGATGT GGGTAATCGC GGGGCGATTT
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGGATTCAA
451 GGTAAATCCTT GGTGGCAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAT
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTTA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA GCGGCTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCGTG ATACCGATTT CACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTGC
801 TGTCGTCGCG GGACAAAACG ATGTGGTCGC AACAGGTAAT GCACATTCGC
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTTATT TGCGATTGAT ACAGGCAAAT TAGGAGGTAT
951 GTATGCCAAC AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATT C
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAAATGTGGC GATTGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCACGATG GCTGCCGCCA ATGCGAAAGA
1101 TACGGATAAT ACAGCGGAAC ACAAGTCAA TATCCGCAGT CAGGGCGTTG
1151 AAAACAGCGG TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA AACTGGCAC ATTATTGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTGCGGC AGCCTGAAAA ATGAAACATC AGGCACATT GAAGCGGCTC
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1351 ACAGGTTTCA AAAAATCCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCTAG GGTTTACAAG ATACCGCACC AACC GCGTCA AATGGTTCAA
1451 GCAATCAAAC CGGCAATAGT TACAATGCAT CTTTCCATT C ATCCACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAAA
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1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTCATC AGTTAAATGC
1701 AAAAGGTTTC GCGTTTGACA ATCACAATGG AACAAATTATC AGTGTATGCG
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1851 GTTATTATCA GCAGAAATAG CGGATTTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCAT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTCAGG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTT TTATGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC GAGGCAGCCT
2151 GAAAAATTCA CATACTTTGC AAGCAGGAAA ACGCATTCGG ATTAAAGCAA
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2251 GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA TTGACGGACA
2301 ACAAAACAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT ACAGGTCCGA
2351 TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGTGAAAACC TGAATTTAGG
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2501 ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGGCCAAGC CACAGGCAAA
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2601 GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGGCGC GAGCATATTG TTGATTACGA AGCATTTGGA
2701 CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG GCTGGTCTGT
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2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCAAAAA AACCCAAGTT
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2951 TCATTGTACA AACAGAAAAA GACGGTTTGC ATAACGAGCA AACCTTTGGC

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3001 GAAAAGAAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA
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3101 TGCCGGAGGA AATCACACGC AACATTTCAC TGGGTTCATT TGCCTATGAA
3151 TCGCATCGCA AAGCATTAAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT
3201 GCCGCAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC
3251 CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT
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3351 TGACTATATG CTGGACAGCC TCAAACCTAGA CCCAAACAAT TTACATAAAC
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3501 ATTTAAAGCC TTAATGGATA ATGGCGCGAC TCGGCACGT TCGATGAATC
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3601 GATATTGTTT GGTGGGTACA AAAAGAAAGT AAGCTTCCTG ATGGCGGCAC
3651 ACAAACCGTA TTGGTGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGACA
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3751 TCAGGCAGCC TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT
3801 TATCAATACC GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA
3851 AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT
3901 TCTGCCGAAC AGACATTATT GCTCAACGCA GGCAACAACA TCAACAGCCA
3951 AAGCACCACC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG
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4101 ATCAGAGCAA GGGCAAACCC GGCTGCAAGC AGGGCGCGAC ATTAACCTAG
4151 ATACGGTACA AACCAGCAAA CATCAAGCAA CCCATTTTGA TGCCGATAAC
4201 CATGTTATTC GCGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA
4251 AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGCTGCCG
4301 AAGTCAGCAG CGCAAAACGGT ACACCTCGTG TGTCTGCCAA AAATGACATC
4351 AACATCAGCG CAGGCATCAA CACGACCCAT GTTGATGATG CGTCCAAACA
4401 CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC
4451 AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT
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4701 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT
4751 TGAAAGGCGA TACCACCATT GTTGCAAGCA AACACTACGA ACAAATCGGC
4801 AGTACCGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT
4851 AGACATTCAA GCGGCACACA ACAAATTAAA CAGTAATACC ACCCAAACCT
4901 ATGAACAAAA AGGCCTAACG GTGGCATTCA GTTCGCCCCG TACCGATTTG
4951 GCACAACAAG CGATTGCCGT AGCACAAGC AGCAAACAAG TCGGACAAAG
5001 CAAAAACGAC CGCGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG
5051 CCTATCAAAC AGGTAAGAGT GCACAAAACCT TAGCCAATGG TACAACCAAT
5101 GCCAAACAAAG TCAGCATCTC CATAACCTAC GCGGAACAGC AAAACCGACA
5151 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAGCAG
5201 GTGGTAAAC CACATTAATC GCCACAGGCG CAGCAGAACA ATCCAATATC
5251 AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC
5301 CGATAACGAC ATCACACTCC AATCAGCCGA GCAAAGCAAT ACCGAACGCG
5351 GCCAAAACAA ATCGGCAGGC TGGAACGCAG GTGCTGCCGT ATCATTCGGA
5401 CAAGGAGGCT GGTCAATAGG CGTTACCGCA GGCGGCAATG TCGGCAAAAG
5451 CTACGGCAAT GGCGACAGCA TCACCCACCG CCATAGCCAT ATCGGCGACA
5501 AAGGCAGCCA AACCTTATC CAAAGCGGTG GCGACACTAC CATCAAAGGC
5551 GCGCAAGTAC GCGCAAAAGG CGTACAAGTC AATGCCAAAA ACCTAAGTAT
5601 TCAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAAACAA CAAACGCCA
5651 GTGCACAAGT TACCGTAGGT TATGGCTTCA GTGCCGGTGC CGATTACAGC
5701 CAAAGCAAAA TCCGAGCCGA CCATGTTTCA GTAACCGAGC AAAGCGGTAT
5751 TTAGTCCGGA GAAGACGGCT ATCAAATCAA GGTCGGAAAC CATAAGACC
5801 TCAAAGGCGG CATCATCACC AGTACCCAAA GCGCAGAAGA CAAGGGTAAA
5851 AACCGCTTTC AGACGGCCAC CCTCACCCAT AGCGACATCA AAAACCCAG
5901 CCAATACAAA GGCAGAAAGT TTGGATTGGG CGCAAGTGGC TCCATAAGCG
5951 GCACAAACACT GGGACAGGGC GCACAAAATA AACCTCAAAA CAAACACCTG
6001 ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG
6051 CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA

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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
6201 CGAACGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
6251 AAAGTGAAC TGGATTACAA AGAACCCTCA GCCAAGATTT TAGTAAAAAT
6301 GTTCAACAAG CCAATACCGA GATTAAACCA CATTTAGACA AACTCAAAGC
6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTAGCC
6601 GGTCAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
6701 ATGCTCTAGC AGGAGCATTG AGTGCGGCGC GGTCGGAAGC GGCTGCGCCT
6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
6901 AATGCGCAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
6951 TGCTCTTAGC CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
7001 ATCCTGGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
7051 CAATTAAATT TATTCCTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTG
7151 GCAAAGATAT TGCTGTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAATACCA
7301 ATAGGTAAAC CACAAAAGAG TTAGTTGGAT TAATCTGGA AACTTATAAA
7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
7401 TGTAAGAAAA AGATTATCTG AAAAAGATTA CCAGAATACA AGCAATATAT
7451 TGATTCACCT AGATAATACT GGTGCCGGAT TAAAATTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAT TTCAGCCAGA CAATGGAGAA GATAA

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

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1 MNKTLRYRVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVFPFTTH
51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIIADKAAP KTQQATILQT
101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIQ
151 GNPWLARGEA RVVVNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
201 GGFNASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
251 LSYHSKIDAP VWGQDVRVVA QONDVVATGN AHSPILNNA ANTSTNTANN
301 GTHIPLFAID TGKLGMYAN KITLISTAEQ AGIRNQGLF ASSGNVAIDA
351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVNSGTAV SQQGTQIHSQ
401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQKLSQ
451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT
501 TPPTATGTGT ATVSISNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA
551 QQGLNNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
601 RQQLIEITDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIHDG
651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSN GTLAADNKLD IALQDDFYVE
701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
751 DIGTQHNLTN RGLIDGQOTK IQAGQMNNIG TGRIYGNIA IAATRLDNQD
801 ENGTAIAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGA LDTNGQATGK
851 AQRHINAGAT IEAAGKMLRG VEKLHNTNEH LKTQLVETGR EHVITYEAFG
901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
1051 SHRKALSHHA PSQGTPLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKGY
1101 LVETDPRFAN YRQWLGSDDY LDLSLKDPNN LHKRLGDGYY EQRLINEQIA
1151 ELTGHRRLDG YQNDEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVWLQKEV KLPDGGTQTV LVPQVYVRVK NGDIDKGAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALINT DTLDNIGGRI HAQSAVTAT QDINNIGGML
1301 SAEQTLNNA GNNINSQSTT ASSQNTQGSS TYLDRMAGIY ITGKEKGVLA
1351 AQAGKDINII AGQISNQSEQ QQTRLQAGRD INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGKDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSTFEGKQV
1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTTQTQSQS ETYHQTQKSG

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855

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1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGSCLKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLNST TQTYEQKGLT VAFSSPVTDL
1651 AQQAIAVAQS SKQVGQSKND RVNAMAANA GWQAYQTGKS AQLNLANGTTN
1701 AKQVSISITY GEQQNRQTTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKASG WNAGAAVSFG
1801 QGGWSLGVTA GGNVKGKGYGN GDSITHRHS IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKKG
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AONKPQNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKLGADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQGGKV ILNMLASGLA APTQSGAGIA AATASPAVSF AIGQHFKDIA
2201 QONANGKLT SAQTAHVLAH AVLGAAVA AV GDNNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGAAVGN SATDAAQGS
2301 NAQSAVENND TVEQVKFALR HPRIAIAIGS VHKDPGSTLE PNISTIASTF
2351 QLNLPNSEF GEGGVGNF RHVLWQATIT REFGKDIQV VGNSHESGK
2401 INYSIRNLS LDKADEMIDQ LNNEIGREIA LNTNRLNTKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```

              10      20      30      40      50
g563.pep      MNKTLRYVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYKVSFIPTH-----SKAFC
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep      MNKTLRYVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
              10      20      30      40      50      60

              60      70      80      90      100     110
g563.pep      FSALGFSLSCLALGTVNIAFADGIITDKAAPKTQQATILQTGNQIPQVNIQTPTSAGVSVN
              || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep      FSLGFSLSCLAVGTANIAFADGIADKAAPKTQQATILQTGNQIPQVNIQTPTSAGVSVN
              70      80      90      100     110     120

              120     130     140     150     160     170
g563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE
              130     140     150     160     170     180

              180     190     200     210     220     230
g563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVVIAGHGL
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVVIAGHGL
              190     200     210     220     230     240

              240
g563.pep      DARDTDFTRIL-----
              ||| ||| ||| |||
m563.pep      DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPILNNAANTSNTANN
              250     260     270     280     290     300

              250     260     270     280     290
g563.pep      -----LYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
              : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep      GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
              310     320     330     340     350     360

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	300	310	320	330	340	
g563 . pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----					
	:: :					:
m563 . pep	AAANAKDNTDAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG					
	370	380	390	400	410	420
g563 . pep	-----					
m563 . pep	SLKNETSGTIEAARLAIDTDTLNNQGKLSQTGSQKLHIDAQGMNDRGRMGLQDTAPTAS					
	430	440	450	460	470	480
g563 . pep	-----					
m563 . pep	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSIISNITAPTADFAGTIRTHGALDNSGSI					
	490	500	510	520	530	540
g563 . pep	-----					
m563 . pep	IANGQTDVSAQQGLNNAQGIDIHQLNAKGSAFDNHNGTIIISDAVHIQAGSLNNQNGNITT					
	550	560	570	580	590	600
g563 . pep	-----		350	360	370	380
	-----	EDLAVSGSLNNQNGEIATNQQLIIHDGQQSTVVIDNT				
m563 . pep	RQOLEIETDQLDNAHGKLLSAEIAIDLAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT					
	610	620	630	640	650	660
g563 . pep	390	400	410	420	430	440
	NGTIQSGRDVAIQAKSLSNNGTLAADNKLKDIALQDDFYVERKIVAGNELSLSTRGSLKNS					
m563 . pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLKDIALQDDFYVERNIVAGNELSLSTRGSLKNS					
	670	680	690	700	710	720
g563 . pep	450	460	470	480	490	500
	HTLQAGKRIRIKANNLDAVQGNIQSGGTTDIGTQHNLTNRGLIDGQQTKIQAGQMNNIG					
m563 . pep	HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLTNRGLIDGQQTKIQAGQMNNIG					
	730	740	750	760	770	780
g563 . pep	510	520	530	540	550	560
	TGRIYGDNIAIAATRLDNQDENG TGAAIAARENLNLGIEQLNNREN SLIYSGNDMAVGGA					
m563 . pep	TGRIYGDNIAIAATRLDNQDENG TGAAIAARENLNLGIGQLNNREN SLIYSGNDMAVGGA					
	790	800	810	820	830	840
g563 . pep	570	580	590	600	610	620
	LDTNDQATGKAQRIHNAGAIIEAAGKMRLGVEKLNHTNEHLKTQLVETGRERIVDYEAFG					
m563 . pep	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLNHTNEHLKTQLVETGREHIVDYEAFG					
	850	860	870	880	890	900
g563 . pep	630	640	650	660	670	680
	RHELLREGTQHELGWVYNNESDHLRTPDGVAHENWHKYDYEKVTQETQVGTGAPAKIIA					
m563 . pep	RHELLREGTQHELGWSVYNDES DHLRTPDGAAHENWHKYDYEKVTQKTQVGTGAPAKIIS					
	910	920	930	940	950	960
	690	700	710	720	730	740

857

g563.pep	GSDLIIDSKAVFNSDSRIIAGGQLLVQTEKDGLHNEQTFGEKKVFSENGKLHNYWRARRK
m563.pep	GNDLTIDGKEVFNTDSQIIAGGNLIVQTEKDGLHNEQTFGEKKVFSENGKLHSYWREKHK
	970 980 990 1000 1010 1020
g563.pep	GHDETGHRQNYTLPEEITRDISLGSFAYESHKALSRHAPSOGTELPQSNRDNIRTAKS
m563.pep	GRDSTGHSEQNYTLPEEITRNISLGSFAYESHKALSHHAPSOGTELPQSN-----
	1030 1040 1050 1060 1070
g563.pep	NGISLPYTPNSFTPLPGSSLYIINPANKGYLVETDPRFANYRQWLGS DYMLGSLKLDPNN
m563.pep	-GISLPYTSNSFTPLPSSSLYIINPVNKG YLVETDPRFANYRQWLGS DYMLDLSKLDPNN
	1080 1090 1100 1110 1120 1130
g563.pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
m563.pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
	1140 1150 1160 1170 1180 1190
g563.pep	SAEQAAQLTSDIVWLQKEVKLPDGGTQTVLMPQVYVRVKNGGIDGKGALLSGSNTQINV
m563.pep	SAEQVAQLTSDIVWLQKEVKLPDGGTQTVLVPQVYVRVKNGDIDGKGALLSGSNTQINV
	1200 1210 1220 1230 1240 1250
g563.pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGILSAEQTLLLNA
m563.pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGMLSAEQTLLLNA
	1260 1270 1280 1290 1300 1310
g563.pep	GNNINNQSTAKSSQNAQGSSTYLDRMAGIYITGKEKGVLAAGAKDINIIAGQISNQSDQ
m563.pep	GNNINSQSTTASSQNTQGSSTYLDRMAGIYITGKEKGVLAAGAKDINIIAGQISNQSEQ
	1320 1330 1340 1350 1360 1370
g563.pep	GQTRLQAGR DINLDTVQTGKYQEIHFADADNHTIRGSTNEVGSSIQTKGDVTLTSGNNLNA
m563.pep	GQTRLQAGR DINLDTVQTSKHQATHFDADNHHVIRGSTNEVGSSIQTKGDVTLTSGNNLNA
	1380 1390 1400 1410 1420 1430
g563.pep	KAAEVGSAKGT LAVYAKNDITISSGIHAGQVDDASKHTGRSGGGNKLVIITDKAQSHHETA
m563.pep	KAAEVSSANGT LAVSAKNDINISAGINTTHVDDASKHTGRSGGGNKLVIITDKAQSHHETA
	1440 1450 1460 1470 1480 1490
g563.pep	QSSTFEGKQVVLQAGNDANILGSNVISDNGTRIAGNHVRIGTTQTQSQSEYHQTKSG
m563.pep	QSSTFEGKQVVLQAGNDANILGSNVISDNGTQIQAGNHVRIGTTQTQSQSEYHQTKSG
	1500 1510 1520 1530 1540 1550
g563.pep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGS LKGDTTIVASKHYEQTGSNVSSPEGN
	1290 1300 1310 1320 1330 1340

[illegible]

859

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDGGSLSNAE					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGSIDLTAE					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFTASDFASSFSYPINMX					
m563 . pep	EKETVTAITNVLTATGA AVGNSATDAAQGSLSNAQSAVENNDTVEQVKFALRHPRIATAI					
	2270	2280	2290	2300	2310	2320

m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLFNSEFGGEGVGNAFRHLVWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564 . seq
1   ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAATGATA TTGCGGGCTT TGCGGGTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTC
201 TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCCAAGG ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTGGTTGG CAAGGGGCGA AGCACGTGTG GTTGTAACC AAATCAACAG
501 CAGCCATTCT TCACAACGA ATGGCTATAT TGAAGTGGC GCACGACGTG
551 CAGAAAGTCG TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAATCG
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACAG TATTCTCAGT
751 TATCATTTCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCGT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCGA GCAAGCAGG ATTCGTAATC
1001 AAGGGCAATG GTTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AACTGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCATTTCAT GCCCGCAATG TTCATAATAG CGGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTGTGTA
1351 TCTGCCGGCA AATTCGATAA CAGTGGAAG ATTGGTGTA GTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCGGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACAAATCCC TTTCACCTAC AGCACCTGCA AAAAATACG CCGTAGGACG
1551 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG
1601 GGCAAAATGA CATTGCCGCC CAAAACGGTT TGGGAAATC GGGTAGTCTG
1651 AATGCGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA
1701 AGGCAAACTC CAGGCACAGC ATCTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAACT CAAACCGGCA AGATTGATAA CCGTGAACTG
1801 CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTCCGG
1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTACAGC
1901 TTGATACCGC CGGTTTACAT AATGCAGGTA ACATTCTTGC CGATAGTGGA
1951 ACCGTTACCA CCAAGAATAA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC
2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
2051 AGGCTGAAAC GGTTAACATC CAAAGTCAGC AACTGACTAA CCAAAGCGGC
2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAACCGGC AAACCTCTAT CTGCAAACCA AGCACAATTA GCTGTTTCAG
2201 ACGGCCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT

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2251 ATTACGATA AAAATCAAAA CACTTTGGCG TTAAACAATG CGGATGGCAC
2301 GATTCAATCT GCCGGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACA
2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT
2401 TTCGTCGTAG AGCGCGACCT CACTGCAGGC AAACAATTAA ATCTAAGCAT
2451 AAAAGGCCGT CTGAAAAATA CCCATACCTT ACAAGCAGGC CATACGCTCA
2501 AACTCAATGC CGGCAATATA GATAACCAAG TTACAGGCAA AATTATTGGT
2551 GGAGAACAAA CGGACATCAC ATCCGAACAG CATGTTGACA ACAGGGGCTT
2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGGTCAA ACCCTGACCA
2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA
2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGGC
2751 AATAGCTGCA AGGAAACGTT TGGATATTGG AGCGAAAGAG ATTCTAATCC
2801 AAGAAGGTGC CCTACTATCC AGCGAAGGTA TTTTGGCCGT AgGTAATCGA
2851 CTGGATGAAC AACATCATGC GGCAGGCATG GCCGATACCT TTGTTAATGG
2901 CAGTGCCGGT TTGGAAGTAC AAGGTGATGC ATTGATGTCC GTTCGGAATA
2951 TGCAGAAATAT CAATAATCAC TTTAAACAG AGACATACTT AGCCAAAGCG
3001 GAAAAGCAAG TCCGCGACTA CACCGTACTG GGGCAAAATA CCTACTATCA
3051 GGCGGGAAAA GACGGTTTAT TCGACAACCT GCAAGGACAA AAAGACCAAA
3101 CTACTGCTAC GTTCCATTTA AAAAATGGTT CTCGTATTGA GGCCAACCAA
3151 TGGCATGTCC GAGACTACCA CATCGAGACT TATAAAGAAC GCATCATCGA
3201 AAACCGGCCG GCACACATTA CTGTGGGCGG TGATTGACT GCCTCAGGTC
3251 AAAATTGGCT GAACAAGAC AGCCGGATTG TAGTAGGCGG GCGTATTATC
3301 ACTGATGATT TAAACCAGAA AGAAATTACC AATCAAAGTA CAACAGGCAA
3351 AGGTGCGACA GATGTGTGCG GCACACAGTG GGATTAGTT ACAAAAAAAG
3401 GATGGTACAG CGGTAGAAAA AGACAACGCC GTACTGAAAG AAACCTACT
3451 CTTACCATG ATACCCAACT ATTTACCCAC GACTTCGACA CGCCTGTATC
3501 CGTCATCCAA CAGAATGCCG CCTCCCTTC CTTTCAACCC GCCGCATCTG
3551 CAATCAAAT GATTGACGGA GTATCCACGG CAGCCGTCAA TGGTCAGCGC
3601 ATCCATACCG GTAATGTGGT CTCGTAAAT AACGCTACTG TTAATCTGCC
3651 TAACAGCAGC CTCTATACCA CCCATCCTGA CAATAAAGGC TGGTTGGTTG
3701 AAACCGATCC TCAATTGCA GACTACCGCC GCTGGTTGGG CAGCGATAC
3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG
3801 CGACGGCTAC TACGAACAAA AACTTGTTAA TGAACAAATC CATCAGTTAA
3851 CAGGCTACCG CCGACTCGAC GGCTACAGGA GTGATGAAGA ACAATTCAAA
3901 GCTCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTCT GTCTCACCCC
3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAACT TCAGATATCG
4001 TTTGGATGGA AAATCAAACC GTCACCCTGT CTGACGGTTC GACTCAAACC
4051 GTACTGGTTC CTAAAGTCTA TGCCCTGGCG CGCAAGGTTG ATCTCAATAC
4101 CTCGGGTGGC CTGATTAGTG CCGAACAAGT CTTACTTAAA CTGCAAAACG
4151 GCAACCTGAC TAACAGCGGT ACCATTGCGG GCGGACAGGC CGTACTATC
4201 CAGGCACGGA ATATTAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG
4251 CTTAAAAGCT GAAAAAAGTA TCAATATCGA CGGCGGGCAG GTACAAGCAG
4301 GCAGACTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC
4351 CAAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC
4401 CGGCATTAAC GTGGTCGGAA GCCATACTGA ACAAGTAGAT AACAGAACTT
4451 CAGACGGCAT CCTATCCCTG CATGCCAGCA ACGATATCAA CCTCAATGCG
4501 GCCACCGTCT CTAACCAAGT TAAAGACGGC ACTACCCAAA TTACCGCCGG
4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG
4601 GTACATTAGA TGACGAGAAC CATCGCCATG TCCGCCAAAG TACCGAAGTC
4651 GGCAGCAGTA TCCGCACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA
4701 CTTAAAAATC CGCCAAGGCG AACTGGAGGC CGAAGAAGGC AAAACCGTCC
4751 TTGCCGAGG ACGTGATGTC ACTATCAGCG AAGGACGCCA AATAACCGAA
4801 CTGGATACCT CGGTAAGCGG AAAAAAGCAA GGCATCCTTT CCAGTACCAA
4851 AACACACGAC CGCTACCGCT TCAGTCATGA TGAAGCAGTC GGCAGCAACA
4901 TCGGCGGCGG CAAAATGATT GTTGCAGCCG GGCAGGATAT CAATGTACGC
4951 GGCAGCAACC TTATTTCTGA TAAGGCGATT GTTTTAAAAG CAGGACACGA
5001 CATCGATATT TCTACTGCCC ATAATCGCTA TACCGGCAAT GAATACCACG
5051 AGAGCAAAAA ATCAGGCGTC ATGGGTACTG GCGGATTGGG CTTTACTATC
5101 GGTAAACCGA AAATACCGA TGACACTGAT CGTACCAATA TTGTCCATAC
5151 AGGCAGCATT ATAGGCAGCC TGAATGGAGA CACCGTTACA GTTGCAGGAA
5201 ACCGCTACCG ACAAAACGGC AGTACCGTCT CCAGCCCCGA GGGGCGCAAT
5251 ACCGTCACAG CCAAAAGCAT AGATGTAGAG TTCGCAACA ACCGGTATGC
5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTCGCCCTCA
5351 ATGTCCCGGT TGTCCAAGCT GCACAAAAT TCATACAAGC AGCCCAAAAT
5401 GTGGGCAAAA GTAAAAATAA ACGCGTTAAT GCCATGGCTG CAGCCAAATG
5451 TGCAATGGCAG AGTTATCAAG CAACCAACA AATGCAACA TTTGCTCCAA
5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAAGCCC CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CCGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAACCTAT CAGAGCAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCTG
6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAACCCAC AGCCGCTACG AAGGCAGAA
6351 CTTCGGCATA GCGGCGAGTT TCGACCTGAA CGGCGGCTGG GACGGCAGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAAACAGCT TCGACAAGA
6651 CGCGGTCGCC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCC
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCG TGAGGCCGCA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGGCGATCCC
6851 TCGGCCAAGT AAACGCCTAT CTGCGCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCAGGCGGC GGCACCTCCC
7001 TTGCCGCACC GTATTGGAC AAAGCGGCGG AAAACCTCGG TCCGCGGGG
7051 AAAGCGGCGG TCAACGCACT GCGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGTTGG AACAAATAGG
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAAGC AGATACTGCG TTGGGTGGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGACTGACGA GCCTTGTCAG CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GCGGGGTGCG GGGAAATATCC GTATCCCTCG
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1  MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LLLLLGSALI LTSSSATAQG IVADKSAPAQ QOPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIOGN
151 PWLARGEARV VVNQINS SHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQFPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW QGDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWQFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVS DVPQTG LNPNP SVIPQ IPSTATSGS STVS VSKPGS
501 NNPVSPAPFA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKLRVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLD TAGLH NAGN ILADSG
651 TVTTKNLNLN TGKVSVARLN TEGQTL DNTR GRIEAE TVNI QSQQLTNQSG
701 HITATEQLTI NSRNV DNQNG KLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGT LTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKL NAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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901 ILLNREETTE GSTKAGIAIA RKRLDIGAKE IHNQEGALLS SEGIFAVGNR
951 LDEQHHAAGM ADTFVNGSAG LEVQGDALMS VRNMQNINNH FKTETYLAKA
1001 EKQVRDYTVL GQNTYYQAGK DGLFDNSQGG KDQTTATFHL KNGSRIEANO
1051 WHVRDYHIET YKERIENRP AHITVGGDLT ASGQNWLKND SRIVVGGRII
1101 TDDLNQKEIT NQSTTGKGRD DAVGTQWDSV TTKGWYSGRK RQRRTERNHT
1151 PYHDTQLFTH DFDTPVSVIQ QNAASPSFQP AASAIKLIDG VSTAAVNGQR
1201 IHTGNVVS LN NATVTLPNSS LYTTHPDNKG WLVEDPQFA DYRRWLGS DY
1251 MLQQLQLDTN HLHKLRLG DY YEQKLVNEQI HQLTGYRRLD GYRSDEEQFK
1301 ALMDNGLTAA KTFGLTPGIA LSAEQVARLT SDIVWMENQT VTLSDGSTQT
1351 VLVPKVYALA RKGDLNTSGG LISAEQVLLK LQNGNLTNSG TIAGRQAVLI
1401 QARNINSNGN IQADQIGLKA EKSINIDGGQ VQAGRLLTAQ AQNINLNGTT
1451 QTSGNERNGN TAIDRMAGIN VVGSHTQVD NRTSDGILSL HASNDINLNA
1501 ATVSNQVKDG TTQITAGNNL NLGTIRTEHR EAYGTLDDEH HRHVRQSTEV
1551 GSSIRTQNGA LLRAGNDLKI RQGELEAEEG KTVLAAGR DV TISEGRQITE
1601 LDTSVSGKSK GILSSTKTHD RYRFSHDEAV GSNIGGGKMI VAAGQDINVR
1651 GSNLISDKGI VLKAGHDIDI STAHNRYTGN EYHESKKSGV MGTGGLGFTI
1701 GNRKTTDDTD RTNIVHTGSI IGSLNGDTVT VAGNRYRQTG STVSSPGRN
1751 TVTAKSIDVE FANNRYATDY AHTQEQKGLT VALNVPVQA AQNFQAAQN
1801 VGKSKNKR VN AMAAANA AWQ SYQATQMQQ FAPSSSAGQG QNNNQSPSIS
1851 VSITYGEQKS RNEQKRHYTE AAASQIIGKQ QTTLAATGSG EQSNINITGS
1901 DVIGHAGTAL IADNHIRLQS AKQDGSEQSK NKSSGWNAGV AVKIGNGIRF
1951 GITAGGNIGK GKEQGGSTTH RHTHVGSTTG KTTIRSGGDT TLKGVQLIGK
2001 GIQADTRNLH IESVQDTETY QSKQNGNVQ VTVGYGFSAS GSYRQSKVKA
2051 DHASVTGQSG IYAGEDGYQI KVRDNTDLKG GIITSSQSAE DKGKNLFTQA
2101 TLTASDIQNH SRYEGRSFGI GGSFDLNGGW DGTVTDKQGR PTDRISPAAG
2151 YGSDGDSKNS TTRSGVNTHN IHITDEAGQL ARTGR TAKET EARIYTGIDT
2201 ETADQHSGLH KNSFDKDAVA KEINLQREVT KEFGRNAAQA VAAVADKLG N
2251 TQSYERYQEA RTLLEAELQN TDSEAEKAAF RASLGQVNAY LAENQSR YDT
2301 WKEGGIGRSI LHGAAGGLTT GSLGGILAGG GTSLAAPYLD KAAENLGPAG
2351 KAAVNALGGA AIGYATGGSG GAVVGANVDW NNRQLHPKEM ALADKYAEAL
2401 KREVEKREGR KISSQEAAMR IRRQILRWVD KGSQDGYTDQ SVISLIGMKG
2451 EDKALGYTWD YRDYGARNPQ TYNDPKLFEE YRRQDKPEYR NLTWLHSGTK
2501 DTKIRQGERK NEEFALNVAE GLTSLVNP NP RIKVPILAGI RNLKNKPTV
2551 TGSDPELLAGA GNIRIPANGN VAKGD RIPDT ALASKGIKHK DRKDQLEKK*

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Computer analysis of this amino acid sequence gave the following results:

Homology with fha

m564/fha

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ID   FHAB BORPE      STANDARD;      PRT;   3591 AA.
AC   P12255;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   FILAMENTOUS HEMAGGLUTININ. . . .

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SCORES      Init1:   190 Initn:   524 Opt:   594
Smith-Waterman score: 866;      21.7% identity in 2427 aa overlap

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          10      20      30      40      50      60
m564 .pep  MNRTLYKVVENKHRNCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS
          || :||:|:|:| :| :| :|:| :| || :| :| :| :| :| :| :| :|
fhab_borpe MNTNLYRLVFESHVRGMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA
          10      20      30      40      50

          70      80      90      100     110     119
m564 .pep  LSLLLG-SALILTSSSATAQGIVADKSAPAQQQPTILQTGNGIPQVNIQTPTSAGVSVNQ
          :|:|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
fhab_borpe WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLQGGNKVPVNVNIADPNSSGGVSHNK
          60      70      80      90      100

          120     130     140     150     160     170     179
m564 .pep  YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQLNGYIEV
          :|:|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
fhab_borpe FQQFNVANPGVVFNNGLTGVSRIIGALTKNPNLTR-QASAILAEVTDTSPSRLAGTLEV
          110     120     130     140     150     160

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180      190      200      210      220      230      239
m564 .pep GGRRAEVIANPAGIAVNGGGFINASRATLTTAQPQYQAGDLSGFKIRQGNVVIAGHGLD
      | : | : : | | | | | : | | | | | | : | : | : | : | : | : | : | : | : |
fhab_borpe YGKGADLIIANPNGLSVNGLSTLNASNLTLTGRPSVNGGRI-GLDVQQTVTIERGGVN
      170      180      190      200      210      220

240      250      260      270      280      290
m564 .pep ARD TDYTRILSYHSKIDAPV---WGQ---DVRVVAGQNDVAATGDAHSPILNNAANTS
      | | : : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
fhab_borpe ATGLGYFDVVARLVKLQGA VSSKQKPLADIAVVAGANRYDHATRRATPI----AAGARG
      230      240      250      260      270      280

300      310      320      330      340      350
m564 .pep NTANNGTHIPLFAIDTGKLGMYANKITLISTVEQAGIRNQGWFFASAGNVAVNAEGKLV
      : | : : | | | | | : | : : | : | : | : | : | : | : | : | : | : | : |
fhab_borpe AAAGA-----YAIDGTAAGAMYGKHITLVSSDSGLGVRQLGS-LSSPSAITVSSQGEIA
      290      300      310      320      330

360      370      380      390      400      410
m564 .pep NTGMIAATGENHAVSLHARNVHNSGTVASQDDANIHSQTLDNSGTVLSSGRLTVRNLGRL
      : | : : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
fhab_borpe ---LGDATVQRGPLSLKGAGVVSAGKLAGSGGAV---NVAGGGAVKIA---SASSVGNL
      340      350      360      370      380

420      430      440      450      460      470
m564 .pep KNQNGTIQAARLDMSTGGLDNTGNITQTGSQALDLVSAGKFDNSGKIGVSDVPQTGLNP
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
fhab_borpe AVQGGGKVQATLLNAG-----GTLVSGRQAVQLGAASSRQALSVNAGGALKADKLSA
      390      400      410      420      430

480      490      500      510      520      530
m564 .pep NPSV-IPQIPSTATGSGSSTVSVSKPGSNNPVSPAPAKNYAVGRIQTGAFD-NAGSIN
      : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
fhab_borpe TRRVVDVGKQAVALGSASSNALSVRAGGA-----LKAGKLSATGRLDVDGKQAVTLGSLVA
      440      450      460      470      480      490

540      550      560      570      579
m564 .pep AGGQIDIAAQNLGNSGSLNAAKLRVSG-----DSFNNT-----VKGKLQAHDLAVNT
      : | : : : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
fhab_borpe SDGALSVSAGGNLRANELVSSAQLEVRGQREVALDDASSARGMTVVAAGALAAARNLQSKG
      500      510      520      530      540      550

580      590      600      610      620      630
m564 .pep QTAKNSGHLTQTGKIDNRELH--NAGEIAANNLTLIHSGRLSNDKKGNIRAAHLQLDTA
      : : | : : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
fhab_borpe AIGVQGGGEAVSVANANSDAELRVGRGQVDLHDLAARGADISGEGRVNIGRARSDSVDK
      560      570      580      590      600      610

640      650      660      670      680      690
m564 .pep GLHNAGNILADSGTVTTKNNLRNTGKVSVARLNTGQTLDNTRGRIEAEVTNIQSQQLTN
      : | : | | : : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | :
fhab_borpe -VSAHGALSIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGG-----AVNLGDVQ---
      620      630      640      650      660

700      710      720      730      740      750
m564 .pep QSGHITATEQLTINSRNVNONGKLLSANQAQLAVSDGLYNQHGEIATNRQLSIHDKNQ
      : | : : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
fhab_borpe SDGQVRATSAGAMTVRDV-----AAAADLALQAGDALQAGFLKSAGAMTVNGRDAV
      670      680      690      700      710
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	760	770	780	790	800	810
m564 .pep	TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTDDFVVERDLTAGKQL-NLS					
fhab_borpe	RL-----DGA-HAGGQLRVSSDQAALGSLAAKGELTVSAAARAATVA-EL---KSLDNIS					
		720	730	740	750	760
	820	830	840	850	860	870
m564 .pep	IKGRLEK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLINSGLT					
fhab_borpe	VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-					
		770	780	790	800	810
	880	890	900	910	920	930
m564 .pep	HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGAIARKRLDI-GAKEIHN					
fhab_borpe	--GSDGAISVSGRDAVRVDQARSLADISLG---AEGGATLGAVEAAGSIDVRGGSTV--					
		820	830	840	850	860
	940	950	960	970	980	990
m564 .pep	QEGALLSSEGIFAVGNRLDEQHHAGMADTFVNGSAGLEVQGDALMSVRNMQINNNHEFT					
fhab_borpe	AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
		870	880	890	900	910
	1000	1010	1020	1030	1040	1050
m564 .pep	ETYLAKAEK--QVRDYTVLGQNTYYQAGKDGLFDNSQGGKQDQTTATFHLKNGSRIEANQ-					
fhab_borpe	ALQSAKASGTLHVQGGELDLGLTAAVGAVDV----NGTGDVVRVAKLVSDAGADLOAGRS					
		930	940	950	960	970
	1060	1070	1080	1090	1100	
m564 .pep	--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNLNKSRIVVGGRIITDDLNQKE					
fhab_borpe	MTLGIVDTTGDQLQARAQQKLELGSVKSDDGGLQAAAGGALSAAAEVAGALELS---GQGV					
		980	990	1000	1010	1020
	1110	1120	1130	1140	1150	1160
m564 .pep	ITNQSTTGKGRDVAVGTDQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe	TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFTPG					
		1040	1050	1060	1070	1080
	1170	1180	1190	1200	1210	1220
m564 .pep	SVI---QQNAASPSFQPAASAIKLIDGVSTAANGQRIHTGNVSVLNNATVTLPNSSLYT					
fhab_borpe	SVVVRAGGNVTVGRGDPHQGVLAQGDIIIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
		1090	1100	1110	1120	1130
	1230	1240	1250	1260	1270	1280
m564 .pep	THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQDLTNHLHKRLGDGYEQLVNEQIHQ					
fhab_borpe	EHSTIESKISQSVLAAKGDGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRQIDV					
		1150	1160	1170	1180	1190
	1290	1300	1310	1320	1330	1340
m564 .pep	LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFGLTPG-IASAEQVARLTSDIVWMENQTV					
fhab_borpe	VDGRPQI---TDAVTGEARKDES SVVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
		1200	1210	1220	1230	1240

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGEQGGSTTHRHVHGTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGIGG-----DVDNRSV-					
		1870	1880	1890	1900		

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE				
		:: :	:::	: : :	: :	:
fhab_borpe		VRTVSAMEYFKTPLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRXEYIWGLYPTY				
		1910	1920	1930	1940	1950

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATLTASDIQNH--RYEGRSFGIGGS					
		:::::		: :		:: :	:: :
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDLRGHTLESAGEGRKI-FGEY					
		1970	1980	1990	2000	2010	

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGSDDGSKNSTTRSGVNTNHIHITDEAG				
		: :	:	: :	:	:
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRRVHDQLG-----QRYGKALGGMDAETKEVDGIIQ				
		2020	2030	2040	2050	2060

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKEFGRNA					
		:	:	:	:	: :	: :
fhab_borpe		EFAADLRITVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRV--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
		::	::	::	:	:	:
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLNNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGS LAAPYLDKAAENLGPAKG					
		: ::	:	:	:	:	:
fhab_borpe		AQNRGRPEGLKIGAHSA TSVSGSFDALRDVGLEKRLDIDDALAAVLVNPHIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccctgcgttt cgcacgcgcg aacgacaccg gctcgcctgc acttctggct
151 acctgcacgc gtgcgatgtc caagtcgagc gcgaaatagc gaatatcctc
201 tttgggcgaa gacgcgtccg accgtctgcc cgccccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

```

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```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCCG CGCCTGTTC CATTCTGGCG AAACCATATC AAGCTGCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGT AGGCTGTGCG CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSIAN SIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90     100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
                |||||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
 51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCG GCCCTGCGC AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCCG CGCCTGTTC CATTCTAGCG AAACCATATC AAGCTGCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGT AGGCTGTGCG CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSIAN SIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||

```

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```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
a565      PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
m565.pep  KAMANTTSAFNTSSIANSSINTCRQPPINAX
           190     200     210
a565      KAMANTTSAFNTSSIANSSINTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggtaac
51  ggttgttcag cccgagtacg tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggt
151 gccggctttg tgggtgattt ccacgcgttc gccgtcggtg gcgaagaggg
201 cgggtgtggc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcgacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGCTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTTGTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTTCGCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACCG GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGTTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCCGA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||

```

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```

g566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG AACAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTACCAG
101 TTTACCCAAA CTGCGGCGCG GACGGCGCCG GCGGCAAAGG TCATGCGGCT
151 GCTTGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGCCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGCG GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFTVYPNCGA DGAGGKGHAA
51  ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVAFAAVNGA
101 LFEVSAERAG DDFAHA*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq.
1  atgcgacgac gggcagcggc atcgacaagg cgggtttgca gtccggcggt
51  tatcaggtct tattgggcga tgcggacgtg cagtcggcgg cggtacgcag
101 caaagagggc ggatacgcg tggtgggtgc gaacgcgcgc gcttgccggc
151 gcggaaatcg agctgggtgc ggaaatcgcc cgggaagtgc gtttgaaaaa
201 cgcgctcaag gcagtgccgg aagattacga ctttatcctg atcgactgtc
251 cgccttcgct gacgctgttg acgcttaacg gcttggtggc gccggggcggc
301 gtgattgtgc cgatgtttg cgaatattac gcgctggaag ggatttccga
351 tttgattgcg accgtgcgca aaatccgcca gccggtcaat cccgatttgg
401 acatcacggg catcgtgcgt acgatgtacg acagccgcag caggctgggt
451 gccgaagtca gcgaacagtt gcgcagccat ttcggggatt tgctttttga
501 aaccgccatc ccgcgcaata tccgccttgc ggaagcgcgc agccacggta
551 tgccggtgat ggcttacgac gcgcaggcaa agggtgccaa gccgtatcct
601 gccttggcgg acgaactggc gccgagggtg tcggggaaat ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAATR RVCSPAFIRS YWAMRTCSRR RYAAKRADTA CWVRTRALAG
51  AEIELVQEIA REVRLLKALK AVAEDYDFIL IDCPPSLTLL TLNGLVAAGG
101 VIVPMLCEYY ALEGISDLIA TVRKIRQAVN PDLDITGIVR TMYDSRSLV
151 AEVSEQLRSH FGDLLFETAI PRNIRLAEAP SHGMPVMAYD AQAKGAKAYL
201 ALADELAARV SGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCACTCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
251 CTGTGTTGGG TCGCAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGACATCACG GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTGCGGGA TTTGCTTTTT GAAACCGTCA TCCCGGCGAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGGC AAAGGATACC AAGCGGTATC TTGCCTTGCG GGACGAGCTG
751 GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101 QEIAREVRLK NALKA VEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAGT KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

60      70      80      90      100     110     119
m567.pep GYVYQVLLGDADVQSAAVRSKEGGYAVLGNALAGAEIELVQEIAREVRLKNALKA VEED
g567      AFIRSYWAMRTCSR RRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKA VAE
20      30      40      50      60      70

120     130     140     150     160     170     179
m567.pep YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
g567      YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
80      90      100     110     120     130

180     190     200     210     220     230     239
m567.pep TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAG
g567      TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAG
140     150     160     170     180     190

240     250
m567.pep TKAYLALADELAARVSGKX
g567      AKAYLALADELAARVSGKX
200     210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
```


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```

251 GCGTGTGGG TCGAACC GCCTGGCCG GCGCGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TCGCAATATT ACGCGCTGGA AGGGATTTCG GATTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGCCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

a567.pep

```

1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGRVVLVVDL DPQGNATTGS
51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

```

m567/a567 97.7% identity in 257 aa overlap

	10	20	30	40	50	60
m567.pep	MSANILAIANQKGGVGKTTT TVNLAASLASRGRVVLVVDLDPQGNATTGSGIDKASLQSG					
a567	MSANILAIANQKGGVGKTTT TVNLAASLASRGRVVLVVDLDPQGNATTGSGIDKASLQSG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m567.pep	VYQVLLGDADVQSAAVRSKEGGYAVLGNRRLAGAEIELVQEIAREVRLKNALKAEEEDY					
a567	VYQVLLGDADVQSAAVRSKEGGYAVLGNRRLAGAEIELVQEIAREVRLKNALKAEEEDY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m567.pep	DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT					
a567	DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m567.pep	GIVRTMYDSRSRLVAEVSQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT					
a567	GIVRTMYDSRSRLVAEVSQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA					
	190	200	210	220	230	240
	250					
m567.pep	KAYLALADELAARVSGKX					
a567	KAYLALADELMARVSGKX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

g568.seq

```

1 atgtctcagg tcagaccggt attatttgcc gtcaaggcct ccgcctcttc
51 gataccttgc agaattctgcc gattaaagcg ttcgcggctg cccaatattt
101 tcaggcgcgt attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
151 tgtaaaaaca gcccacatcag gaacgaaact tcgtcttcg ggcgacgcca
201 gttttcgggt gaaaaggcaa acacggctcag atattgcacg ccagttttg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgcg tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```

401 tgctgctctt catatctgcc tttcgcggtt cggcggtcaa atgccgtctg
451 aacgccgcgc cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep
1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
151 NAAP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51 GATGCCTTGC AGAATCTGCC GGTGAAGCG TTCGCGGCTG CCCAATATCT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAAACT TCGTCTTCGG GCGGCGGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTGCGGTT CCGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTGCGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCTG TGGCATCGCG GCGCACGTTG CCGATAGAGA
651 CCGCGCCTTC TTCCGCTTCG CCGCGTACGA CTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CCGATCAGGT CCGCGACAGC
751 TGCCGGGTTC AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep..
1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVGIA AHVADRDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	ICLGMAVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
g568	MCLGMAVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	130	140	150			
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTGAC  GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTAAAAACA GCCCATCAG  GAACGAACT TCGTCTTCGG GGCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATGACACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCG CAACGGCCGT TGCCGTCCAT
351 AATCAGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCTGCG
401 TGCTGCTTTT CATGCTGCG TTTGCGGTT CGGCATTCAA ATGCCGCTG
451 AACGCCGAAC CGTGCAGGT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTGCTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG .CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1  MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFDVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIXRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADGDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADGDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1  atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgcctt gaccgccttg tgggagtatg cccgatggc cggtttgctg
```

874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgcctgctaa ttggtttgg tatgttgttt
251 tggcattttg gctcgccgtt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgcctatgcc
351 gttttggttc gcgtcgtat ccctggcgcc cgcattccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRPKWR
101 LGGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGC GGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTG CCTCGCCGCA ACCTTGCTTT TCGGCGTGCT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCTTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTAAATCGG TTTGGTGTCT ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAGGCTGCT GCCCGGACAC GCGGCGGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRPKWR
101 LGGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPASPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDLSL
251 IAVISVYAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRPKWRLNGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRPKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHDDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPASPGKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGC GGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCCCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACC GG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTAAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GGCAGCGTGT TCGACCGCAC CGACAGCTAG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALLIAL WEYARMGGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRTDSL
251 IAVISVYAAM MSVLN*

m569/a569 99.6% identity in 265 aa overlap

          10      20      30      40      50      60
m569.pep  MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGGLCKIKTNHYLAA
          |||
a569       MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGGLCKIKTNHYLAA
          10      20      30      40      50      60

          70      80      90      100     110     120
m569.pep  TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
          |||
a569       TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
          70      80      90      100     110     120

          130     140     150     160     170     180
m569.pep  ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
          |||
a569       ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
          130     140     150     160     170     180

          190     200     210     220     230     240
m569.pep  VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVSVCGDLLSWLKRAAGIKDSSKLLPGH
          |||
a569       VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVSVCGDLLSWLKRAAGIKDSSNLLPGH
          190     200     210     220     230     240

          250     260
m569.pep  GGVFDRTDSLIAVISVYAAMMSVLNX
          |||
a569       GGVFDRTDSLIAVISVYAAMMSVLNX
          250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

```

g570.seq..
1  atgatccggtt tgaccgcgcg gtttgccgcc gccctgatcg gtttatgctg
51  caccacaggc gcgcacgcgc acaccttcca aaaaatcggc tttatcaaca
101 ccgagcgcgt ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc cgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttgaaa ggcagctcgc cggcgcaaaa cttaaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggt cgaagcgctt
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtgttgc tccctccagc aaaacgcaaa ccgctcatc gtcaaaatcg

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876

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
 451 acccaatacg acgttaccga cagcgtcatt aaagaaatga acgcccgcgtg
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MIRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
 101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151 TQYDVTDSVI KEMNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTGTCCGCG GCTCTGATCG GTTGTGCTG
 51 CACCGCAGGC GCGCAGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAP
 101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIIYN
 151 TQYDVTDSVI KEMNAR*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD					
g570	MIRLTRAFAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLTLDGEFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAPFRKKQAQFEEDYNLRRNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRRNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTGTCCGCG GCTCTGATCG GTTGTGCTG
 51 CACCGCAGGC GCGCAGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151  TQYDVTDSVI KEMNAR*

m570/a570  97.6% identity in 166 aa overlap

              10      20      30      40      50      60
m570.pep    MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
a570        MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
              10      20      30      40      50      60

              70      80      90     100     110     120
m570.pep    ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA
a570        ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA
              70      80      90     100     110     120

              130     140     150     160
m570.pep    SLQQNANRVIVKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX
a570        SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttgtt gttaccgttt tcggcggcgg
 51  tataggttct gccgtcccac acgctgcctg cgtcggcaaa caggctcagg
101  cggacggtgc gtgcgtcttt cgcaccgggc atcgggaaga gcagctcggc
151  ggagacgttg gcttttttgt tgcgcgcgta gctgattttt tcgcgcgtatt
201  cgtcatacac ttccgggccc agcgtgccgc ttctgtagcc gcgcaccgaa
251  cccaggccgc cgccgtagaa gttttcaaag aaggggattt ctttggttct
301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRV VTVFGGIGS AVPHAACVVK QAQADGACVF RTGHRREEQLG
 51  GDVGFFVAAV ADFFAVFVIH FRAERAAVFA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCCCTGCCG CCGGTCCGCG
 51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTCGCC GTATTCGTCA TAGACTTTG GACCGAGCGT GCCGCTTTG
251  TATCCGCGCA CCGAACCAGG GCCGCCGCCG TAGAAGTTT CAAAGAAGGG
301  GATTTCTTTG GTTCTGCCGT AGCCGCCGCG AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTGCGCGTT
451  CACGCCCGTC AGGTAGCCGC GCGTCGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLGGDVGF FVAADVDFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  DFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDFFGV
151  HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLPAAAGRGTA VVVGVFAVPHAACVGKQAQADGARVFRAGHREEQLGGDVGF
      :| ||||| ||||| ||||| ||||| ||||| |||||
g571      MRVFRVNRFFVTVFGGGIGSAVPHAACVGKQAQADGACVFRTGHREEQLGGDVGF
      10      20      30      40      50

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571      FVAAVADFFAVFVIHFRAERAAAFVAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      60      70      80      90      100     110

      130     140     150     160
m571.pep  EGFAQGEPEGLVVGGGVVLQFAARQDGFVHARQVAARRPX
      |||
g571      EGFA
      119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTCGCGG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTGTTGCCG CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCCGCG TAGAAGTTT CAAAGAAGGG
301 GATTTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGSTTTG CTTAAGGGGA AGAACCAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTGCTGCCG GGCAGGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNVLPAAAGRGTA VVVGVFAVPHA ACVGKQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQ EGFA*GEEPG LVVGGGVVLQ FAAGQGDFGV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLPAAAGRGTA VVVGVFAVPHAACVGKQAQADGARVFRAGHREEQLGGDVGF
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      MGIAGAVNVLPAAAGRGTA VVVGVFAVPHAACVGKQAQADGARVFRAGHREEQLGGDVGF
      10      20      30      40      50      60

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
      70      80      90      100     110     120

      130     140     150     160
m571.pep  EGFAQGEPEGLVVGGGVVLQFAARQDGFVHARQVAARRPX
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      EGFAXGEPEGLVVGGGVVLQFAAGQDGFVHARQVAARRPX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

1	atgtgcgccca	tcgtcgggggc	ggcgggggctg	ccttcgcgcgc	tcgcagcgggc
51	gcaaaaagggc	aaaaccattt	atctggcaaa	caaagaaacg	ctgggtggttt
101	ccgcgctgta	ggttatggaa	accgcccgcc	caaacggcgc	ggcagtggtt
151	cgcgtgcaca	ctgaacacaa	cgccattttc	caagttttgc	cgcgcgtta
201	cacagaccgt	ctgaacgaac	acggcatcga	ttcgattatc	ctgaccgcctt
251	ccggcgggccc	gttttttaaca	acggatttaa	gcacgttcga	cagcatatcc
301	cccgagcaag	cggtagcaaca	ccccaatggg	cgtatggggc	gcaaaatcgc
351	cgctgcattc	ggcactatgg	caaacaaggg	ctgtgaactg	attgaagcgc
401	attggctggt	caactgtccg	cccgacaaac	tcgaagtctt	catccatccc
451	caatccgtga	tacacgatat	tgtgcgctac	cgcgacggct	cgcgtgatcc
501	gcaactgggc	aatcccgata	tgcgaacgcc	catcgccat	tgtttggtgc
551	tgcccgcagc	catcgattcg	gggtgcggca	aactcgattt	cggcgcattg
601	tcgcgcgtga	ccttcacaaa	gcccgacttc	ggcgcgttcc	cctgcctgaa
651	gttcgcctat	gaaacataaa	acgcaggcgg	agccgcgcc	tgcgtataga
701	acgcgcctaa	caaaccggcc	ctgcgcgctt	tttggacgc	acagattaa
751	ttatccgaca	ttgcgcaaac	cgtcgccac	tgctctgcac	aagacttttc
801	aaacggcatg	ggcgatatag	aaggactgtt	ggcgtaagat	gcccggcac
851	qcqcacaagc	qcqqcattt	atqcqacac	tcqcctga	

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

q572.pwp..

```

1  MCAIVGAAGL PSALAAAKQG KTIYLANKET LUVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYTDR LNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PEQAVKHPNV RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVTHP
151 QSVIHSMPVY RDGGSVLAQGS NPDMRTPIAY CILGLPERIS GVGKLDVFGV
201 SALTFOKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGOIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1715>:

m572. seq. .

1	ATGTGCGCCA	TCGTGGGGG	GGTGGGGCTG	CCTTCCGCGC	TGCGAGCGGC
51	GCAAAAAGCG	AAAACCATTT	ATCTGGCAAA	CAAAGAAACG	CTGGTGGTTT
101	CCGCGCGGTT	GTTATGGAA	ACCGCCCGTG	CAACCGGCGC	GGCAGCTGCT
151	CCCGTCGACA	CGGACACAA	CGCGTTTTC	CAAGTTTTCG	CGCGGATTAA
201	CGCGCGCGGT	CTGAACGAAC	ACGGCATCGC	TTCGATTATC	CTGACCGCTT
251	CGCGCGCGCC	GGTTCTGACC	GCGCAATTTA	ACACGTTTCA	CCGCAATTACG
301	CCGCGCCAAG	CTGTCAAACA	CCCAATTTGG	CGATTGGGAG	GCAAAATCTC
351	CGTCGATTCC	GCCACCATGA	TGAACAAAGG	TTTGGAGCTG	ATTGAAGCGT
401	ATTGGCTGTT	CAACTGTCCG	CCCGACAAC	TCGAAGTCTG	CATCGTCCGG
451	CAATCCGTGA	TACACGCAT	GTGCGCTAC	CGCGACGGCT	CCGTGCTCGG
501	GCAACTGGGC	AATCCCGATA	TGCGAAGGCC	CATCGCTTAT	TGTTTGGGTT
551	TGCCCCGAGCG	CATCGATTCT	GGTGTGCGCG	ACCTGGATTT	CGACGCATTG
601	TCGCGCGTGA	CAATTCAAAA	GCCCGACTTT	GACCGCTTCC	CCTGCTTGAG
651	GCTGCGCTAT	GAGGCCATGA	ACGCAGGCGG	AGCCGCGCCC	TGCGTATTGA
701	ACGCGCGCAA	CGAAGCGGCC	GTCGCGCCT	TTTTGGACGC	ACAGATTAA
751	TTTACCGACA	TTGCGAAAA	CGTGCGCCAC	TGTCCTTGAC	AAGACTTTTC
801	AGACGGCATA	GGCGATATAG	GCGGGCTCTT	GGCGCAAGAT	GCCCGGACAC
851	CGCACAAGC	GCGAGCATTT	ATCGGCACAC	TGCGCTGA	

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

m572.pap..

1	MCAIVGAVGL	PSALAAAKQG	KTIYLANKET	LUVSGALFME	TARANGAAVL
51	PVDSEHNAAF	QVLPFRDYAGR	LTNEHGASII	LTAASGGPFL	ADLNTFDRIT
101	PAQAVKHFNW	RMGRKISIVS	ATMMNKGLEL	IEAHVLFNCP	PKDLKEVHP
151	QSVIHSMPVR	RDGSLAQLG	NPDMRTPIAY	CLGLPERIDS	GVGDLDFDAL
201	SALTFFMQPY	DRFPCLRLAY	EAMNAGGAAP	CVLNAANEAA	VAAFLDGGQIK
251	FTDIAKTVAH	CLAQDFSDGI	DIGGLGLAAO	ARTRAARAF	IGTLR*

m572/g572 92.9% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPVDSEHNAVF					
g572	MCAIVGAAGLPSALAAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPVDSEHNAIF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572 . pep	QVLPRDYAGRLNEHGIIASIIILTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
g572	QVLPRDYTDRLNEHGIDSIILTASGGPFLTTDLSTFDSITPEQAVKHPNWRMGRKISVDS					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m572 . pep	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
g572	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572 . pep	CLGLPERIDSGVGDLDLFDALSALTFOKPDFRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGKLDLFDALSALTFOKPDFRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572 . pep	VAAFLDGQIKFTDIKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGQIKFTDIKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```

a572 . seq
1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTGACC GCCGATTAA ACACGTTTCA CAGCATTACG
301 CCCGACCAAG CGGTCAAACA CCCAATTGG CGTATGGGAC GCAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATGAAGCGC
401 ATTGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTTGCG
501 GCAACTGGGC AATCCCGATA TGCGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTG GGTGTCGGCG ACCTGGATTT CGACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCGCGACTTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCCT TTTTGACGG ACAGATTAG
751 TTTACCGACA TTGCCAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGGCATA GCGGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGCACAAAG CGGGGCATTT ATCGGCACAC TGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```

a572 . pep
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGA AVL
51  PVDSEHNAV FQVLPRDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFOKPDF DRFPCLKLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGA AVL PVDSEHNAV F					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGA AVL PVDSEHNAV F					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572 . pep	QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPRDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSVMVRYRDGSLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFOKPDFDRFCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDFDALSALTFOKPDFDRFCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIKTVAHCLAQDFSDGIGDIGGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIKTVAHCLSDQDFSDGIGDIGGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1   atgccctgtt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccgcc aggttaatct cggcagggtc ttccgcccgt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 cccgaacccg tcggaccggt taccagcacc atcccgtaag gacggtgaat
301 cgcttccaac acaattttt tctggaacgg ctcaaaacgg agctggtcga
351 tgttcaaaga cgcggcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tcctaccgtc ctggcgtaac cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc gggaaagcaag ctgccccctt
551 accgcaatgg gcggctgaac cacctcgagg agctgcccgt ccacacggaa
601 acggatacgc gcatttgtgt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcatccgac aaagttttat ggataaacct cggaacaggg
701 ccgtcttctg cctcctcgtc gtcgataata aggggtgtgc tttcctcttc
751 ctcttgcccc tccccaagct cctgaagcag cgatgtcgaa cggaaccca
801 ccaatcgag caaacccgcc aactggtcat cctcgacaat gaccaactca
851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcattctggg
901 cggatcgga accgcaaaaa atactttgtc gccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgcctctccg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgaataac tgaacaccc
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacaccg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1   MPCLRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHPVVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYFFFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPATQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNRNPGCR NRLFNLRHIG
301 RIGNRKKYFV APTENRHIVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1   ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCGGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGGTACCAAC aCaw.TTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGAAG GTGAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

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551 ACCGCAATGG GCGGCTGAAC CACCTGCGG AGCTGCCCCG CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTC
751 CTCTGCCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

```

m573.pep..
  1 MPCLCLRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
 51 DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLFQKRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
	MPCLCLRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLI					
g573	10	20	30	40	50	60
	MPCLCLRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQTLIIIDVNLI					
m573.pep	70	80	90	100	110	120
	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVMRYQHXFFLKR					
g573	70	80	90	100	110	120
	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVRTVMRFQQQFLE					
m573.pep	130	140	150	160	170	180
	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQ					
g573	130	140	150	160	170	180
	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPFGNVQ					
m573.pep	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIRQSLMDK					
g573	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVGCPTQGIRQSFMDK					
m573.pep	250	260	270	280	290	300
	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCR					
g573	250	260	270	280	290	300
	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNRNPGCR					
m573.pep	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHP					
g573	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHP					
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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a573.seq

```
1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAAATTTT TCTGAAACGG CTCAAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCA ACACGACATT ACCTTAATCC GGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCTT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```
1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLGRV FRRNCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPBH DLFQRRQC ADTEIDRLAA
151 LLKQLHPAV LRYPFPGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIQSLMDKP RNRVFCLLV VDIQVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*
```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQTLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	FRRNCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHFFLKR LKTELVDVQR					
a573	FRRNCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	FRRNCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHFFLKR LKTELVDVQR					
a573	FRRNCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFPGNVQTRHYLNPGSK					
a573	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFPGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIQSLMDKPRNRVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIQSLMDKPRNRVFCLLV					
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIQSLMDKPRNRVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIQSLMDKPRNRVFCLLV					
	190	200	210	220	230	240
m573.pep	VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNLDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNLDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1  atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct ttgcccgcgc ttcttcacga
101 tgggctgggt tggcgccgcg gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggtcgaccg
201 caacagcggg cgcgcggcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaaacttta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaa ggcgggtttg gtcgatcggt ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaaagg agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgctt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tggcgccgct
751 gaagcctatg ccgccatcga gcagcaaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaacgg tctgacagga tatatgcaga cgtttccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg ctttaaggcg agaaagaagc
951 cgcgcaaacg gccgtcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgtaccgcct gctcgggttg aaactcagcg atttggatcc ggcttggaaa
1051 gccgatgccg acatgatgag ttcggttacc ggacggcagc tccagcgagc
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtcttttctt
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1  MLNPLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREB RQHLNLIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQAALEFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMOTFPELDL
301 INVVEKESLL LKGEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLDPAAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1  ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTGCCCCTGC TTCTTCGCGA
101 TGGGCTGGTT TGGCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCCGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GGCAGAAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GCGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTCGGG
451 CTGCAAGACG GTAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGCGTTT

```

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```

651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCAGAGAAG CTTTACGAAG CCTATGCCGC GCAGGAAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCT TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCGC CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACCTCAGC ATATGAATCC GGCTTGGAAA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCCTGCCCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```

1 MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFES NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GKPEGLNRLTG YMQTFPELDL
301 INVVEKSL LKKEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

m573/g573 97.8% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA KSIPSGFYKS					
g574	MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA KSIPSGFYKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m574.pep	LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQ GENDKAINIH RTMLDSPDTV					
g574	LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQ GENDKAINIH RTMLDSPDTV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m574.pep	GEKRARVLF ELAQNYQSAGL VDRAEQIFLG LQDGKMAREARQHLLNIYQQ DRDWEKAVET					
g574	GEKRARVLF ELAQNYQSAGL VDRAEQIFLG LQDGEMAREARQHLLNIYQQ DRDWEKAVET					
	130	140	150	160	170	180
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVG KALEANKKCT RANMILGDIE					
g574	AQLLSHDEQTYQFEIAQFYCELAQAALFKSNFDAARFNVG KALEANKKCT RANMILGDIE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEGLNRLTG YMQTFPELDL					
g574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEGLNRLTG YMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVEKSL LKKEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK ADADMRSVI					
g574	INVVEKSL LKKEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLPAWK ADADMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI EVX					
g574	GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI EVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1  ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GGCAGAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATGTC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGC AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCAGC CTCAACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAATCAGCG ATTTGGATCC GGCTTGGAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACA GTCTTTTCT
1151 GGCATTGTCC TGCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1  MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLDSPDTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSLDPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFWHCPACN KWQTFTPNKI
401 EV*

m574/a574 97.5% identity in 402 aa overlap

          10      20      30      40      50      60
m574.pep MRPNLPNSLKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
          |||
a574      MRPNLPNSLEKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
          10      20      30      40      50      60

          70      80      90      100     110     120
m574.pep LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV
          |||
a574      LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLDSPDTT
          70      80      90      100     110     120

          130     140     150     160     170     180
m574.pep GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET
          |
a574      GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET
          130     140     150     160     170     180

          190     200     210     220     230     240
m574.pep ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE
          |||
a574      ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE
```


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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGKPEEGLNRLTGYMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGKPEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDINGVYRLGLKLSDMNPAWKADADMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDINGVYRLGLKLSDLDPWKADADMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1 ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51 cccgtcaaaca gtcgcgtttc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
151 gttcggaac ggtgttaccg gtttcgtcgg tcggcgtgtc gatggcagaa
201 gcggcggtt cttggggggg cggattcggc agcgggttcc gatgcggcag
251 tatttgcagc ggttacaggt ccgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt gggttcgggt cgaacggccg gttttccgc
351 ttttgcctcg ggccgggcaa ctttgccttc aggtttttca accgggtttt
401 cgacaggttt ctctatcggt ttctccacag ttgctgttt ggacgggtca
451 gacggcatgg atgcagtttc ggtttgggt ttcgccgttt gcggtttggg
501 ttgttccgct ttgattttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1 ..MPCLLRQAAR CTNRRTRDQT VRFRLLRQK PVRQVRQVR RQLHNLFPQQ
51 VRKRCYRFR SACRWQKRRL LGGADSAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGS RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDS
151 DGMDAVSALG FAVCGLGCSA LI FLGAALI LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq..
1 ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51 GCGAGGTTTT GCGGAAGCTG TTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTGTGC GGAGAAATCG GTATCGACGG TTTCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAAATGCC GTTTGCGCG GCTGCCAGGC TGTCGAAATC
351 CAAGTCGATG CGGTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGCTGTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCCGAGTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCG GTCGTCAAG TCAGGCTCTT
551 CTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAAATCC GCGCCTCCG CGGCAAGCAG
651 CAAGGTGTAC GAACCGCCGA ACAGACCGTC AACAGTCCG CTTTCGGTTT
701 CTCTTTCGGC AGAAACCTGT TCGACAGGTT CGGAACCGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTCTGAT GGCAGAAGCG GCGGCTCTT GGGGGCGGGA
801 TTCGGCAGCG GTTTCGGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 GTCGAACCGC CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTTGGGTT
1001 GTTCCGCTTT GATCCTGTTC AGATTGGAA TGTGA

```

888

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep
 1 MVSGERAFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA
 51 VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201 RKSSSRAINA APPPASSKVY EPPNRPNSP LSVSSSAETC STGSETALPV
 251 SSVGVSMAEA AASWGADSA VSDAAVFAAG TSGRTAGFS AFASGAATFA
 301 SGFSTGFSTV ACLDGS DGM DAVSALGFAVC GLGCSALILF RFGM*

m575/g575 70.2% identity in 114 aa overlap

	240	250	260	270	280
m575.pep	SSAETCSTGSETALPVSSVGVSMAEAAAASWGADSAVSDAAVFAAGTG-----				
g575	LHWLFPQVRKRCYRFRRSACRWQKRLLGGADSAVSDAAVFAAGTGPGRSVAEAGVS				
	50	60	70	80	90 100

	290	300	309	310	320
m575.pep	-----SGRTAGFSAFASGAATFASGFSTGFST-----VACLDGSDGMDAVSALGFA				
g575	DTAGLGSGRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA				
	110	120	130	140	150 160

	330	340
m575.pep	VCGLGCSALI-----LFRFGMX	
g575	VCGLGCSALIFLGAAALILFRFGMX	
	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

a575.seq
 1 ATGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
 51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
 101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
 151 GTTTGGGCGA CAGATCCCG TFCGGCGTG TCGATACGA TTTCGACAGG
 201 GTTGACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCGA
 251 TGGCGTTCCA ATCGGCATCC GCGCGTTTT GGGTTTCTTC ATCCTGCGTA
 301 AGTGCCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTCGAAATC
 351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
 401 TTGCCGACAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
 451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
 501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
 551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
 601 CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG
 651 CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
 701 AAACCTGTTC GACAGGTCG GAAACGGCGT TACCGGTTTC GTCGGTCGGC
 751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
 801 TTCCGATGCG GCAGTATTG CAGCGGTAC AGGTTGCGGT CGAACGCGCG
 851 GTTTTCCCG TTTTGCTTCG GCGCGGCAA CTTTGTCTTC AGGTTTTTCA
 901 ACCGTTTCT CTACCGTTGC CTGTTTGGAC GGTTCCGACG GCATGGATGC
 951 GGTTTCGGCT TTGGGTTTCG CCGTTTCCG TTTGGGTTGT TCCGCTTTGA
 1001 TCCTGTTTCA ATTCCGAATG TGA

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep
 1 MVSGERAFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA
 51 VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201 RKSSSRAINA APPPASSKVY EPPNRPNSP LSVSSSAETC STGSETALPV
 251 VSMEEAASW GADSAVSDA AVFAAGTGS RTAGFSAFAS GAATFASGFS
 301 TGFSTVACLD GSDGMDAVSA LGFAVCGLCG SALILFRFGM *

889

m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEAAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEAAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m575.pep	SMTISTGLYGLKVSGSYTLSDMAFQASARFWVSSSCVSA PDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVSGSYTLSDMAFQASARFWVSSSCVSA PDKMPFCAAARLSKSKSM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m575.pep	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m575.pep	SGSSSGTDSVRRARLDWARRKSSSRAINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSVRRARLDWARRKSSSRAINAAPPPASSKVYEPN----SPLSVSSSAETC					
	190	200	210	220	230	
	250	260	270	280	290	300
m575.pep	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTSGSRTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTSGSRTAGFSAFASGAATFA					
	240	250	260	270	280	290
	310	320	330	340		
m575.pep	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atggcgctgg acatcggacg ctcctgaaa caaatgaagg aacagggcgc
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttcttgacag agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcggtt ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcggcgc acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51 FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAEEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

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```

51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCCA
501  AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGGCG
551  GCGACAAATC CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

	10	20	30	40	50	60
m576.pep	MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLO					
g576	MGVDIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLO					
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQGE GKQPTKDDIV					
g576	EQQAKAVEKH KADAKANKEK GEAFLENAA EDGVKTTASGLQYKITKQGE GKQPTKDDIV					
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ VIPGWTEGVQLLKEGGEATFYIPSNLAYRE					
g576	TVEYEGRLID GTVFDSSKAN GPATFPLSQ VIPGWTEGVRLLEKGEATFYIPSNLAYRE					
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPNATLVFDVKLV KIGAPENAPAKQPAQVDIKKVN					
g576	QGAGEKIGPNATLVFDVKLV KIGAPENAPAKQPDQVDIKKVN					
	180	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTCCGCG CAGGGCGACA CCTCTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA

```

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```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
  1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

                                10      20      30
m576.pep                                MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
a576                                CGKKEAAPAS ASEPAASSA QGDTSSIGST MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m576.pep FTEAMQAVYDGKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
a576 FTEAMQAVYDGKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m576.pep KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
a576 KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m576.pep VIPGWTEGVQLLKEGGEATFYIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
a576 VILGWTEGVQLLKEGGEATFYIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
                                210     220     230     240     250     260

                                220
m576.pep KQPAQVDIKKVN
a576 KQPAQVDIKKVN
                                270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

```

g576-1.seq
  1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TCGGCGAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCCG TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAATGAAG GAACAGGCGC CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCTGCAG GAGCAGCAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTCCGGT
451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASAA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTDAMQAVYD  GKEIKMTEEQ
101 AQEVMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA  KDGVKTTASG
151 LQYKITKQGE  GKQPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPATFPLSQ
201 VIPGWTEGVR  LLKEGGEATF  YIPSNLAYRE  QGAGEKIGPN  ATLVFDVKLV
251 KIGAPENAPA  KQPDQVDIKK  VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA  TTTTCAAAT  CAGCGCACTG  ACCCTTTCCG  CCGCTTTGGC
51  ACTTTCCGCC  TGGCGCAAAA  AAGAAGCCGC  CCCCGCATCT  GCATCCGAAC
101 CTGCCGCCGC  TTCTTCCGCG  CAGGCGCACA  CCTCTTCGAT  CGGCAGCAGC
151 ATGCAGCAGG  CAAGCTATGC  GATGGGCGTG  GACATCGGAC  GCTCCCTGAA
201 GCAAATGAAG  GAACAGGCGC  CGGAAATCGA  TTTGAAAGTC  TTTACCGAAG
251 CCATGCAGGC  AGTGTATGAC  GGCAAAGAAA  TCAAAATGAC  CGAAGAGCAG
301 GTCAGGAAG  TCATGATGAA  ATTCCTTCAG  GAACAACAGG  CTAAAGCCGT
351 AGAAAAACAC  AAGCGGACG  CGAAGGCCAA  TAAAGAAAAA  GGCGAAGCCT
401 TTCTGAAAGA  AAATGCCGCC  AAAGACGCCG  TGAAGACCAC  TGCTTCCGGC
451 CTGCAATACA  AAATCACCAA  ACAGGCGGAA  GGCAACAGC  CGACCAAGA
501 CGACATCGTT  ACCGTGGAAT  ACGAAGGCCG  CCTGATTGAC  GGTACGGTAT
551 TCGACAGCAG  CAAAGCCAA  GCGCGCCCGG  TCACCTTCCC  TTTGAGCCAA
601 GTGATTCCGG  GTTGGACCGA  AGCGGTACAG  CTTCTGAAAG  AAGCGCGCGA
651 AGCCACGTT  TACATCCCGT  CCAACCTTGC  CTACCGCGAA  CAGGGTGGCG
701 GCGCAAAAAT  CGGTCCGAAC  GCCACTTTGG  TATTGTATGT  GAAACTGGTC
751 AAAATCGGCG  CACCCGAAAA  CGCGCCCGCC  AAGCAGCCGG  CTCAGTCCGA
801 CATCAAAAA  GTAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASSA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTEAMQAVYD  GKEIKMTEEQ
101 AQEVMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA  KDGVKTTASG
151 LQYKITKQGE  GKQPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPVTFPLSQ
201 VIPGWTEGVQ  LLKEGGEATF  YIPSNLAYRE  QGAGDKIGPN  ATLVFDVKLV
251 KIGAPENAPA  KQPAQVDIKK  VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	190	200	210	220	230	240
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			
g576-1.pep	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGC GG
701 GCGACAAAT CCGGCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCTGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAE KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISAL TLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISAL TLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMMKF LQEQQAKAVEKH					
m576-1	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMMKF LQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMMKF LQEQQAKAVEKH					
m576-1	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMMKF LQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	KADAKANKEK GEAFLENAE KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAE KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	KADAKANKEK GEAFLENAE KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAE KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	GTVFDSSKAN GGPVTFPLSQ VILGWTEGVQ LLKEGGEATFYIPSNLAYRE QGAGDKIGPN					
m576-1	GTVFDSSKAN GGPVTFPLSQ VILGWTEGVQ LLKEGGEATFYIPSNLAYRE QGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKAN GGPVTFPLSQ VILGWTEGVQ LLKEGGEATFYIPSNLAYRE QGAGDKIGPN					
m576-1	GTVFDSSKAN GGPVTFPLSQ VILGWTEGVQ LLKEGGEATFYIPSNLAYRE QGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	ATLVFDVKLV KIGAPENAPAKQPAQVDIKK VN					
m576-1	ATLVFDVKLV KIGAPENAPAKQPAQVDIKK VN					
	250	260	270			
a576-1.pep	ATLVFDVKLV KIGAPENAPAKQPAQVDIKK VN					
m576-1	ATLVFDVKLV KIGAPENAPAKQPAQVDIKK VN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1  atggaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaaaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggt
151 tttatttacg gagcaaacat gaaacttatc tataccgtca tcaaaatcat
201 tatcctgctg ctcttcctgc tgcttgccgt cattaatatg gatgccgtta
251 ccttttcta tctccgggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgtcgt cggcatcgtg ttcggaatgt ttgccctgtt
351 cgggaggctg ctgtccttgc gggcgaaaa cagccgctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1  MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLTQSW FRVRSCPCGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINM DAVTFSYLPQ QSVNPLPLIV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAAESAKQP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1  ATGGAAGGA ACGGTGTATT TGGTAAATT GTCGGAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAGTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTACG GAGCAAACAT GAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAATACG GATGCCGTTA
251 CCTTTTCTA CTGCGGGGG CAAAATTCTG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CATTTGTAGT CGGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGCV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577.pep	MERNVFGKIVGNRILRMS	SEHAAASYPKPCKSFKLAQSW	FRVRSC	LG	GVFIYGANMKLI	
g577	MERSGVFGKIVGNRILRMP	SEHAAAFYPKPCKSFKLTQSW	FRVRSC	PC	PGVFIYGANMKLI	
	10	20	30	40	50	60
	70	80	90	100	110	120
m577.pep	YTVIKIIILL	LFLLLAVINT	DAVTFSYLPQ	KFDLPLIV	VLF	GAFVVGII
						FGMFALFGRL

895

```

|||||
g577      YTVIKIIILLFLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFFVVGIVFGMFALFGRL
          70      80      90      100     110     120
          130     140     150     160
m577.pep  LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||:|||||:|||||:|||||
g577      LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAESAQKPX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAAGGA  ACGGTGTATT  TGGTAAAATT  GTCGGCAATC  GCATACTCCG
51  TATGTCGTCC  GAACACGCTG  CCGCATCCTA  TCCGAAACCG  TGCAAATCGT
101 TTAACCTAGC  GCAATCTTGG  TTCAGAGTGC  GAAGCTGTCC  GGGCGGCGTT
151 TTTATTTACG  GAGCAAACAT  GAAACTTATC  TATACCGTCA  TCAAAATCAT
201 TATCCTGCTG  CTCTTCCTGC  TGCTTGCTGT  CATTAAATACG  GATGCCGTTA
251 CCTTTTCCTA  CCTGCCGGGG  CAAAATTTCG  ATTTGCCGCT  GATTGTCGTA
301 TTGTCGGCG  CGTTTGTCGT  CGGCATCGTG  TTCGGAATGT  TTGCCTTGTT
351 CGGACGGTTG  TTGTCGTTAC  GTGGCGAGAA  CGGCAGGTTG  CGTGCCGAAG
401 TAAAGAAAAA  TCGCGGTTTG  ACGGGGAAGG  AGCTGACCGC  ACCACCGGCG
451 CAAATGCGC  CCGAATCTGC  CAAACAGCCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1  MERNGVFGKI  VGNRILRMSS  EHAAASYPKP  CKSFKLAQSW  FRVRSCPGGV
51  FIYGANMKLI  YTVIKIILL  LFLLLAVINT  DAVTFSYLPQ  QKFDLPLIVV
101 LFGAFVVGIV  FGMFALFGRL  LSLRGENGRL  RAEVKKNARL  TGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

          10      20      30      40      50      60
m577.pep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
          |||||
a577      MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCPGGVFIYGANMKLI
          10      20      30      40      50      60
          70      80      90      100     110     120
m577.pep  YTVIKIILLFLLAVINTDAVTFSYLPQKQFDLPLIVVLFGAFFVVGIIIFGMFALFGRL
          |||||
a577      YTVIKIILLFLLAVINTDAVTFSYLPQKQFDLPLIVVLFGAFFVVGIVFGMFALFGRL
          70      80      90      100     110     120
          130     140     150     160
m577.pep  LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||
a577      LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESAQKPX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1  atgggaaagc  tcgacatcgg  gatattgttt  gccgatttct  tcaaagattt
51  cgcgccacag  ttcggtggtt  tccaaaacgt  tggctttgcc  tacggagcag
101 acttttttgc  tgcgtttttg  ggcggattgg  aaggccacgt  gggcgatgcy
151 gcggatttcg  ctttcgctgt  atttcaggtt  gttgtagcct  tcgtgttcgc
201 cgttttccaa  aacacggatg  ccgcgcggtt  cgccgaaata  aatatcgccg
251 gtaagtccgc  gcacaatcaa  aatatccaaa  ccggcaacga  tttcagggtt
301 gagcgtggag  gcgttggtta  a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1  MGKLDIGILF  ADFFKDFAPQ  FGGFQNVGFA  YGADFFAAFL  GGLEGHVGDA
51  ADFAFVFGH  VVAFVFAVFQ  NTDAARFAEI  NIAGKFAHNQ  NIQTGNDPRL

```

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101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTCT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTCG TCGTTTTCG GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCAG AACGCGGATG CCGCGCGGTT CGCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGCAACGA TTTCAGGCTT

```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	:					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	:					
g578	VVAFAFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTCT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTCG TCGTTTTCG GCGGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	:					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	:					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```

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```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCCCTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TCGGACGACG CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCGG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGACT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TCGGACGACG CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

```

          10      20      30      40      50      60
m579.pep  MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
          |||||||
g579       MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
          10      20      30      40      50      60

          70      80      90     100     110     120
m579.pep  KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM
          |||||||
g579       KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM
          70      80      90     100     110     120

```

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : :					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAABEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	: : : : :					
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```

a579.seq
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATGCCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGC GCGGGT TGGCGGTGGC GTTGTCTTGA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCCACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

a579.pep	1	MRAAMTRAQV	DATLISFLCN	VANIGLLILV	IIAALGRLGV	STTSVTALIG
	51	GAGLAVALSL	KDQLSNFAAG	ALIILFRPFK	VGDFIRVGGF	EGYVREIKMV
	101	QTSRLRTDNE	EVVLPNSVVM	GNSIVNRSTL	PLCRAQVIVG	VDYNCDLKVA
	151	KEAVLKAAVE	HPLSVQNEER	QAAAYITALG	DNAIEITLWA	WANEADRWTL
	201	QCDLNEQVVE	NLRKVNINIP	FPQORDIHIIN	S*	
m579/a579	100.0% identity in 231 aa overlap					
	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	: : : : :					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	: : : : :					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : :					
a579	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	: : : : :					
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

```

1  ATGGACTTCA AACAAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTGCGC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGT GCGGTTGTCC TTAAGAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCTGA TTATCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTCGGCGGT TTGAAGGAT ATGTCCGGGA AATCAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACAG CTGCCGCTTT
551 GCGCGGCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCGCGCGCC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGCCCG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH LISVSGWHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAA EHPLSVQNEE RQPAAYITAL GDNAIETLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA AACAAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGTGGTC GGGAAATGGG CGGCGAAACG CATTGTGCGT
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGT GCGGTTGTCC CTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGACTGA TTATCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACAG CTGCCGCTGT
551 GCGCGGCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCGCGCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCTG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRST LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIETLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
g579-1	MDFKQDFDLHLISVSGWHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPSNVVMGNSIVNRST					

900

```

|||||:
g579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180

          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||:
g579-1  LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240

          250      260      270      280
m579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          |||||:
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA AACAAATTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCGG
101 CGCTGCTTAT TTTTGTGTC GGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTGATGAGGG CGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATGGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGGG GTTGGCGGGT GCGTGTGTC TTGAAAGACC AGCTGCCAA
351 TTTTGGCGCC GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCGAGA GATTAAATG
451 GTGCAGACTT CTTGCGGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGCAGGCCG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGCAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.pep
1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVLPNSVV MGNSIVNRST LPLCRAQVIV GVDYNDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRW
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          |||||:
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          10      20      30      40      50      60

          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||:
m579-1  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120

          130     140     150     160     170     180
a579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          |||||:
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          130     140     150     160     170     180

          190     200     210     220     230     240
a579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||:
m579-1  LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240

          250     260     270     280
a579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX

```

```

|||||
m579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

```

g580.seq
1  atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51  cgcgtcgcag cccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
151 tcgaaaatca gcttggtaaa gcggtgtcgc caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt .ggtaattttg cggcctgatg
251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg
301 tag

```

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

```

g580.pep..
1  MDSPKVGCWG MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

```

m580.seq..
1  ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTTGTGC CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCCAGGGA AGTTGGCTTT GGTGATTTTG CGCCCGGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
301 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

```

m580.pep..
1  MDSPKVGCWG MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

```

m580/g580 97.0% identity in 100 aa overlap

```

          10      20      30      40      50      60
m580.pep  MDSPKVGCWMMVLPMASASQPISMARQTSPISPPFGPTMPPPMRPVSASKISLVKPLS
          |||||
g580       MDSPKVGCWMMVLPMASASQPISMARQTSPIMSPPFGPTMPPPMRPVSASKISLVKPLS
          10      20      30      40      50      60

          70      80      90      100
m580.pep  QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX
          |||||
g580       QPLAIARPEAAHGKLALVILRPDALADNSVSPHATSGEVX
          70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

```

a580.seq
1  ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTGC CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGCCCGGAGG
251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
301 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

```

a580.pep
1  MDSPKVGCWG MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

```

902

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPSAASQPISMARQTSPIISPPFGPTMPPPMRVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPSAASQPISMARQTSPIISPPFGPTMPPPMRVSASKISLVKPLS					
	10	20	30	40	50	60

	70	80	90	100
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX			
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1 atgcacttcg cccagcttgt gggcacaacc ggtatagaac aaaatacgtt
51 ctgtcgctcg ggttttaccg gcatcgatat gggcggaaat accgatgttg
101 cggtagacggc tgatcggggg cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagtgagaga atgctttgtt ggcttcagcc atacggtgta
201 cttcttcacg ttttttcaac gcaccgccac ggccctcgga cgcataaatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttgcgggc
301 cgcgtcgcca acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51 CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CCGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCCTCGGA CGCATCAATC
251 AATTGCGCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTVQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLLTFAGRIANPAHCQSQTAX				
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLTTFAGRVANPTHQCSQTAX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:


```

a581.seq
1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRG	LTSHFISLSKLETEVRECFV				
	::					
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTQADRG	LTSHFISLSKLETEVRECFV				
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX			
a581	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX			
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
1  atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
51  agagaccgcy ctgcaatgcy ccgctttgac ggacaatggt acgcgtttgg
101  cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151  gaaggcgagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201  cagcttggat aaggcgagg cggtcattgt tgttgaaaaa ggcggggatg
251  cgcttcctgc cgacagtgcg ggcgaaccg ccgatatcta tacgcctttg
301  agcctgatgt acgacttgga caaaaacgat ttgcgcgggc tgttggcggt
351  acgcgaacac aatccgatgt acctatgcc gtttgggtat aacaattcgc
401  ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451  ttcggacagc agaaacgtgc ggaaaccaa ttgcaggttt cgttcaaaag
501  caaaattgcc gaaaatttgt ttaaaacccg cgcggatctg tggttcggct
551  acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601  ccgttcgcga atacggatta caaacctgaa attttcctga cccagcctgt
651  gaaggcggat ttgcggttcg gcggcaggct gcgtatgctc ggtgcggggt
701  ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcgtggaac
751  aggtatttat ccatggcagg catggaatgg ggcaaatga cggtgattcc
801  gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851  ccgatatgac cgactatatg gggatatggc acgtgaagct gcagtaccgc
901  ctgaacgaca ggcagaatgt gtattccgta ttgcgctaca accccaaaac
951  gggctacggc gcgattgaag ccgcctacac gtttccgatt aaggggaaac
1001 tcaaaggcgt ggtacgcgga ttccacgggt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
1  MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EQQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101  SLMYDLKND LRGLLVREH NPMYLMPPFY NNSPNYAPSS PTRGTTVQEK
151  FGQQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTRQSDW QIYNQGRKSA
201  PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNG QSRPESRSWN
251  RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVVLQYR
301  LNDRQNVYSV LRYNPKTYGY AIEAAYTFPI KGKLGKVVGR FHGYGESLID
351  YNHKQNGIGI GLMFNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
  1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
 51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101  CGTGTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151  GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201  CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GCGGGGATG
251  CGCTTCTGCG CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301  AGCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351  ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAITCGC
401  CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451  TTCGGACAGC AGAAACGTGC GGAACCAAAA TTGCAGTTT CGTTCAAAAG
501  CAAAAATTGCC GAAGATTGT TAAAAACCGC CCGGATCTG TGTTCCGGCT
551  ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601  CGCTTCCGCA ATACGGATTA CAAACCTGAA ATTTCTCTGA CCCAGCTGT
651  GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701  TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751  AGGATTATCG CCATGGCAGG CATGGAATGG GGCAAATGA CCGTGATTCC
801  GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CCGCGATAAA AACGACAATC
851  CCGATATGCG CACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901  CTGAACGACA GGCAGAAATG GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951  GGGCTACGGC GCGATTGAAG CCGCTTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
  1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
 51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101  SLMYDLKND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151  FGQQRKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201  PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251  RIYAMAGMEW GKLTIVIPRVW VRAFDQSGDK NDNPDADYD GYGDVKLQYR
301  LNDQRNVYSV LRYPNKTGYG AIEAAYTFPI KGKLGKVVVG FHGYGESLID
351  YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

```

      10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||||
g582      MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||||

      70      80      90     100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSIMYDLKNDLRGLLGVREH
          |||||
g582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSIMYDLKNDLRGLLGVREH
          |||||

     130     140     150     160     170     180
m582.pep  NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQRKRAETKLQVSFKSKIAEDLFKTRADL
          |||||
g582      NPMYLMPLWYNNSPNYAPSSPTRGTTVQEKFGQQRKRAETKLQVSFKSKIAENLFKTRADL
          |||||

     190     200     210     220     230     240
m582.pep  WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
          |||||
g582      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
          |||||

     250     260     270     280     290     300
m582.pep  QSRPESRSWNRIYAMAGMEWGKLTIVIPRVVWRAFDQSGDKNDNPDADYMGYGDVKLQYR
          |||||
g582      QSRPESRSWNRIYAMAGMEWGKLTIVIPRVVWRAFDQSGDKNDNPDADYMGYGDVKLQYR
          |||||

     310     320     330     340     350     360
```

905

```

m582.pep  LNDQRNVYSVLRYPNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          |||
g582      LNDQRNVYSVLRYPNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          |||
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||
g582      GLMFNDWDGIX
          |||
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTTT GCAGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAG CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCAATTGT TGTTGAAAAA GGCAGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGG CAAAACGAT TTGCGCGGGC TGTTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGTG TTAACACCGC CGCGGATCTG TGTTCCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTCG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCGCTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGCG GCGATTGAAG CCGCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGT ACAGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNG QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH
          |||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH
          |||
          70      80      90      100     110     120

          130     140     150     160     170     180

```

906

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAETKLQVSFKSKIAEDLFKTRADL
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAETKLQVSFKSKIAEDLFKTRADL
               130      140      150      160      170      180

               190      200      210      220      230      240
m582.pep      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
               190      200      210      220      230      240

               250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
               250      260      270      280      290      300

               310      320      330      340      350      360
m582.pep      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582          LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
               310      320      330      340      350      360

               370
m582.pep      GLMFNDLDGIX
               |||||||||||
a582          GLMFNDLDGIX
               370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgaaccgat gccacgcgtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaacgca ctcaacgcat cgtcatcgc cgcccgccgt ttgtcggcgg
351 ttacgccggt tactgcgacc aaccgcgagg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcgcca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtggca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT HLAFCAPCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51  QFGKSETVTD AQRFPSSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIAGR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLD VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTACC CATCTGCCTT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCATGGCA ATCAGCCAAA TCAACGGATT
301 GCGGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACCAGCAGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACAGGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

551 CCCAATTTC A TCATATTGAC CTC CGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pwp.

```

1  MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAA GIGRNGSQO
51  QFGKSETVTD AQRFSKNGD KQISDTHPQ CFEQTARNHN CDGNQPNQRI
101 QERTQRTAHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 GQRPSRLRDP VGYGQCQNOG AQYCGNGEGY RFETQFHHID LRRKKDRPEKS
201 EK*

```

m583 / q583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583 . pep	MIVDQSQIFTHLAFCAFCGIGAVTAGNRLNHRMYNAAAARGIGRGNSSQQQFGKSETVTD					
	:					
g583	MIIDQSQIFTHLAFCAFCGIGAVTAGNRLNHRMYNAAAARGIGRGNSSQQQFGKSETVTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m583 . pep	AQRFSKSKNGDKQISDTHPQPCFEQTARNHNCNQGPNQRIGERTQRIAHRRARFVGGYAG					
g583	AQRFSKSKNGDKQISDTHPQPCFEQTARNHNCNQGPNQRIGERTQRIAHRRARFVGGYAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m583 . pep	YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLLDPVGYGQCQNQGAQYCGNGEGY					
g583	YCDQPDGNNRQRAQRHGLADNGGNHTDKHSGQQRPSLRLLDPVGYGQCQNQGAQYCGNGEGY					
	130	140	150	160	170	180
	190	200				
m583 . pep	RFETQFHHIDLKKDRPEKSEKX					
g583	RFETQFHHIDLKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1795>:

a583.seq

1	ATGATAGTTG	ACCAAAGCCA	AATATTTACC	CATCTTGCCT	TCTGTGCCTT
51	TTGCGGGATT	GGAGCCGTAA	CTGCCGGCAA	TCGACTGCAT	AATCGGATGT
101	ATAATGCCCGC	CGCCGCGCGC	GGTATTGGAA	GGGGTAACGG	GAGCCAGCAG
151	CAGTTCCGAA	AGAGCGAGAC	TGTAACCGAT	GCCACGCGT	TTTCTTCCAA
201	AAACGCGCAT	AAACAATAT	CGGATACGCA	TCCCGACGCC	TGTTTTGAGC
251	AAACCGCGCG	AAATCATAAC	TGCGATGGCA	ATCAGCCAAA	TCAACGGATT
301	GGCGAACGCA	CTCAACGCAT	CGCTCATCGC	CGACCCGGT	TGTGCGGCGG
351	TTACGCGCGT	TACTGCGACC	AACCCGACGG	CAATAATCGA	CAGCGCACCC
401	AACGCGCAT	CCTTGCCGAT	AATGGCGGCA	ATCACACGGA	TAAAGTATGGC
451	CAGCAGCGTC	CAAGCCTGAG	GCTTGACCCC	GTCGGGTACG	GGCAGTGCCA
501	AAACAAGGC	GCACAATACT	GCGGCAATGG	CGAGGGGTAT	CGGTTTGAAG
551	CCCAATTTC	TCATATTGAC	CTCCGTAAAA	AAGACCGTCC	CGAAAAATCG
601	GAATAATAA				

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pap

```

1  MIVDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAA GIGRGNQSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GORTQRIAGR RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VYGQCQNQG AQYCGNGEGY RFETQFHHD LRKKDRPEKS
201 EK*

```

m583/a583 99.0% identity in 202 aa overlap

m583.pep MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQFGKSETVTD

908

```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQFGKSETVTD
           10      20      30      40      50      60

           70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQPQRIGERTQRIAHRRARFVGGYAG
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQPQRIGERTQRIAHRRRTFVGGYAG
           70      80      90      100     110     120

           130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLLDPVGYGQCQNQGAQYCGNGEGY
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLLDPVGYGQCQNQGAQYCGNGEGY
           130     140     150     160     170     180

           190     200
m583.pep  RFETQFHHIDLRRKKDRPEKSEKX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a583      RFETQFHHIDLRRKKDRPEKSEKX
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1  atgetgcgtt ctattttggc ggcttcctg ctggcggtat cttttcggc
51  ggcggtcag gcaattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcgcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggat
251 cgcgcagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggaggcca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcgttctg ggtgcgtccg gttataaaat cgtcaaatg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggt aaggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:..

```

1  MLRSILAASL LAVSFPAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNAVNA EFVKKFNNFT RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK AEGRDFDALN RFIADVQTD SLEDTFPSVS RRRRNEVIDQ
151 VSKDAVLRFK ARAEKLAGVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEBISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1  ATGTTGCGTC TTGTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTCATC AGAAAATCGA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCCGGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTAAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGMAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

909

m584.pep..

```

1 MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51 EGRDKNAVNA EFVKKFNKFI RSKNGSFKT ELVSR SAMPR YQYTN GRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKL AVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

      10      20      30      40      50      60
m584.pep MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTA EGRDKNAVNA
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      MLRSILAASLLAVSFPAAAEALNYNIVEFS ESAGIEVAQDTMSARFQVAAEGRDKNAVNA
      10      20      30      40      50      60

      70      80      90     100     110     120
m584.pep EFVKKFNKFI RSKNGSFKT ELVSR SAMPR YQYTN GRRIQ TGWEERAEFK VEGRDFDELN
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      EFVKKFNKFI RSKNGSFKT ELVSR SAMPR YQYTN GRRIQ TGWEERAEFK AEGRDFDALN
      70      80      90     100     110     120

      130     140     150     160     170     180
m584.pep RFIADIQADA ALXYTDFHVS RERRNEVIXQ VSKDAVLRFK ARAEKL AVL GASGYKIVKL
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      RFIADVQTDASLED TDFS VSRERRNEVIDQ VSKDAVLRFK ARAEKL AVL GASGYKIVKL
      130     140     150     160     170     180

      190     200     210     220     230
m584.pep NLGHIGSHIAGGGAAQAKML RAMPMAASVN MEGADSAAPG VEEISISVNG TVQFX
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584      NFGQIGSHIAGDGAVRAKML RAMPMAASVNMKG TDSAAPG VEEISISING TVQFX
      190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

```

a584.seq
1 ATGTTGCGTT CTATTTTGGC GGCTTCCTG CTG.....
51 ..... ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG AAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAACCC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TCGGTTGAAC CGTTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGTTGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

```

a584.pep
1 MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51 EGRDKNAVNA EFVKKFNKFI RSKNGSFKT ELVSR SAMPR YQYTN GRRIQ
101 TGWEERAEFK VEGRDFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKL AVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

      10      20      30      40      50      60
m584.pep MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTA EGRDKNAVNA
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584      MLRSILAASLL----- IVEFS ESAGVEAVQDTMSARFQVTA EGRDKNAVNA
      10      20      30      40

```

910

	70	80	90	100	110	120
m584.pep	EFVKKFNKFIKRSKNGSFKTELVSRSAMPYQYTNRRITQTGWEEAEFKVEGRDFDELN					
a584	EFVKKFNKFIKRSKNGSFKTELVSRSAMPYQYTNRRITQTGWEEAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  tttcgccaca  ttttgccggg  ttatcgctctg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctgggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattatgt  ccgcattcaa  gacacggggc  gacacggcg  cgccgcaaat
201  cctgaccgaa  tggaaaaaca  gcccggtctc  atccgcggtt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaacc  gctatatcga  caattacacc
301  atagaacgcg  cccggctggt  tgccgccaac  aacccccatt  ccaaccttgt
351  ccgcacgaa  tacgaccgtt  tcggcgaaga  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggccctgcgc  ttgccccgat  ttggcacgaa  ttcatcatcc  tctccttcac
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aacccatcag  aatcttaggc  aacggcatgg  acagggtggc  agaacgagaa
601  cttgaagacc  gcgtttgcca  acagggttcg  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgaattcgc  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFORIFAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQGEKKD  ILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGEEYLF  FIKGWDNHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCCQVR  DRDELADVA  MQPDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTGCCACA  TTTTGCGCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCAG  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCGG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCTGACGGAA  TGGAAAGACA  GCCCGGTCTC  ATCGGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCCGGCTTTT  CGCCGCCGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTT  TTCACCAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCCTGC  CCAGCCCCCT  GTTGATCCCC
451  GGCCTGCCGC  TCGCCCCGAT  TTGGCACGAA  CTCATCATAT  TGTCTTCAT
501  CATCATCGTC  GGAATGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGGTGGC  AAACGGAGAA
601  CTTGAAACCC  GTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCTCTTGCC  ATCCAATTGG  ACAAAATGGT  GGAAAACTC  GAAAACTCG
701  TTGCCAAGA  ACGCCACCTG  CTCCATCAG  TCTCCCATGA  AATGCGTTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTCCGA  CTGATTGAGG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAACTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAACGT  TTAACCTGT  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTGG  AAAAAGAAAG  CCTGAAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAAGAC  AATCAAAGCA  TTGCCAGAA  AAACGGACAA  ACGGTTACCC
1001  TGTCTGCCGA  CGGAAAAATC  CCCGAAACA  CAACCATCCT  TGCCAACGAA

```



```
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAAACGGC CCGGCGTGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAAGGGGCG TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```
1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDD IILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDELHSLA IQFDKMVEKL EKLVAKEHRL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQKE QYLRLEGELE TRMDTLAGELE LTLRSLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNYSPG GSTILINIGQ DHKHWIIDVT DNGPGVDEMGO
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*
```

m585 / g585 88.3% identity in 231 aa overlap

```
10 20 30 40 50 60
m585.pep MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG
|||||
g585 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFKTRG
10 20 30 40 50 60

70 80 90 100 110 120
m585.pep DAGAREILTEWKDSPVSSGVYVIQGDEKDD IILNRYIDSYTIERARLFAAGHPHNSNLVHIE
|||||
g585 DNGAREILTEWKNSPVSSAVYVIQGDEKDD IILNRYIDNYTIERARLFAANNPHNSNLVRIE
70 80 90 100 110 120

130 140 150 160 170 180
m585.pep YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
|||||
g585 YDRFGEEYLF FIKGWDNHQAQRLPSPLFIPGLPLAPIWHEFIILSFIIIVGLLMAYILAG
130 140 150 160 170 180

190 200 210 220 230 240
m585.pep NIAKPIRILGNMMDRVANGELETRISQQVDDRDDELHSLAIQFDKMVEKLEKLVAKERHRL
|||||
g585 NIAKPIRILGNMMDRVAERELEDVRCQVDRDDELADVAMQFDTMVEKLEX
190 200 210 220 230

250 260 270 280 290 300
m585.pep LHHVSHEMRSPLARMQAIVGLIQAQPKQKEQYLRLEGELETRMDTLAGELELTLRSLRLETSN
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```
1 ATGAAACTGT TCCAACGCAT CTTGCCACAA TTTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCCTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCGG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGCTTTT CGCCGCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCTGC CCAGCCCTCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCGCAT TTGGCACGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTGCAC GACCGCGACG ACGAATTGTC
```

```
651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTGCGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAACTG TTAACCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCGAAAAACA CAACCATCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGCGGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACGCG TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

a585.pep

```
1 MKLFQRI FAT FCAVIVCAIF VASFSEWL VQ NTLAENQFNQ RRTIETTL MG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGD EKKD ILHRYIDS YT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWD KLQA RRLPSPL LIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIR ILG NGMDRVAN GE
201 LETRISQQVD DRDDEL SHLA IQFDKMVEKL EKLVAKE RHL LHHVSHEM RS
251 PLARMQAIVG LIQAQPQKQE QYLKRLE GEL TRMDTLA GEL LTLRLETS N
301 MALEKESLKL LPFLGNL VED NQSIAQK NGQ TVTLSAD GKI PENTTILA NE
351 SYLYRAFDNV IRNAVNY SPE GSTILINI GQ DHKHWI DVT DNGPGVDE MQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQ HI IEQHCGKI IA ENIKPNGL RM
451 RFILPKKKTG SKTEKSAN*
```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FATFC	AVIVCAIFV	ASFSEWL VQNT	LAENQFNQ	RRTIETTL MG	SIISAFRARG
a585	MKLFQRI FATFC	AVIVCAIFV	ASFSEWL VQNT	LAENQFNQ	RRTIETTL MG	SIISAFRARG
	70	80	90	100	110	120
m585.pep	DAGAREILTEW	KDSPVSSGV	YVIQGD EKKD	ILNRYIDS YT	IERARLFAAG	HPHSNLVHIE
a585	DAGAREILTEW	KDSPVSSGV	YVIQGD EKKD	ILHRYIDS YT	IERARLFAAG	HPHSNLVHIE
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF	FTKDWD KLQARR	LPSPLLIPGL	PLAPIWHE	LIILSFIIIV	GLLMAYILAG
a585	YDRFGEEYLF	FTKDWD KLQARR	LPSPLLIPGL	PLAPIWHE	LIILSFIIIV	GLLMAYILAG
	190	200	210	220	230	240
m585.pep	NIAKPIRILGN	GMDRVANGE	LETRISQQV	DDRDEL SHLAI	QFDKMVEK	EKLVAKE RHL
a585	NIAKPIRILGN	GMDRVANGE	LETRISQQV	DDRDEL SHLAI	QFDKMVEK	EKLVAKE RHL
	250	260	270	280	290	300
m585.pep	LHHVSHEMRS	PLARMQAIV	GLIQAQPQKQE	QYLKRLE GEL	TRMDTLA GEL	LLTLRLETS N
a585	LHHVSHEMRS	PLARMQAIV	GLIQAQPQKQE	QYLKRLE GEL	TRMDTLA GEL	LLTLRLETS N
	310	320	330	340	350	360
m585.pep	MALEKESLKL	LPFLGNL VED	NQSIAQK NGQ	TVTLSAD GKI	PENTTILA NE	SYLYRAFDNV
a585	MALEKESLKL	LPFLGNL VED	NQSIAQK NGQ	TVTLSAD GKI	PENTTILA NE	SYLYRAFDNV

913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKKWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKKWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1  atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatatatt
51  ttggaaaacc acgggcaa at ggctgtttgc cctgctgatt ttggcggcac
101 tccggtactt gggatacacg gtttaccaaa accgtgcggc ttcccaaat
151 caggaagcgg cggcgggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcaa agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acccccatct catttccgcc gcccaagcca cgctgatggc ggccggcaacc
301 gaatttgacg cgcagcggtta cgatgttgcc gaaggtcatt tgaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttggcg gcgcagcgctc
401 tggcggttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctcgacacgc cgggttgaggc ggacttcgcc cccctgctga tggaaactaa
501 aggcgatgtt tatgccgcac agggaaaaag ccaggaagcc ttaaaaaact
551 acggacaggc ttggaaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1  MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNRRAASQN
51  QEAAAVLANI VEKAQNKAPO SEINAEISKI QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLVLSN QKDSLIALA AQLRGVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1  ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATATT
51  TTGGA AAAACC ACGGGCAAAT GGCTGTTTGC CTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GACCAAATC CAACAAAGCT
251 ACCCGCATTC CATTTCGCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTTCAAC CAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACATGCCGC GCTTGCCGCG
451 CTCGATACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTA AAAAAT
551 ACGGACAGGC TTAGAAAAA ATGCCTCAAG ATTCTGTCG TCGCAATTG
601 GTTCAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1  MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNRKVSQN
51  QEAAAVLANI VEKAQSKAPO SEINAEITKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLVLSN QKDSLIALA AQLRGVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNRKVSQN QEAAAVLANI					

g586	MAAHLEEQQELDNFKYFWKTTGKWLFPALLILAAALGYLGTYVYQNRAASQNQEEAAVLANI	10	20	30	40	50	60
		70	80	90	100	110	120
m586.pep	VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATFEFDAQRYDVAEGHLKQWVLSN						
	:						
g586	VEKAQNKAPQSEINAELSKLQQSYPHSISAAQATLMAAAATFEFDAQRYDVAEGHLKQWVLSN						
		70	80	90	100	110	120
		130	140	150	160	170	180
m586.pep	QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA						
g586	QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQKSQEA						
		130	140	150	160	170	180
		190	200	210			
m586.pep	LKNYGQALEKMPQDSVSGRELVMKLDLSLXX						
	:						
g586	LKNYGQALEKMPQDSVSGRELLMKLDLSLXX						
		190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```
a586.seq
1  ATGGCAGCCC  ATTTGGAAGA  ACAACAAGAG  TTGGACAATT  TTAAATATTT
51  TTGGAAAACC  ACGGGCAAAT  GGCTGTGTGC  CGTGCTGATT  TTGGCGGCAC
101 TCGGCTACTT  GGGATACACG  GTTTACCAAA  ACGGTGCGGC  TTCCCAAAAT
151 CAGGAAGCGG  CGGCGGTGCT  GGCAACATC  GTGGAAAAGC  CGCAAAACAA
201 AGCCCCGCAA  AGCGAAATCA  ATGCCGAATT  GGCCAAGCTC  CAACAAGAAGT
251 ACCCCCATTC  CATTTCCGCC  CCGCAAGCCA  CGCTGATGGC  GGCAGCAACC
301 GAATTTGACG  CGCAGCGTTA  CGATGTTGCC  GAAGGCCATT  TGAATGGGT
351 ATTGTCCAAC  CAAAAGACA  CCCTGTATCA  GGCCTTGGCG  GCGCAGCGTC
401 TGGCGGTGT  GTTGTTCGAA  CAAAATAAAT  ACGATGCCGC  GCTTGC CGCA
451 CTCGACACGC  CGGTGAAGC  GGACTTCGCC  CCGCTGCTGA  TGGAAACCAA
501 AGGCGATGTC  TATGCCGCAC  AGGGA AAAAG  CCAGGAAGCC  TTAAAAAACT
551 ACGGACAGGC  TTTAGAAAAA  ATGCTCTAAG  ATTCTGTCGG  TCGCGAATTG
601 GTTCAAATGA  AACTTGATTC  GCTGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

a586.pep

1	MAAHLEEQQE	LDNFKYFWKT	TGKWLFAVLI	<u>LAALGYLGYT</u>	<u>VYQNRAASQN</u>
51	QEAAAVLANI	VEKAQNKAPO	SEINAEALAKL	QQSYPHSTSA	AQATLMAAAT
101	EFDAQRYDVA	EGHLKWVLSN	QKDSLIIQALA	AQRLGVVLLQ	QKKYDAALAA
151	LDTPEVADF	PLLMETKGDV	YAAQGSQEA	LKNYGQALEK	MPQDSVGREL
201	VQMKLDSLK*				

m586/a586 97.6% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQELDNFKYFWKTTGKWLFALLILAALGYLGTYVYQNKRKVSQNQEAAAVLANI					
	: : : : : : : : : : : :					
a586	MAAHLEEQQELDNFKYFWKTTGKWLFVALLILAALGYLGTYVYQNRAASQNQEAAAVLANI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m586.pep	VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN					
	: : : : : : : : : : :					
a586	VEKAQNKAQSEINAELAKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m586.pep	QKDSLIIQALAAQRLGVVLLQKKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA					
	: : : : : : : : : : :					
a586	QKDSLIIQALAAQRLGVVLLQKKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA					
	130	140	150	160	170	180

915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRELVQMKLDSLKX
                |||||
a586          LKNYGQALEKMPQDSVGRELVQMKLDSLKX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
  1  atgaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
 51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101  aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151  gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201  ccccatcccg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251  ccggcacgct cggtttgcgc tacggactga ccggcaatac cgacatttac
301  ggcagcggca gctatctgtg gcacgaagaa cgcaaactcg acggcaacgg
351  caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
401  ctttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451  acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501  gctttgcccc ttttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
  1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENSR
 51  AALAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLAGTLGLR YGLTGNTDIY
101  GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKD GK NPALISFLES
151  TVYEKSRNKA SLIKKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
  1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
 51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101  AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151  GCCGAACTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201  CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251  TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301  GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTCG ACGGCAACAG
351  CAAAACCCGC AACAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401  CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451  ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501  CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551  CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601  TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGCTG
651  CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701  CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751  GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCCAGG CTTTAAACGC
801  ATCCGACAGT TCAACGTTT CAGGGCAAAG CAGTTCGAA CTGAAATTG
851  GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
  1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
 51  AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLR YGLTGNTDIY
101  GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151  TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLSDGIR
201  YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251  AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

916

```

m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587       MKRIFLPALPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENRAALAAPVYIQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m587.pep  TGATSFIPITEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587       TGATSFIPITEIQENGSDMLAGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

          130     140     150     160     170     180
m587.pep  NKRMDSVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587       NKRMDSISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKKRGLCPFFYNLRINYEY
          130     140     150     160     170     180

          190     200     210     220     230     240
m587.pep  LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587      X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587.seq
1  ATGAAGCGCA TCTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAACT GGAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGET TTACATCCAA ACCGGCGCAA CTCGTTTAT
201 CCCCATTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGC GC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACGG
351 CAAAACCGGA AACAAACGGA GTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCGTCGTC CTCTCATTTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCAATATAT CTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCT GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587.pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGSDMLVGTGLRL YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMDSVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

m587/a587 95.2% identity in 289 aa overlap

```

          10      20      30      40      50      60
m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587       MKRIFLPALPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m587.pep  TGATSFIPITEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587       TGATSFIPITEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

```

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLKGQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

g588.seq

```

1   atgcttaaac atctcgcat cctactgcc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacc
101 aaggcgggat cggaagagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgcggg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaagc gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aacctctttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

g588.pep..

```

1   MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

m588.seq..

```

1   ATGCTTAAAC ATCTCGCATT CCTACTGCCG GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCCTGA CTTCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAGAC GGTAAACCCG CCGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTC TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAGG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCTCTTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

m588.pep..

```

1   MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENMIK EVKLPHNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g588         MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGLP SGKGIWRCRDGRGYTGS
             10      20      30      40      50      60

             70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g588         FKNGKFDGQGVYTVAAAGREVLEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
             70      80      90      100     110     120

             130     139
m588.pep    IMKCENGMIKEVKLPKNKX
g588        YYEMRTRHDX
             130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CGCCGCGTCC GCCGTCTCTGA CTTCCCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCCTACTA TACCGGTTTCG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAGG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAGC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1   MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPKAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

m588/a588    96.4% identity in 138 aa overlap

             10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588         MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKD GKPKAGKGTWRCQDGRNYTGS
             10      20      30      40      50      60

             70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588         FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
             70      80      90      100     110     120

             130     139
m588.pep    IMKCENGMIKEVKLPKNKX
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588        IMKCENGMIKEVKLPKNKX
             130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq.
1   atgcaacaaa aaatccggtt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgcgc attgaaaaag tgttgaaaca aaaagatttt gtcgaatcgg
101 cgggagtgaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgy ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcgaggaa aaaacggaag atacattgcc gcaacctgaa gcagaaacacc
251 atacggctg gcggtgtggt ctttctgtga ccatcaatat cccgttcctt

```



```

301 atcggatatgg tagggatgat gctaaaaggg ctgaattgga caccggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgcAAC
401 tttggctggc aatcccgttt taaaaagcg cgtgggcaag cattaaggcg
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcattgt gtattttgaa gcgggcgtga tgggtatcgg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgcgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaacg catcgtctgc gacggcatta tcgaaagcgg
801 cagcggttgg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggg gggcgcaaaa gtgttggcgg gcgcgtgat gaccgaaggg
901 agcgtggtgt accgcgcgcg gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgcttggctg attaagggcg attggacggt
1101 cgcactgatg caccgcgttg ccgttttggg gattgcctgc ccgtgcgcg
1151 tcggtctggc gaccctgcc gcgattatgg tcggcatggg caaagcggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtattgg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgcggtttat tacgttccc acagcggtt tgacgaagac
1351 gctttgtacc gcatcgccgc cgcgctcgag caaaacgccc cccaccgct
1401 cgcgcgcgcc atcgtctccg ccgcacaagc gcgcggtttg gagattccc
1451 ctgcacaaaa tgcgcaaacg gttgtcggag caggcattac cgccgaagt
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgcggaag ttttcagacg gcgtttggga aatcgccagt gcggttacc
1601 tatctgtaaa cggcaaacgg atcggcgcat tcgcactctc cgacgcgtt
1651 aaagccgata ccgccaagac cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggtg atatgagtcc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccc tggcgatgg
1851 cggcgacggc atcaacgacg cgcgcgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttctctaca
2051 atatattggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcgcgg caatggcggc aagctcgggt tcggtattgg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

```

g589.pep.
1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIKI IEKTYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSWG ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSCK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

```

m589.seq.
1  ATGCAACAAA AAATCCGTTT CCAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGTAA CTTCGCCAGC GAAGAGGCGC AGGTAGTGTG TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGCTGTGG CTGCTGTTC CACATCAACG CCCGTTCCCT

```

```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTACAA AAGCGCGTGG GCGAGCATTG AGGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCACTGGG TAAATTTTTG
601 GAACACCGTA CAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGCGGGGCG
851 GCAAAGTGTG GCGGGGCGCG TTAATGACCG AAGGCACTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GCGGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TCGCGCGCTA GCCGATAAAG
1001 CGGCTGCGGT ATTCGTGCGT GCCGTGCTGG GCATTGCGGT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CGCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTAAACA CGGTATTTGG
1201 TTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCAGCTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCCG
1301 TTTATTGCGT TCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCCGCCG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTGGACAT TCCCGCCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGGC ATTACCGCCG AAGTGGAAAG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TCGGGTCTCA GTCGATAACA
1601 AACCATCGG CGCATTGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCCT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCTCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTC
2051 CTCTCGCCGC GCTTGCTTTT TTAAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

m589.pep..

```

1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIARI IEKTYGAKKE KTEDTLPOPE AEHHIGWRLW LLFTINVPEFL
101 IGMAGMMIGR HDWMIPPLWQ FALASVQLW LAIPFYKSAW ASIKGGLANM
151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVEFEVGMV IGFVSLGKFL
201 EHRTKKSSLN SLGLLLKLTP TQNVQNRGE WKQLPIDQVQ IGDILIRANHG
251 ERIAADGIEE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSVVYR
301 ATQLGSQTQL GDMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTF
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEEA AHVDAVVDK TGTLEGSPO VAAVYCVFDS GFDEDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501 VKAGKAEFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFA LADALKADTA
551 EAIGRLKKNH IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601 KLKAAGKTVA MVDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIARI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

921

g589 MQQKIRFQIEAMTCQACASRIEKLNLKKDFVESAGVNFASEEAQVTFDGSKTSVADI
 10 20 30 40 50 60

 70 80 90 100 1 110

m589.pep IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVFPFLIGMAGMMIG-----RHDWMI
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

g589 IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMMLKGLNWRHDWMI
 70 80 90 100 110 120

 120 130 140 150 160 170

m589.pep PPLWQFALASVVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

g589 PPVWQFVLASIVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
 130 140 150 160 170 180

 180 190 200 210 220 230

m589.pep AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
 |:|||||:|||||:|||||:|||||:|||||:|||||:|||||

g589 AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
 190 200 210 220 230 240

 240 250 260 270 280 290

m589.pep IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKAGGKVLALMTEG
 |||||:|||||:|||||:|||||:|||||:|||||:|||||

g589 IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKAGGKVLALMTEG
 250 260 270 280 290 300

 300 310 320 330 340 350

m589.pep SVVYRATQLGSQTQLGDMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFFIVTWL
 |||||:|||||:|||||:|||||:|||||:|||||:|||||

g589 SVVYRAAQLGSQTLLGDMNALSEAQGSKAPIARVADKAAAVFVPTVVVGIALLTFFIVAWL
 310 320 330 340 350 360

922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAYVCVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEVEGVGLVKSAGKAEFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAIIGRLKKNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAIIGRLKKNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALVLSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLSNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

a589.seq

1	ATGCAACAAA	AAGTCCGTTT	CCAAATCGAA	GGCATGACCT	GCCAGGCATG
51	TGCTTCGCGC	ATTGAAAAAG	TGTTGAACAA	AAAAGATTTT	GTGCAATCGG
101	CGGGGGTAAA	CTTCGCCAGC	GAAGAGGCTC	AGGTAGTGT	TGACGACAGC
151	AAAACCTCAG	TAGCCGACAT	TGCCAAAATC	ATTGAGAAAA	CCGGTTACGG
201	CGCGAAGGAA	AAAACGGAAG	ATACATTGCC	GCAACCCGAA	GCAGAACACC
251	ATATCGGCTG	GAGGTTGTGG	CTTTTGCTGG	CCATCAATAT	CCCGTTCCTT
301	ATCGGTATGG	TAGGGATGAT	GCTAAAAGGG	CTGAATTGGA	CACGGCATGA
351	TTGGATGTTG	TCGCCCTTGT	TGCAGTTTGC	ATTGGCGAGT	GTGGTGCAGC
401	TTTGGCTGGC	GGTGCCATTT	TACAAAAGCG	CGTGGGCGAG	CATTAAAGGC
451	GGGCTGGCGA	ATATGGACGT	ACTCGTTACC	ATCGGCACGG	TCTCGATTTA
501	CCTGTATTCC	GTCTATATGC	TGTTTTTCAG	CCGCGACGCG	GCGTACGGTA
551	TGGCGCATGT	GTATTTTGAA	GTAGGCATAA	TGGTGATTGG	TTTGTGTGTA
601	CTGGGTAAAT	TTTGTGAACA	CCGCACCAA	AAATCCAGCC	TGAACAGCTT
651	GGGCTTGCTG	CTCAAACCTCA	CGCCAACCCA	AGTCAACGTG	CAACGCGATG
701	CGCAATGGCG	GCAGCTACCC	ATCGACCAAG	TGCAAAATCGG	CGACCTAATC
751	CGCGCAATC	ACGCGCAACG	CATTGCCGCC	GACGGCATCA	TAGAAAGCGG
801	CAGCGGCTGG	CGCGACGAAA	GCCATCTTAC	CGGCGAATCC	AATCCCAGAG
851	AGAAAAGGC	AGGCGGCAAA	GTATTGGCGG	GCGCGCTGAT	GACTGAAGGC
901	AGCGTGGTGT	ACCGCGCCGC	GCAGCTCGGC	AGCCAAACCC	TGCTCGGCGA
951	CATGATGAAC	GCGCTCTCCG	AAGCGCAAGG	CAGTAAAGCA	CCGATTGCGC
1001	GTGTGGCGGA	CAAGGCGGCG	GCGGTATTCT	TGCCTGCCGT	TGTGGGCATC
1051	GCACTTTTGA	CTTTTATCGC	TACTTGGCTG	ATTAAGGGCG	ATTGGACGCT
1101	CGCATTGATG	CACGCCGTCG	CCGTTTTGGT	GATTGCCTGC	CCGTGTGCAC

923

```
1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCGC CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCAGGC GCGCGGTTTG GAGATCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTGCGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAG CGGCAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCCGCGCT CGCCGCCGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTAAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCTGAAA CGGGTAAAAA TCGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

```
a589.pep
1  MQQKVRFOIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIARI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMMLKG LNWTRHDWML SPLQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIA PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKPQVAAYV CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAEHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKONLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*
```

m589/a589 94.9% identity in 725 aa overlap

```
10 20 30 40 50 60
m589.pep MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIARI
|||||
a589 MQQKVRFOIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIARI
10 20 30 40 50 60

70 80 90 100 110
m589.pep IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
|||||
a589 IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMVGMMMLKGLNWTRHDWML
70 80 90 100 110 120

120 130 140 150 160 170
m589.pep PPLWQFALASVVQLWLAIFFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
||
a589 SPLQFALASVVQLWLAVFFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
130 140 150 160 170 180

180 190 200 210 220 230
m589.pep AYGMHVYFEVGMVIGFVSLGKFLHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
|||||
a589 AYGMHVYFEVGIMVIGFVSLGKFLHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
190 200 210 220 230 240
```

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	240	250	260	270	280	290
m589.pep	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
a589	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
	250	260	270	280	290	300
	300	310	320	330	340	350
m589.pep	SVVYRATQLGSQTQLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VP	PAVVGIAL	LTFTVTWL	
a589	SVVYRATQLGSQTQLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VP	PAVVGIAL	LTFTVTWL	
	310	320	330	340	350	360
	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIA	CPCALGLATPAAIMVGM	GKAVKHGIWFKDAAAMEE	AAHVDA		
a589	IKGDWTVALMHAVAVLVIA	CPCALGLATPAAIMVGM	GKAVKHGIWFKDAAAMEE	AAHVDA		
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVA	AVYCV	PDSGF	DEDALYRIA	AAVEQNAAHPLARAI	VSAAQARGL
a589	VVLDKTGTLTEGSPQVA	AVYCV	PDSGF	DEDALYRIA	AAVEQNAAHPLARAI	VSAAQARGL
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQT	VVGAGITA	VEGVGLVKAGKAE	FAELALPKFLD	GVWDIASIVAVSV	DNKP
a589	DIPAAQNAQT	VVGAGITA	VEGVGLVKAGKAE	FAELALPKFLD	GVWDIASIVAVSV	DNKP
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAE	AIGRLKKNIDVYIM	SGDNQGTVEYVAKQLG	IAHAFGNMSPRDK		
a589	IGAFALADALKADTAE	AIGRLKKNIDVYIM	SGDNQGTVEYVAKQLG	IAHAFGNMSPRDK		
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAM	VGDGINDAPALAAAN	VSFAMKGGADVAEHT	ASATLMQHSVNQLA		
a589	AAEVQKLKAAGKTVAM	VGDGINDAPALAAAN	VSFAMKGGADVAEHT	ASATLMQHSVNQLA		
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQN	LFFAFFYNILGIPLA	ALGFLNPVIAGAAMA	ASSSVSVLSNALRLK		
a589	DALLVSQATLKNIKQN	LFFAFFYNILGIPLA	ALGFLNPVIAGAAMA	ASSSVSVLSNALRLK		
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:
g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaacg agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtggttga acagccggtt acgctggtta accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaag ttttgaacg ctttttggg aaacaagttc
401 cggtttcctt tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc cgcgttttca ttatgaagaa ctgtcgggca tcaggctgca

```

```

501 ctgggaaggc ctgacggggg aaacgggtta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccc cgtttgaaaa agcgcatctc gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatctt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaat gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcggggcgcg ttatcgaca gcaagggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaataatc ggcgcgtgg acatccatat
951 cgctgcccga cactcgcg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgcgg cagtcaaaag cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaatct tccgtttcac cctgcctcag ggaataattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaa
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttgccggt aagtcaggct ggaatatctt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatgggtggc agtacggtcc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cctttaaaaa caacgcctg aagttaaacg ggaataacgt gcaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttcggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVKAES LTQQQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKPEL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEPKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDVNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMKKEDLN
401 QLGLMLKKTE ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIA
451 INETLRIMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 ..TGTTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAATACC TGCCGGATAA CCTGAAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCAGCG AGGCGTACAT TGAAACCGAG TTCAAATACG CGCCTGAAAC
201 GGA AAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG.CTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTGTGTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAG TGCAATTCGA TTCGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
601 ACCGATTGTC AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCAAC AACAATCCCG TATTGGACAT
951 TAAACTTTC CGATTACGC TGCCATCGGG AAAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTGGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590.pep..(partial)

```
1  .WFTSMETTVI RLKPELLNNA RLYLPDNLKT VLEQPVTLVN HITHGPFAGG
51  FGTQAYIETE PKYAPETEKV LERFFGKQVP ASLANTVYFN GSGKMEVSVP
101 AFDYEELSGI XLHWEXLTGE TVYQKGPKSY RNYDAPLFFK IKLADKGDAA
151 FEKVHFDSET SDGINPLALG SSNLTLEKFS LEWKEGVDYN VKLNELVNLV
201 TDLQIGAFIN PNGSIAPSKI EVGKLAFSTK TGESGAFINS EGQFRFDTLV
251 YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMT E QIRNDLIAA
301 VKGEASGLFT NNPVLDIKTF RFTLPSGKID VGGKIMFKDM KKEDLNQLGL
351 MLKKTEADIR MSIPQKMLED LAVSQAGNIF SVNAEDEAEG RASLDDINET
401 LRLMVDSTVQ SMAREKYLT L NGDQIDTAIS LKNNQLKING KTLQNEPEPD
451 FDEGGMVSEP QQ*
```

m590 / g590 93.1% identity in 462 aa overlap

```

                                     10      20      30
m590.pep                          WFTSMETTVI RLKPELLNNA RLYLPDNLKT
g590      VKAESLTQQQKILQKTGFLT VESHQYDRGWFTSTETT VIRLKPPELLHNAQKYLDPNLKI
          30      40      50      60      70      80

          40      50      60      70      80      90
m590.pep  VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
g590      VLEQPVTLVNHITHGPFAGGFGTQAHIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
          90     100     110     120     130     140

          100     110     120     130     140     150
m590.pep  GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGPKSYRNGYDAPLFKIKLADKGDAA
g590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGPKSYRNSYDAPLFKIKLADKGDAA
          150     160     170     180     190     200

          160     170     180     190     200     210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
g590      FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
          210     220     230     240     250     260

          220     230     240     250     260     270
m590.pep  PNGSIAPSKIEVGKLAFSTKTGESGAFINSEGGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
g590      PNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRFDTLVYGDEKYGPLDIHIAAEHLDA
          270     280     290     300     310     320

          280     290     300     310     320     330
m590.pep  SALTVLKRKFAQISAKKMTBEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
g590      SALTVLKRKFAQISAKKMTBEEQIRNDLIAAVKGDASGLFTHDPVLNLIKIFRFTLPQGKID
          330     340     350     360     370     380

          340     350     360     370     380     390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
g590      VGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQKMLEDLAVSQAGNIFSVNAEDEARA
          390     400     410     420     430     440

          400     410     420     430     440     450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTNGDQIDTAISLKNQLKINGKTLQNEPEPD
g590      RASLADINETLRLMVDSTVQSMAREKYLTLDGNQIDTVISLKNALKLINGKTLQNEPDPP
          450     460     470     480     490     500

          460
m590.pep  FDEGGMVS-EPQQX
          ||| ||| :|
g590      FDEGDMVSGQPHX
          510
```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGAT AACCTGAAAA
251 CAGTGTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCTT
301 TTTGCCGCG GATTCCGGCAG GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTTGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTT CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGATGCCG CGTTTGAAAA AGTGCATTTC GATTCCGAAA CTTCAGACGG
651 CATCAACCCG CTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACCTG
751 GTCATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTCAACCA
851 AGACCGGGA ATCGGGGCGG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCCTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAATACTT TCCGATTCAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGTAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAA ATGCTGGAAG ACTTGCGCGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE AGFLTVESHQ
51  YERGWFSTSE TTVIRLKPPEL LHNAQKYLDP NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDVNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRETLPS GKIDVGKIM FKDMKKEDLN
401 QLGLMLKKE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNQNL KLNKGTQLQNE
501 PEPDFDEGGM VSEPQQ*
```

m590/a590 97.8% identity in 462 aa overlap

```
m590.pep
10 20 30
WFTSMETTIVIRLKPPELLNNARKYLPDNLKT
|||||
a590 VKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTETTIVIRLKPPELLHNAQKYLDPNLKT
30 40 50 60 70 80

40 50 60 70 80 90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
|||||
a590 VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
90 100 110 120 130 140

100 110 120 130 140 150
m590.pep GSGKMEVSVPAFDYEEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
```

928

```
|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAfstktGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAfstktGESGAFIDSEGQFRFGTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPsgKID
          |||||
a590      SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLPsgKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTlNGDQIDTAISLKNQLKLNGKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTlNGDQIDTAISLKNQLKLNGKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEPQQX
          |||||
a590      FDEGGMVSEPQQX
          510
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```
1  ATGAAAAAAC CTTTGATTTC GGTTCGGCCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGGCG GATTCCGGCA GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGGCCTCGAA ACGGAAAAAG TTCTGGAACG CTTTTTGGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAATGGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGAAGGCG CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCAGATGCCG CGTTTGAAAA AGTGCAATTC GATTGGGAAA CTTGAGACGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAAAT GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 GTCAAATCTG TTACCGATTG GCAGATTGCG GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCGTTTTC
901 GATACATCGG TGTACGGCGA TGAATAATAC GGCCCGCTGG ACATCCATAT
951 CGTGCCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101 CGTATTGGAC ATTAATACTT TCCGATTAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTTTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
```

1251 TCCCCAAAAA ATGCTGGAAG ACTTGCGCGT CAGTCAAGCA GGCAATATTT
 1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
 1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
 1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
 1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
 1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
 1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE TGFLTVESHO
 51 YERGWFSTME TTIVRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
 101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
 151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
 201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL
 251 VNLVTDLQIG AFINPNNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
 301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KKKFAQISAK KMTEEQIRND
 351 LIAAVKGEAS GLFTNNPVLD IKTRFTLPSP GKIDVGGKIM FKDMKKEDLN
 401 QLGLMLKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
 451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNQNL KLNKGTILQNE
 501 PEPDFDEGGM VSEPPQ*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	10	20	30	40	50	60
g590	10	20	30	40	50	60
m590-1.pep	70	80	90	100	110	120
g590	70	80	90	100	110	120
m590-1.pep	130	140	150	160	170	180
g590	130	140	150	160	170	180
m590-1.pep	190	200	210	220	230	240
g590	190	200	210	220	230	240
m590-1.pep	250	260	270	280	290	300
g590	250	260	270	280	290	300
m590-1.pep	310	320	330	340	350	360
g590	310	320	330	340	350	360
m590-1.pep	370	380	390	400	410	420
g590	370	380	390	400	410	420
m590-1.pep	430	440	450	460	470	480
g590	430	440	450	460	470	480
m590-1.pep	490	500	510			
g590	490	500	510			

g590	TVISLKNALKLNKGLTQNEPDPDFDEGDMVSGQPHX	490	500	510	
a590/m590-1	98.3% identity in 516 aa overlap				
a590.pep	10 20 30 40 50 60				
m590-1	10 20 30 40 50 60				
a590.pep	70 80 90 100 110 120				
m590-1	70 80 90 100 110 120				
a590.pep	130 140 150 160 170 180				
m590-1	130 140 150 160 170 180				
a590.pep	190 200 210 220 230 240				
m590-1	190 200 210 220 230 240				
a590.pep	250 260 270 280 290 300				
m590-1	250 260 270 280 290 300				
a590.pep	310 320 330 340 350 360				
m590-1	310 320 330 340 350 360				
a590.pep	370 380 390 400 410 420				
m590-1	370 380 390 400 410 420				
a590.pep	430 440 450 460 470 480				
m590-1	430 440 450 460 470 480				
a590.pep	490 500 510				
m590-1	490 500 510				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

```
g591.seq
  1  TTGCAAACCC  TTCTAGCTTT  TATCTTCGCC  ATCTTGATT  TGGTCAGCCT
51  GCACGAATTC  GGACACTACA  TCGTGCSCAG  GTTGTGCGGC  GTCAAGGTTG
101 TCGGTTTTC  CGCTCGCTTC  GGCAAAACCG  TTTTCACCG  AAGCGCGCG
151 GACACCGAAT  GGTGCCTCG  CCCGATTCG  TTGGCGCGCT  ACATCAAAAT
201 GGTGATACG  CGCGAAGCG  AAGTATCAGA  AGCGGATTA  CCCTACGCTT
251 TTGCAAAAC  ACACCCGCG  AAGCGCATCG  CCATCGTCTG  CGCCGGTTCG
301 CTGACCAAC  TCGCActgac  ggTTTTCGT  TACGGATCG  cctTttcctt
351 cggcgtaaCC  GAACTGCGGC  CCTatgtcgg  cacagtcgaa  ccgcaacacc
```

```

401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGc ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCGg ggcAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCCTCA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTACAG
1051 CATATTTCG GCGCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1 LQTLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRGR
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFGALMM LMMAAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51 GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCTCAAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCCTCA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCG GCGCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRG
51 DTEWCLAPIP LGGYVKMVD REGEVSEADL PYAFDKQHFA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV PDIARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPAEGA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMAVAFFND VTRLIG*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRG DTEWCLAPIP					
g591	LQTLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRG DTEWCLAPIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m591.pep	LGGYVKMVD TREGEVSEADLPYAFDKQHFA KRIAIVAAGPLTNLALAVLL YGLSFSFGVT					
g591	LGGYVKMVD TREGEVSEADLPYAFDKQHFA KRIAIVAAGPLTNLALAVLL YGLSFSFGVT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m591.pep	ELRPYVGTV EPDTIARAGF QSGDKIQSVNGTPVADWGS AQTEIVLNLEAGKVAVGVQTA					
g591	ELRPYVGTV EPDTVAARTGFQSGDKIQSVNGVSVQDWSSAQTEIVLNLEAGKVAVGVQTA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m591.pep	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPAEGAGL KPGDRLTA					
g591	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPAEGAGL KPGDRLTA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
g591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRFAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
g591	PDRAWDAQIRRSYRPSVVRFAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
g591	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTVIEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLIGX					
g591	GLRFGALMMLMAAAFFNDVTRLIGX					
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:
a591.seq

```

1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCTTGATT TGGTCAGCCT
51 GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGGGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACAG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCGGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGCA AACCCATCGC CTGATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCATACCGC CGACATCCG CCCGATACG
851 TCGAACAGCC CGACCACACC CTGATCGGCG GCGTCGGCCT CCGTCCGCGC
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCGCTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCCTCA ATTTTTCGGC AACTAATCA GCGGCAACGC CTCCGTCAGC
1051 CATATTTCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCGCA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTT GGCATGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCGG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGT TCGGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1 LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRK
51 DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GKVAVGVQT A SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGL M PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLYER AGQHTADIR PDTVEQPDHT LIGRVGLRFPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGLVNL L PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMMAVAFEND VTRLLG*

```

m591/a591 99.6% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRGDTEWCLAPIP					
a591	LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRGDTEWCLAPIP					
	10	20	30	40	50	60
m591.pep	LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGPLTNLALAVLL YGLSFSFGVT					
a591	LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGPLTNLALAVLL YGLSFSFGVT					
	70	80	90	100	110	120
m591.pep	ELRPYVGTV E PDTIARAGF QSGDKIQSVN GTPVADWGS AQTEIVLNLEA GKVAVGVQT A					
a591	ELRPYVGTV E PDTIARAGF QSGDKIQSVN GTPVADWGS AQTEIVLNLEA GKVAVGVQT A					
	130	140	150	160	170	180
m591.pep	SGAQTVRTID AAGTPEAGKIAKNQGYIGL MPFKITTVAGGVEKGSPEAKAGL KPGDRLTA					
a591	SGAQTVRTID AAGTPEAGKIAKNQGYIGL MPFKITTVAGGVEKGSPEAKAGL KPGDRLTA					
	190	200	210	220	230	240
m591.pep	SGAQTVRTID AAGTPEAGKIAKNQGYIGL MPFKITTVAGGVEKGSPEAKAGL KPGDRLTA					
a591	SGAQTVRTID AAGTPEAGKIAKNQGYIGL MPFKITTVAGGVEKGSPEAKAGL KPGDRLTA					

934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLNLPVPVLDGGHLVFTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVSISLGVNLNLPVPVLDGGHLVFTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51  cgcggcagca ggcggcttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgcgc cgcgcgcgcg cgaagtgaac caccctgttt cgcaaggatg
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 cgccttcatt catcttgatt taccaacagc cttatggcga tttgagcggg
301 gcgcgcgtga cgcaggcgcg gattgtcagc caagtggggc aatggggcgc
351 ggggtttcct gccgtcatcc tggttatggt tgccttttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctggtt ttggcgtggg tctatttcgg
501 cgcggttgcc aatgtgcctt tggctcggga tatggcggat atggcgatgg
551 gcatcatggc gtggatcaac ctgcgcgcca tcctgctgct ctcgccattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFQIF SGAFKFDAAA GLLGLISQ TMMGIKRL YSNEAGMGS
51  PNAAAAEVK HPVSQGMQM LGVFVDTIIV CSCTAFIILI YQPPYGDLSG
101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQPIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTTTC TCGGGCGCGT TCAAATTCGA
51  CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCCTG TATTCCAACG AGGCGGGTAT GGGTTCGCGC
151 CCGAACGCGC CCGCGCGCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTGATAC CATCATCGTT TGTCTTGCA
251 CCGCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 CCGCGCTGTA CGCAGGCGGC GATTGTGAGC CAAGTGGGGC AATGGGCGGC
351 GGGCTTCCTC GCCGTCATCC TGTATTATGT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTATCAA AAGCCATTGG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCGG
501 CGCGGTTGCG AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTGCGCA TCCTGCTGCT CTCGCCCTTG

```


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601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCGAGTTC AACTTTCCG AACATCCGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDIIIV CSCTAFIILI YQOPYGDL SG
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQOPYGDL SGAALTQAAIVSQVGQWAGFL					
g592	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQOPYGDL SGAALTQAAIVSQVGQWAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLV LAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLV LAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEFKLSHPGLKRRIKSDVW					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEFKLSHPGLKRRIKSDVW					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGGCGGGTAT GGGTCCGCG
 151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTATTATGT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCG TATGCTGGT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTGACC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCGAGTTC AACTTTCCG AACATCCGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDIIIV CSCTAFIILI YQOPYGDL SG
 101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAGGLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAGGLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1   atgcttgaac tgaacggact ctgcaaatgc ttcggcgcca aaacggctcgc
51  cgacaacatc tgcctgactg tcgggcccgg caaaatactc gccgtactgg
101 ggccggtcggg ctgcccgaac tccaccctgc tgaatatgat tgcgggcatc
151 gtccggccgg acggcgccga aattcggctg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaagcgcga agccgaacgc ctgccttgtg cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcactggcgc gcgctttggt tgcgcgccct
451 tccctgctgt tgcctgatga atcgttttcc agtttggaac cgcatttcgc
501 cgaccggctg cgccgtatga ccgcccgaac catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcac tcgcccgaag aggcctgcac ggcggcggac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgcccga
651 aaccttgatt caaacgcctg ccggcggtga ggtcgccctg ctgatggggc
701 gcccaatac cgacgatgac cgccatattc cgcaaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgctc gcctgcccga
801 ctgctccggg ctttccgccc tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccgaaa cggtacggtc
901 cgcattccgg tcgatgaagg gcgtatcgct cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1   MLELNLGCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNQTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1   ATGCTTGAAC TGAACGGACT CTGCAACGCG TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GGCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGAGAAA ACATTACCCG

```

```

201 TATGCCGCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCA TATGAGTGCG CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AACTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTCC AGTTGGACA CGCATTTGCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GGCAGCATCC
551 CTGCCGTTT GGTAAACGAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTCGCCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep  ..
          1 MLELNLCKR FGKNTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
          51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAFLGLKM
          101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
          151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
          201 EIAVMHKGRI LQYGTPELTV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
          251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWLNLMRHA GAVSGKDTV
          301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGKNTVADNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
	:					
g593	MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPP EKRRISLMFQDYALFPHMSALENAFLGLKM QKMPKAEAEER LAMAALAEVG					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKM QKMPKAEAEER LALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRI LQYGTPELTVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIAVMHEGKILQCGTPETLIQTPAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240

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	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDDGMECRVLSRTCLPESFSLSVLHPEHGILWLNLDLDM-RHAGAVSGKDTV					
	: : : : : : : : : : : : : : : : : :					
g593	RHIPQNAVCLDNHGTECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISGNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	: : : :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGCGTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TCGGGGCATC
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201 TATGCCGCCC GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCA CTGGAATGCG CGGCATTCCG TTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAATACG AGGCGCACCG CAAGCCTGAN AAACCTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTTGGACGA ATCGTTTCC AGTTTGGACA CGCATTGCG
501 CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GGCGGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCGAAG AGGCCTGCAC GGCGGCAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAATC CTTCAATGCG GTACGCCCGA
651 AACCTTGTTT CAAACGCTG CCGCGTGCA GGTGCGCCAT CTGATGGGGC
701 TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTGCCCGA
801 ATCGTTCAGC CTGTCCTGCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAACAGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAES LAMAALAEVG LENEHRKPX KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDD RHIPQHAVRF
251 DDGMECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
a593	MLELNLCKRFGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEERLAMAALAEVG					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
a593	LENEAHRKPXKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTADEIAVMHKGRILQYGTPTLVKTPSCVQVARLMGLPNTDDN					

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```

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a593  GGIPAVLVTHSPEEACTAADEIAVMHEGKILQCGTPETLVQTPAGVQVAHLMGLPNTDDD
      190      200      210      220      230      240

      250      260      270      280      290      300
m593.pep RHIPQHAVRFDQDGMECRVLSRTCLPESFSLSVLHPEHGILWLNLDMRHAGAVSGKDTVR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a593  RHIPQHAVRFDQDGMECRVLSRTCLPESFSLSVLHPEHGILWLNLDMPHAGEISGNDTVR
      250      260      270      280      290      300

      310
m593.pep IHIEEREIVRFRX
|||||:|||||:
a593  IHIEDREIVRFRX
      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

```

g594.seq..
1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgTTTT agcatactcc ggctgctgtt ccgcacgga attgggatcg
101 gtaagttcgc cgttcaggcc tttcaggtct ttaagctgct gatctgtacg
151 gttgagcacc caaatcgggt tgccttgcca ctcggcggtc agcagctgac
201 ccgcttcgat tttactgaca tccacctcga cggcagcacc ggaggccttg
251 gctttttccg aagggaAAAA actggccaca aacggcgttg ccacacccaa
301 tgctgccact ccgcccgcgc cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttggt gatttcttga ttatccatta ttcagtcgtc ctaatatTTT
401 gggaatgccg agccattaaa cattgcaatt ttaccagtt tgcagtgata
451 ctcaaagcat tatttaaaat aaggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

```

g594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCOETAAAVV DFLIIHYSV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

```

m594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGGCGCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCgcgc CGCAGGTGCG GAGTGTcAGG AAACGGCGGC
351 GGCCGTtGTT GATTtCTTGA TTATCCATTA TTCAGTcGTC CTAATATTTT
401 GGGAATACCG AGCCATTAaA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTtAAAAA AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

```

m594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECOETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRCQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```
a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGCGCCTTG
251 GCTTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTGAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAG CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```
a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*
```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```
g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttgggttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcggtt cggtcggtat cgccgtcaac
```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgtgat ggtggtggac gaacgcgaaa atatcgccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaa aactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacga accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttcac cgtatcgaac
701 acgcccttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcgaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg caaaaaaca agccttggtg gaaaaaacgg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcacaaa
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942

1051 gacggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga cttgccccaa cttcgcgga
 1151 tactcggctt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGI AVN
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
 151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGCGGAGAAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAATAT CGCCGTCAC
 151 GACAATGCCT GCGAACCAGT GGAAGTACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTC AAGCGAGGTT AAAGAGCTGG TGGCGAAAAC
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
 551 CCCTGTTGCG CGACACCGCG GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCGGTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
 751 AAAGTATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTTGG
 801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACCT ATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 GTTCCGTCCG CTGATCGAGG CAAAAACAA AGCCTTGTG GAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCTCTT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSI AVN
 51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSI	AVNDNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGI	AVNDNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

m595.pep	VPSGQVVFN	IKNN	SGRKL	EWI	LKGM	VVDER	ENI	APGL	SDKMT	VTLL	PG	YEMT	CGLLT
	: :												
g595	VPSGQVVFN	IKNN	SGRKL	EWI	LKGM	VVDER	ENI	APGL	SDKMN	RNRL	LPGE	YEMT	CGLLT
	70	80	90	100	110	120							
	130	140	150	160	170	180							
m595.pep	NPRGKLV	VTDSG	FKDTA	NEAD	LEKLS	QPLAD	YKAY	VQGE	VKEL	VAKT	TKTF	EAVK	AGDIE
	: :												
g595	NPRGKLV	VADSG	FKDTA	NEAD	LEKL	PQPLA	DYKAY	VQGE	VKELA	AKT	TKTF	EAVK	AGDIE
	130	140	150	160	170	180							
	190	200	210	220	230	240							
m595.pep	KAKSLF	ADTRV	HYERIE	PIAEL	FSELD	PVIDA	REDDF	KDGAK	DAGFT	GFHRI	EYAL	VWEK	
g595	KAKSLF	AA TRV	HYERIE	PIAEL	FSELD	PVIDA	CEDDF	KDGAK	DAGFT	GFHRI	EHAL	VWEK	
	190	200	210	220	230	240							
	250	260	270	280	290	300							
m595.pep	DVSGVKE	IAAKL	MTDVE	ALQKE	IDALA	FP	PGKV	VGGAS	ELIEE	VAGS	KISGE	EDRY	SHTD
	: :												
g595	DVSGVK	ETAAKL	MTDVE	ALQKE	IDALA	FP	PGKV	VGGAS	ELIEE	AAGS	KISGE	EDRY	SHTD
	250	260	270	280	290	300							
	310	320	330	340	350	360							
m595.pep	LSDFQAN	ADGSK	KIVDL	FRPL	IEAKN	KALLE	KTDT	NFKQ	VNEI	LAKY	RTKD	GFET	YDKLG
g595	LSDFQAN	ADGSK	KIVDL	FRPL	IEAKN	KALLE	KTDT	NFKQ	VNEI	LAKY	RTKD	GFET	YDKLS
	310	320	330	340	350	360							
	370	380	389										
m595.pep	EADRKA	LQAS	INALA	EDLA	QLRG	ILGL	KX						
g595	EADRKA	LQAP	INALA	EDLA	QLRG	ILGL	KX						
	370	380											

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

a595.seq

1	ATGAGAAAAT	TCAATTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCGCG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGCGGGTT	CGGTCAGTAT	CGCCGCTCAAC
151	GACAAATGCCT	GCGAACCAGT	GGAAGCTGACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGTGTAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGAT	CCGTCACCCT	GTTGCCGGGC	GAATACGAAA	TGACTTTGCGG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAAACGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAG	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTC	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCAATCG	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTATC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAGAA	GAGCTGTCCG	CGAGTAAGGA	AATTGACGGC
751	AAACTGTATG	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCAATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGGCG	GTCCGAAGTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATACAGC	TGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGCAT	TCCAAGCCAA	TGTGGACCGA	TCGAAAAAAA	TCGTTCGATT
951	TTTCGCTCCG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTGT	GAAAAAACCC
1001	ATACCAACTT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTTG	AACTCAACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCTCTT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGCGCT	GAATAATA			

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

a595.pep
1 MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQ TAN EGGSVSI AVN
51 DNACEPMELT VPSGQVVFNI KNSGRKLEW EILKGMVVD ERENIAPGLS

101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTAHSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSIIVNDNACEPMELT					
a595	MRKFNLTAHSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSIIVNDNACEPMELT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m595.pep	VPSGQVVFNIKNNNGRKLWEILKGVMMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
a595	VPSGQVVFNIKNNNGRKLWEILKGVMMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m595.pep	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
a595	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m595.pep	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
a595	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m595.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
a595	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m595.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFEYTDKLG					
a595	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFEYTDKLG					
	310	320	330	340	350	360
	370	380	389			
m595.pep	EADRKALQASINALAEDLAQLRGILGLKX					
a595	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1  ..atgctgctct tggacgagcc gaccaaccac ttggatgctg aatcggtgga
51  atggctggag caattcctcg tgcgttccc cggcacagtg gtcgcggttaa
101 cgcacgaccg ctacttcctc gacaacgcgc cgaatggat ttggaactc
151 gaccgaggac acggcattcc gtggaaggc aattactcgt cttgctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

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945

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451   ttcggcgata aagtgtgat tgacggtttg agcttcaaag tgccggcggg
501   cgcgattgtc ggcacatcgc gcccgaaacg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcga agtgaaaatc
601   gggcaaaccg tgaaaatgag cttgattgac caaagccgcg aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggctgc gatattttgc
701   aggtcggaca gtttgaaatc cccgccccgc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801   acgcggccgt ctgcacttgg caaaaacctt gttgggcgcg ggcaatgtgt
851   tgctgtctga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgcg
901   ttggaagacg cattgttgga atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactcaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   .MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLENEAKSE AARVKAMKQE LEWVRQNAKG
101 ROAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLNE VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGFQEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRLGKEG AKPKRIKYK VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCTAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTG AAGATATTTT CCTTTCTTTC TTCCCGGGCG
101 CGAAAATCGG CCGTCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CCGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 GCGCAGGTTT GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCC
451 GCCGACGCGC TCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTGTGTC
501 CCGCGGTGAA AAACGCCGCG TTGCCTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGCA CAGTCGTGTC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAAAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGCCGCCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTGTA AATGTTTCCA
1001 AATCGTTCGG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCC
1051 CCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCCTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCGCGACAT
1251 TTTGCAGGTT GGTCAAGTTG AAATCCCGC CCGCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351 GGCGAACGCG GTCGCTGCA CTTGGCAAAA ACCTTGTTGA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGTC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTCCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGCGCAC TCTAAATGGG TGTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCAGTAAC GCGTTAA

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This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

```

1 MSQQYVYSML RVSKVVPPOK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51 RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAAVRK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGLHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYEADEKRR LGEEGAKPKR
551 IKYKPVTR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

	160	170	180	190	200	210
m596.pep	LPEWDAKIDNL	SGGEKRRVALCKLL	LSKPDMLLD	DEPTNHLDAES	VEWLEQFLVR	FPGTV
g596				MLLD	DEPTNHLDAES	VEWLEQFLVR
				10	20	30
	220	230	240	250	260	270
m596.pep	VAVTHDRYFLDNAAEW	ILELDRGHGIPWKGNYSW	LEQKEKRLNEAKSEAAVR	KAMKQE		
g596	VAVTHDRYFLDNAAEW	ILELDRGHGIPWKGNYSW	LEQKEKRLNEAKSEAAVR	KAMKQE		
	40	50	60	70	80	90
	280	290	300	310	320	330
m596.pep	LEWVRQNAKGRQAKS	KARLARFEEMS	SNYEYQKRNETQEIFIPVAER	LGNEVIEFVN	VS	KS
g596	LEWVRQNAKGRQAKP	KARLARFEEMS	SNYEYQKRNETQEIFIPVAER	LGNEVIEFVN	VS	KS
	100	110	120	130	140	150
	340	350	360	370	380	390
m596.pep	FGDKVLIDDLSEKVP	PAGAI	VGIIGP	NGAGKSTLFK	MISGKEQPDG	GEVKIGQTVK
g596	FGDKVLIDGLSEKVP	PAGAI	VGIIGP	NGAGKSTLFK	MISGKEQPDG	GEVKIGQTVK
	160	170	180	190	200	210
	400	410	420	430	440	450
m596.pep	QSREGLQNDKTVFDN	IAEGRDILQVGQFEI	PARQYLGRFNFKGSD	QSKIAGQLSG	GERGR	
g596	QSREGLQNDKTVFDN	IAEGRDILQVGQFEI	PARQYLGRFNFKGSD	QSKIARQLSG	GERGR	
	220	230	240	250	260	270

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLD	DEPSNDLDVETL	RALEDALLEFAGSVMVISHDRWFLDRIATHIL			
g596	LHLAKTLLGGGNVLLLD	DEPSNDLDVETL	RALEDALLEFAGSVMVISHDRWFLDRIATHIL			
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGN	QYEADKKRRLG	EAGAKPKRIKYKPVTRX		
g596	ACEGDSKWVFFDGN	QYEADKKRRLG	EAGAKPKRIKYKPVTRX		
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTCTTTTC TTCCCGGGCG
101 CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGG TAAAGAATTG GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTGGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GCGATTTTAC GCGTTGGCGG AAGAGCAGGG GCGTTTGGA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAATCGCT
451 GCCGACGCGC TCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGCTTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGAAAAAC GAGGCGAAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTCA AGCCAAGTCC AAAGCGCGTT TGGCGCGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTTCG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTGCGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCGC CCGCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCCGCG
1351 GGCGAACGCG GACGTTTGCA CTGGCAAAA ACCTTGTGTT GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG CTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCAAATGGG TGTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHELEIA
151 ADALRLFEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAAVRK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNIEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451 GERGLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGN YQEYADKKRR LGEEGTEPKR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

948

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTLFKMGISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFKMGISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGRHLAKTLLGGNVLLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGRHLAKTLLGGNVLLLDEPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYQYEADKKRR					
a596	ETLRALEDALLEFAGSMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYQYEADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGTPKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTACAGCA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTGGGACAA ATTCCAAAAA

```

```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTCGTAT CGGGGAAC TAACAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGAAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAG GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAaagcc
601 gaacaccgCA TtcaggAtgc ggAagcaaaa agaAAATTGG CTGAagcCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGCGCAG CAGAAAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACggtT TCAGCCGCAT
801 GCAGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GCGAGAACC GAGCGGcgC GATGTTTGA AAGCGGTGT TATTCCACT
901 GCGCTGCAA CGGTTGAAAG CATTGCGCg gGAACggtaa GCTATGCGGA
951 cgaGTTGAC GGCTACGGCA AAGTGGTCGT GATCGATCAC GGCAGAACT
1001 ACATCAGCAT CTATGCCGT TTGAGCGAAA TTTCCGCCG CAAGGGTTAT
1051 ACGGTTCGCG CAGGAAGCAA AATCGGCACG AGCGGGTCG TCGCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTGCGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.pep

```

1 MLLHVSNSLK QLQEEIRQ ERIQERIRQA RGNLASVNRK QREAWDKFKQ
51 LNTLNRLKT EVAATKAQIS RFVSGNYKNS RPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKQNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ QKAEARRAEM SNLTAEARNI
251 QAPVSMGTGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLRIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAACAGCG CGAGGCTTGG GACAAAGTCC AAAAAGTCAA TACCGAGCTG
151 AACCCTTTGA AAACGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTCC
251 TGA AAAACGCG CGAACCGGGT CAGAAAAACC GCTTTTTCG TTATACGCGT
301 TATGTAACG CCTCCAATCG GGAAGTTGTC AAGGATTGG AAAAACAGCA
351 GAAGGCTTTG CGCGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAT TCAGGCAAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAAGCCGC AGACAGAAAT CCAAATCGC
501 CAAAGATGCC CGAAAATGCG TGGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTTG GAGAAGAAAA AGGCCGAACA CCGCATTCAG
601 GATCGCGAAG CAAAAGAAAA ATTGGCTGAA GCCAGACTGG GCGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCCGGCAG AACCGGAGCG
851 GCGGCGATAT TTGGAAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTT CGCCGGGAAC GGTAAGCTAT CCGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTCG ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAATA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEEIRQ ERIQARGNLA SVNKRQREAW DKFQKLNTL
51 NRLKTEVAAT KAQISRFSV NYKNSQPNV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREV KDLKQKQKAL AVQEQKINNE LARLKKIQAN VQSLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKQNE QQLNKLNSNL EKKKAEHRIQ
201 DAEAKRKLAE ARLAAAARAR KEAAQKQKAE RRAEMSNLTA EDNRNIQAPSV
251 MGGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELDSYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEEGLYLQI RYQGQVLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLSVNRKQREAWDKFQKLNTELNLRLKT					
m597	MLLHVSNSLKQLQEERIRQ-----ARGNLSVNRKQREAWDKFQKLNTELNLRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEOKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEOKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIIQAPSVMGIGSADGFSRMQGRLLKPKVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIIQAPSVMGIGSADGFSRMQGRLLKPKVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVKGGMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

1	ATGCTGCTTC	ATGTCAGCAA	TTCCTCAAG	CAGCTTCAGG	AAGAGCGTAT
51	CCGCCAAGAA	CGTATCCGCC	AAGAGCGTAT	CCGTCAGGCG	CGCGGCAACC
101	TTGCTTCCGT	CAACCGCAAA	CAGCGCGAGG	CTTGGGACAA	GTTCCAAAAA
151	CTCAATACCG	AGCTGAACCG	TTTGAAAACG	GAAGTCGCCG	CTACGAAAGC
201	GCAGATTTC	CGTTTCGTAT	CGGGGAACTA	TAAAAACAGC	CAGCCGAATG
251	CGGTTGCCCT	GTTCTTGAAA	AACGCCGAAC	CGGGTCAGAA	AAACCGCTTT
301	TTGCGTTATA	CGCGTTATGT	AAACGCCTCC	AATCGGGAAG	TTGTCAAGGA
351	TTTGAAAAA	CAGCAGAAGG	CTTTGGCGGT	ACAAGAGCAG	AAAATCAACA
401	ATGAGCTTGC	CCGTTTGAAG	AAAATTCAAG	CAAACGTGCA	ATCCCTGCTG
451	AAAAAACAGG	GTGTAACCGA	TGCGGCGGAA	CAGACGGAAA	GCCGCAGACA
501	GAATGCCAAA	ATCGCCAAAG	ATGCCCGAAA	ACTGCTGGAA	CAGAAAGGGA
551	ACGAGCAGCA	GCTGAACAAG	CTCTTGAGCA	ATTTGGAGAA	GAAAAAGGCC
601	GAACACCGCA	TTCAAGATGC	GGAAGCAAAA	AGAAAATTGG	CTGAAGCCAG
651	ACTGGCGGCA	GCCGAAAAAG	CCAGAAAAAG	AGCGGCGCAG	CAGAAGGCTG
701	AAGCACGACG	TGCGGAAATG	TCCAACCTGA	CCGCGGAAGA	CAGGAACATC
751	CAAGCGCCTT	CGGTTATGGG	TATCGGCAGT	GCCGACGGTT	TCAGCCGCAT
801	GCAAGGACGT	TTGAAAAAAC	CGGTTGACGG	TGTGCCGACC	GGACTTTTCG
851	GGCAGAACCG	GAGCGGCGGC	GATGTTTGA	AAGGCGTGT	CTATTCCACT
901	GCACCGGCAA	CGGTTGAAAG	CATTGCGCCG	GGAACGGTAA	GCTATGCGGA

951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GCGGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTCGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pap
1  MLLHVSNSLK QLQEEIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51  LNTLNRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEFGQKNRF
101 LRYTRYVNAS NREVVKDLEK QKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISYIAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQQG VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

```

m597/a597 98.5% identity in 389 aa overlap

      10      20      30      40      50      60
a597.pap MLLHVSNSLKQLQEEIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTLNRLKT
          |||
m597      MLLHVSNSLKQLQEEIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTLNRLKT
          10      20      30      40      50

      70      80      90      100     110     120
a597.pap EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          |||
m597      EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          60      70      80      90      100     110

      130     140     150     160     170     180
a597.pap QKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          |||
m597      QKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          120     130     140     150     160     170

      190     200     210     220     230     240
a597.pap QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          |||
m597      QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          180     190     200     210     220     230

      250     260     270     280     290     300
a597.pap SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST
          |||
m597      SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST
          240     250     260     270     280     290

      310     320     330     340     350     360
a597.pap APATVESIAPGTVSYADELDGYGKVVVDHGENYISYIAGLSEISVGKGYMVAAGSKIGS
          |||
m597      APATVESIAPGTVSYADELDGYGKVVVDHGENYISYIAGLSEISVGKGYMVAAGSKIGS
          300     310     320     330     340     350

      370     380     390
a597.pap SGSLPDGEEGLYLQIRYQQGVLPSSWIRX
          |||
m597      SGSLPDGEEGLYLQIRYQQGVLPSSWIRX
          360     370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
  1 ATGTTCCCAA CCGGCAATTT GGTCGACGAA ATTGATGTGC CGAATATAGG
 51 TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCGGA CTGGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTTGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCGGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
351 GAGCATGGGC AAAGTGCACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
401 TCGCCGCGGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCCTT CGGGCATCCG TCAGGTACGC TCGTGTTCGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCG aaagcggtca
551 tgaGCCGCGC CGCACgcgtg attatggaaa gttgGGTGCg cgttcccgat
601 gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
  1 MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
 51 NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDQGWTAA KAVMSRSARV IMESWVRVPD
201 DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
  1 ATGTTCCCAA CCGGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
 51 CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCTTGA
101 ATGCCGCGGA CTGGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCGGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AAAGTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCGGTA CCGGTACGC TGGTCAACCT TGCCGAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTCCG GCACATGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CCGTCATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTCAAGGTG
601 CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
  1 MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
 51 NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

      |||
g601  TIRAYGALKMGLISDVSEAAARATPKPAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.pep KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
      |||
g601  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
      130     140     150     160     170

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |||
g601  AAKAVMSRSARVIMESWVRVPDDCFX
      180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTCTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAG GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC  ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTGGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAATG  GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTGTCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTACGGGTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFH HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

      10      20      30      40      50      60
m601.pep MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      |||
a601  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      10      20      30      40      50      60

      70      80      90      100     110     120
m601.pep KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      |||
a601  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.pep KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
      |||
a601  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
      130     140     150     160     170     180

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |||
a601  ATKAVMSRSARVMMEGWVRVPEDCFX
      190     200

```



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```

g602.seq
1      ATGTTGCTCC  ATCAATGCGA  CAAAGCGCGA  CATATGCGTC  CCTTTCTGCT
51     CGCGGGGCGAG  ATAAACGCTC  ATCGTCAGGC  GAGCAACCGT  GGATTGTGTT
101    CTTTCGGCGGG  TTTTCAGGGT  ATCCGGGAAG  CGCAGGTTCT  TAATGCCGAC
151    CTGATTGATC  GGCCAGGTTG  GCAAACTCTT  GCTGGATTCT  ACCGTGCGAA
201    TGGCGTTCAT  GCGTTGTTTG  TCCTTAATAT  TCGAGATAAT  ATGAGATGTG
251    GTGATATGTA  TGGCAGGcag  atccgctctg  aAAAAAcgct  gtcgCGCCc
301    TGCCCTGAAA  Tgcgcagatta  tatCACTTgc  TTTtgcgcGC  TGCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

g602.pap
1 MLLHQCDKAR HMRPFLGGQ INRHRQASNR GLCSFGGFGQ NREAQVFNAD
51 LIDRQVAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLAA
101 CLOMRDYITC FWRLH*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1      ATGTTGCTCC  ATCAATGCGA  CAAAACGCGA  CATATGCGTC  CCCTTCTGCT
51     CAGCAGGCAG  GTAACACGTC  ATGTGTCAGC  GGGCAATGGT  GGACTGGATG
101    CCTTCTGCAG  TTTGACAGGT  ATCCGGAAGC  CGCAGGTTCT  TGATACCGAC
151    CTGATTGATC  GGCAGATTGC  GCAAAATCTC  GCTGGATTCT  ACGTCTGCAA
201    TAGTGTTTCA  GAGTTGTTTT  TCCTTAATAT  TCTAGTAATT  TGTGAGATGT
251    GTGCATGGTA  TGCGGTTTCC  CGCGGGGAAT  ATACCGTCAA  TCTGCAAATG
301    CGAGATTATA  TCCATCGCTT  TTACGACGTC  CATTG
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

m602.pap
1 MLLHQCDKTR HMRPLLSRQ VNRHGQTNG GLDAFCSLQG NRKAQVFTD
51 LIDRQIAQS AGLHVCNSVH ELFFLNIIHVI WEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPILLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTLIDRQIAQIS					
	: : : : : : : : : :					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSA-GEYTVN---LQMRDYITRFQQLHX					
	: : : : : : : : : : : :					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGROMPSEKTLAACLQMRDYITCFWRLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```

a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAGGCAG GTAACCCGTC ATGGTCAGAC GGGCACACTG GGACTGGATG
101 CTTCTGTCAG TTTGCAGGGT AATCGGAAAG CGCAGGCTTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTGTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTGTTC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACCTGCCT TTACGACGTG CATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

a602.pep
1 MLLHQCDKAR HMRTLLGRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51 LIDRQIAQIS AGLHVCNSVH ELFFLNHIVI VEMCAWYGVs TGEYTVNLQM
101 RDYITRF*QL H*

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
a602	MLLHQCDKARHMRLLLGROVNRHGQTGNCGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAGEYTVNLQMRDYITRFQQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTTT
101 CAGACGGCCC CGCACCAAAA AAACAACCAC AAATACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCTGAAC TGCCTCAGTT CATCGCTCAA
201 AGCGCCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCTTA AGCTGCCTCG
251 GGGAAACGCT GACTACGCCC GAAGCGGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCTCT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGCGCG GCGAAAAATA TCACGAGTCC
451 GTCTCATCG ACCAAGACGT CTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCGGCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaagACATC
751 CGCTCATGTA TTGCCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGTAATGGG TACACGTTGC GCGACACCG ATCCGGCGCT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTTCCCGG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGCCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCCGCT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTTAC CGGCGGTATC GGCGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCTT ATCTTGATT CTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAAA CGTACGGCA ATTCCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGNDA RKYGIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISLPN DCRTLEIAAD EGREGARLAL
351 EVMTCLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDPLGL
401 HIDTKANMEK RYGNSGIISP TDSSPAVLVV PTNEELMIAC DTAEAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCCTCGC GTAGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCCTGAT GTCTGC.CTT
101 TTTACAGCGA CCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCAG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

956

```

301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGAAATTGCC ACGCCGGCGC
351 GGTGGGTATG CTTTGAACG AACTGGAAAA ACACGGTCTG CACGACCGCA
401 TCAAAGCCAT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTGCGCGCAC
551 AGGAACATTT CCCCCTGCTG CCCAATGTCG GCGTGATGGA TACTTCGTTC
601 CACCAAAACCA TGCCGGAGCG TGCTTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCGCTACCG TTTCCACGGC ACCAGTATGC
701 GTTACGTGTC CCCTGAAGCC GCACGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTAGGCAAC GCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGTACACGT TGCGGCGACA TCGATCCGGG CGTATACAGC
901 TATCTGACTT CCCACGCCGG GATGGATGTT GCCCAAGTGG ATGAAATGCT
951 GAACAAAAAA TCAGGTTTGC TCGGTATTTC CGAATTTC AACGACTGCC
1001 GCACCCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTCA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGTGTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 CATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAAGT GATGATTGCC TCGGACACTG CCGAACTTGC CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1898; ORF 603>:

m603.pep

```

1  LSSRRRGRNN DRKCGIRFAQ RGRCLKHLAPD VCXFSDDPTL KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRXSGSVV LSCLGERLTT PEAVITFNKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHGL HDRIKAIGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPNANISGI LAAQEHFPLG PNVGVMDTSF
201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ARILGKPLED
251 IRMIIAHLGN GASITAING KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301 YLTSHAGMDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
351 LEVMTYRLAK YIASMAVCGG GVDALVFTGG IGENSNRNIRA KTVSYLDFLG
401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELAGIL
451 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

```

              10      20      30      40      50      60
m603.pep  LSSRRRGRNNDRKCGIRFAQRGRCLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL
          ::|| || |: || ||||| ||||| ||:: ||| |: ||||| ||||| |||||
g603      MDSRLRG-NDARKYGIRFAQRGRCLKHTPPNAHPFSDGPAPKKQPQTTRRNIMSDQLILVL
              10      20      30      40      50

              70      80      90      100     110     120
m603.pep  NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNKRQVPLSGRNCHAGAVGM
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      NCVSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNKRQVPLSGRNCHAGAVGM
          60      70      80      90      100     110

              130     140     150     160     170     180
m603.pep  LLNELEKHGLHDRIKAIGHRIAHGGEKYESVLIDQAVMDELNACIPLAPLHNPNANISGI
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      LLNELEKHGLHDRIKAIGRIAHGGEKYHESVLIDQDVLDELKACIPFAPLHNPNANISGI
          120     130     140     150     160     170

              190     200     210     220     230     240
m603.pep  LAAQEHFPLGNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

g603      LAAQEHFPGLPNVGMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISELPNDCRTLEIAADEGREGARLALEVMTCRLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVCGGVDALVFTGGIGENSRNIRAKTVSYLDLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||:|||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTTCAGACGA CCCACACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAAGTCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCGC CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCGTCTG CCAATGTCG GCGTGATGGA TACTTCGTTC
601 CACCAAAACCA TGCCGGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTC GCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAAAC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGTAAT GGGTACGCGC TGCGGCGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TGCGACACTG CCGAACTTGT GGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RRLKHTPPN AHPFSDPTX KKQPQTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHN PANISGI LAAQEHFPGLP NVGVMDDTSF

```

201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
 301 YLTSHAGLDV AQVDEMLNKK SLLGISELS NDCRTLEIAA DEGHEGARLA
 351 LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGNSRNIRA KTVSYLDFLG
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL
 451 *

m603/a603 96.7% identity in 450 aa overlap

m603.pep	10	20	30	40	50	60
	LSSRRRGRNDRKCGIRFAQRGLKHLAPDVCXFSDDEPTLKKQPQTRRNIMSDQLILVL					
a603	10	20	30	40	50	60
	LSSRRRGRNDRKCGIRFAQRGLKHTPPNAHPFSDDEPTXKKQPQTRRNIMSDQLILVL					
m603.pep	70	80	90	100	110	120
	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNKQVPLSGRNCHAGAVGM					
a603	70	80	90	100	110	120
	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFSKDGKNKQVPLSGRNCHAGAVGM					
m603.pep	130	140	150	160	170	180
	LLNELEKHGLHDRIKAIGHRIAHHGGEKYESVLIQAVMDELNACIPLAPLHN PANISGI					
a603	130	140	150	160	170	180
	LLNELEKHELHDRIQAVGHRIAHHGGEKYESVLIQAVMDELNACIPLAPLHN PANISGI					
m603.pep	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHG TSMRYVAPEA					
a603	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHG TSMRYVAPEA					
m603.pep	250	260	270	280	290	300
	ARILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	250	260	270	280	290	300
	ACILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
m603.pep	310	320	330	340	350	360
	YLTSHAGMDVAQVDEMLNKKSGLLGISELSND CRTLEIAADEGHEGARLALEVMTYRLAK					
a603	310	320	330	340	350	360
	YLTSHAGLDVAQVDEMLNKKSGLLGISELSND CRTLEIAADEGHEGARLALEVMTYRLAK					
m603.pep	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
a603	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
m603.pep	430	440	450			
	PTDSSPAVLVPTNEELMIACDTAELAGILX					
a603	430	440	450			
	PTDSSPAVLVPTNEELMIACDTAELVGILX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:
 g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
 51 CCAGCGTACC GAGCACGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
 151 GTCGGCGGCG TTTACGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG
 201 GCGCGACGAA GGCGGGTTTC GGCGTGCGCG CGCGGGCGGC GGCTTCGGAT

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251 ACGTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC
 301 AAATTTTCC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT
 351 TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAACACGGT CGGAATGCCC
 401 GCCTTGATGA GCGTGGCTTT CAGACGACCT ATATTCGGCA CATCAATTTC
 451 GTCGACCAAA TTGCCGGTTG GGAACATACT GCCTTcgCG TCGGCTGGAT
 501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604.pep

1 MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQAYRQID
 51 VGGVYGFAAG GGVIGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
 101 KFFQRGIVV DVVLQLFARV AQVGGVQENG RNARVDERGF QTTYIRHINF
 151 VDQIAGWEHT AFAVGWI*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604.seq

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
 51 CCAGCGTACC GGGTACGGCG GCGGCGGTTC CAATGGCAAC AGAGGCGGTA
 101 CCCATCATCG CGTGGTGCAAG TTGCCCATG CTCAGGGCGC GTACCAGCAA
 151 ATCGATGTCG GCGGCGTTCA CGGTTTTGCC ACTGGAGGCG GTGTAATCGG
 201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG AGCGGCAGCT
 251 TCGGATACGT CGCTGATCAG ACCATTTC AGCGCACCGT AAGCGCGGAT
 301 TTTCTCGAAT TTTTCCAAAG CCGCGGCATC GTTGTGTATG TCGTCTTGCA
 351 ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
 401 ATGCCCGCGT TGATAGCGGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
 451 AATTTTCATG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
 501 CTGGATC

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604.pep

1 MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVVQ FAHAQAYQQ
 51 IDVGVHGF A TGGVIGGGR DEGDFRRVRA SGSGFYVADQ THFORTVSAD
 101 FLEFFQSRGI VVDVVLQLF A CVAQVGGIQE NGRNARVDER GFQTAYIRHI
 151 NFIDQIAGWE HTAFAVGWI

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

	10	20	30	40	50	60
m604.pep	MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQAYQQIDVGGVHGF					
	: : : : : :					
g604	MPEAHFFTRSAACGKVDQRTGHEGG--DGDGRDAHHSVVQFAHAQAYRQIDVGGVYGFA					
	10	20	30	40	50	
	70	80	90	100	110	120
m604.pep	TGGGVIGGRDEGDFRRVRASGSFGYVADQTHFORTVSADFLEFFQSRGIVVDVVLQLF					
	: : : : : : :					
g604	AGGGVIGGRDEGDFRRARAGGGFGYVADQTHFQRAICADGFKFFQRGIVVDVVLQLF					
	60	70	80	90	100	110
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI					
	: : : : : :					
g604	RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX					
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604.seq

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
 51 CCAGCGTACC GGGCACGGCG GCGGCGGTTC CAATGGCAAC AGAGGCGGTA
 101 CCCATCATCG CGTGGTGCAA TTGCCCATG CTCAGGGCGC GTACCAGCAA
 151 ATCGATGTCG GCGGCATTCA CGGTTTTGCC ACTGGAGGCG GTGTAATCGG

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201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTACAGGAA AACGGTCGGA
401 ATGCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAAACT GCGCCGTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTGC CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWIK KFDLYFGCRE RYAVELKIAC FQNCVAVLHRY
201 MGNNGFADVF LPDFDCADAV *

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m604/a604 97.0% identity in 169 aa overlap

```

m604.pep      10      20      30      40      50      60
MPEAHFFTRSAAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
|||||
a604          10      20      30      40      50      60
MPEAHFFTRSAAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA

m604.pep      70      80      90      100     110     120
TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA
|||||
a604          70      80      90      100     110     120
TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFLEFFQSCGIVVDVVLQLFA

m604.pep      130     140     150     160     169
CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
|||||
a604          130     140     150     160     170     180
RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWIKKFDLYFGCRE

a604          190     200     210     220
RYAVELKIACFQNCVAVLHRYMGNNGFADVFLEPDFDCADAVX

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGTTTA TCAGCGAAAA CTTACCCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGACAG
201 CATCATCACG CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgccgccga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTAcccgT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCTT TAAAGGCGTG GCGGAACTCG ATTTCCGCCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAATA CGCcgC AAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGCGAGGA
651 GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGAGGCGGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACACAC CACCTACAAC CTCGCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATCCA CATCGAATTG GCGCACACGC
851 TGACCAACCC CAAACTCAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgat

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATc CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGOEKVN KIYDPACGSG SLLLOAKKQF DEHIEEGFF
251 GQEINHHTYN LARMNMF LHN VNYNKFHIEL GDTLTNP K LK DSKPFDVAVS
301 NPPYSIDWIG SDDPTLIND RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPPI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCAVNI
401 LVL SKHKDNT DIQFIDASGF FKKETNN NVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQT V KDNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGACG TCAACACCAA GCTGAAAGAA ATTTTACC GATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACTCG ATTTCGGCAA
501 TTTTGAAAAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGTGCCAAAC GCAGGCAAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
 151 KRLA AVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
 201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF
 251 GQEINHHTYN LARMNMF LHN VNYNQFHIEL GDTLTNP K LK DSKPFDAIVS
 301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
 351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
 401 LVLSKHKDNT DIQFIDASGF FKKETNNNV L IEEHIAEIVK LFADKADVP H
 451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
 501 LRREIDEVIA EIEA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng)
from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADEVRGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQRAQLHRQIWKIADEVRGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVGKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVGKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFENHHIDLFGDAY					
g605	GYPSEQGIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFEDHRIDLFGDAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFT PQSVSKLIAR LAVHGQEKVN KIYDPACGSGSLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFT PQSVSKLIAR LAVHGQEKVN KIYDPACGSGSLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIEEGFFGQEINHHTYN LARMNMF LHN VNYNQFHIEL GDTLTNP K LK DSKPFDAIVS					
g605	DEHIEEGFFGQEINHHTYN LARMNMF LHN VNYNQFHIEL GDTLTNP K LK DSKPFDAIVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFIL HALNYLSGRGRAAIVSFPGI					
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAFIL HALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNNNV L IEEHIAEIVK LFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					
g605	FKKETNNNV L IEEHIAEIVK LFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					

963

	430	440	450	460	470	480
	490	500	510			
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
	: : : : :					
g605	VIDIRQLNAEISETVAKIERLRREIDEVIAEITX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1911>:

```

a605.seq
1  ATGATGACCG  AAATACAACA  ACGCGCCCAA  CTGCACCGCC  AAATTTGGAA
51  AATTGGCCGAC  GAAGTACGCG  GCGCGGTGGA  TGGCTGGGAC  TTCAAACAAT
101 ACGTTTCTCGG  CACACTTTTC  TACCGCTTTA  TCACGAAAAA  CTTTACCGAC
151 TATATGCAGG  CAGGCGACAG  CAGTATTGAT  TACGCGCGTA  TCGCGGACAG
201 CATCATCAGC  CCCGAAATCA  AAGACGATGC  CGTCAAAGTC  AAAGGCTATT
251 TCATCTACCC  CGGCGACGTT  TTTTGGAAATA  TTGCCGCGCA  AGCCCCATCAA
301 AACGAAGAGC  TCAACACCTA  GCTGAAGAA  ATTTTACCG  CGATTGAAG
351 CTCCGCCTCC  GGCTATCCGT  CCGAACAAAG  CATTAAGCG  CTGTTTGACG
401 ACTTCGACAC  CACCAGCAGC  CGGCTCGGCA  GCACCGTTGC  CGACAAGAAC
451 AAACGCCTTG  CCGCCGTCTT  AAAAGCGCTG  CGGGAACTCG  ATTTCCGCGAC
501 TTTTGAAGAC  CACCATCATG  ACCTTTTCGG  CGATGCCTAC  GAATACCTGA
551 TTTCCAATA  CGCTGCCAAC  GCAGGCAAAT  CCGGCGCGCA  ATTTTTACC
601 CCGCAAAGCG  TATCCAAGCT  GATTGCGCGG  CTGGCGGTGC  ACGGGCAGGA
651 GAAAGTAAAC  AAAATCTACG  ACCCAGCTTG  CGGCTCGGGC  AGCCTGCTCT
701 TGCAGCGCGA  AAAACAGTTT  CACGAGCACA  TCATCGAAGA  AGGCTTCTTC
751 GGGCAGGAAA  TCAACCACAC  CACCTACAAC  CTCGCCCGCA  TGAATATGTT
801 TCTGCACAAC  GTCGAATTACA  ACAAATTCCA  CATCGAATTG  GCGCAGACAC
851 TGACCAATAT  CAAACTCAA  GACAGCAAA  CCTTTGATGC  CGTCGTTTCC
901 AATCCGCCCT  ATTCATCAA  CTGTGATAGC  AGCGGCCGAC  CACCTTAAAT
951 CAACGACGAC  CGCTTTGCCC  CTGCAGGCGT  ACTCGCCCCG  AAATCCAAAG
1001 CCGATTTTGC  CTTCTATTCT  CACGCGATCA  ACTACCTTTC  CGGCAGAGGC
1051 CGCGCCGCCA  TCGTCTCATT  CCCCGCATT  TTCTATCGCG  GCGGCGCGCA
1101 GCAGAAAAATC  GCCCAATATC  TGGTGGAGGG  CAACTACGTG  GAAACCGTGA
1151 TCGCCCTTGC  GCCCAATCTC  TTTTACGGCA  CCGGCATCGC  CGTCAATATA
1201 CTGGTTTGTG  CCAACACAA  AGACAATACC  GACATCCBAAT  TCATCGACGC
1251 AGCGGCTTTC  TTTAAAAAAG  AAACAACAA  CAACGTCTTA  ACCGAAGAAT
1301 ACATTGCCGA  AATCGTCAAA  CTCTTCGCGC  ATAAAGCCGA  TGTGCCGCAT
1351 ATCGCCCAAA  ACGCCGCCCA  GCAAACGCTC  AAAGACAACG  GCTACAACCT
1401 CGCGGTACGT  AGCTATGTTG  ACCCGGAAG  CACCCGCGAA  ATTATCGACA
1451 TCAACAGACT  TAACGCGGAA  ATCAGCGAAA  CCGTTGCCAA  AATCGAACGG
1501 CTGCGGCGTG  AAATTGACGA  AGTGAATTGA  GAGATTGAAG  CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

```
a605.pep
1  MMTEIQQRAQ LHRQIWKIAD EVRGAVDGDWDFKQYVLGTLFYRFISENFDT
51  YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDFTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGSFED HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLOAKKQF DEHIEEGFF
251 GQEQINHTTYN LARMNMFLHN VYNKFKHIEL GDTLTNPCLK DSKPFDVAVS
301 NPPYSINWIG SGDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDAGGF FKKETNNNVL TEEHIAEIVK LFDADKADVP
451 IAQNAAQOTV KDNQYNLAVS SYVEPEDTRE IIDIKQLNAE ISETVAKIER
501 LRREIDEVIA ETEA*
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m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQQR	QLHRQIWK	IADEV	RGAVD	GWDFKQY	VLGTLF
	:					
a605	MMTEIQQR	QLHRQIWK	IADEV	RGAVD	GWDFKQY	VLGTLF
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDS	IITPEIKD	DAVKVK	GYFIYP	QGLFCN	IAAEAHQ
						NEELNT
						KLKEIFT
						AIASSA

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a605	YAAMPDSIIITPEIKDDAVKVGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS	70	80	90	100	110	120
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEIDFGNFENHHIDLFGDAY	130	140	150	160	170	180
a605	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEIDFGSFEDHHIDLFGDAY	130	140	150	160	170	180
m605.pep	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF	190	200	210	220	230	240
a605	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF	190	200	210	220	230	240
m605.pep	DEHIIEEGFFGQEIINHHTTYNLARMNMFLHNVNYNQFHIELGDTLTNPCLKDSKPFDAIVS	250	260	270	280	290	300
a605	DEHIIEEGFFGQEIINHHTTYNLARMNMFLHNVNYNKFHIELGDTLTNPCLKDSKPFDAVVS	250	260	270	280	290	300
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI	310	320	330	340	350	360
a605	NPPYSINWIGSGDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI	310	320	330	340	350	360
m605.pep	FYRGGAEQKIRQYLVVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF	370	380	390	400	410	420
a605	FYRGGAEQKIRQYLVVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDAGGF	370	380	390	400	410	420
m605.pep	FKKETNNNVLIIEEHIAEIVKLFADKADVPHIAQNAAQTVKDNNGYNLAVSSYVEAEDTRE	430	440	450	460	470	480
a605	FKKETNNNVLTTEEIHAEIVKLFADKADVPHIAQNAAQTVKDNNGYNLAVSSYVEPEDTRE	430	440	450	460	470	480
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX	490	500	510			
a605	IIDIKQLNAEISETVAKIERLRREIDEVIAEIEAX	490	500	510			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

g606.seq

1	ATGTCCAAA	TTATCGCCAA	ACAATCGGTC	GGTGC	GGAAG
51	GCCGcgCACC	GAAGAAGAAG	CCTGGCTTCT	GAACACTGTC	GAAGCCCAag
101	cgcGGCAATG	CAATCTGAAA	AGGCCAGAAG	TGCCCATCTA	CCACTCCCC
151	GAACCCAATG	CGTTTGCCAC	GGCGCATCG	AGAAACAGCT	CCCTGATCGC
201	CGTCAGCacc	ggtttctctcg	accaTatgaC	GCGCGACgaa	tggaagccg
251	tgTTGGCGCA	CGAAATGGCG	CACGTCGGCA	ACGGCGACAT	GGTTACGCTG
301	ACGCTGatTC	AAGGCGTGGT	CAATACCTTT	GTGCTGTTCC	TGTCGGCGAT
351	TATTGCCAAC	CTGATTGCCC	GAACAACAAG	CGGCACGCCA	TCCCAGGGAA
401	CTTATTCTCT	AGTCAGCATG	GTAATCCAAA	TCTGTGTGGG	TTCTCTTGCC
451	AGCCTGATTG	TCATGTGGTT	CAGCCGCCAA	CGGAATACCC	GCGCCGAgc
501	gggCGcgGCA	AAACTGGTCG	GCGCACCGAA	AATGATTTCG	GCCCTGCAAA
551	GGCTTAAAGG	CAACCCGGTC	GATTTGGCCG	AGCAAAATGA	CGCAATGGGC
601	ATCGCCGGAG	ATACGCGCGA	CTCCCTGCTC	AGCACCACCC	CTTCGCTGGA
651	CAACCGAATC	GCCCGCCTCA	AATCGCTTTA	A	

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSLL STHPSLDNRI ARLKSL*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1 ATGTCCAAAT TTATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51 GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GTTACGCTG
301 ACGCTGATT C AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCGGAA AATGATTTC GCCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGTATC GCCCGCTCA AATCGTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSLL STHPSLDNRI ARLKSL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRRIAN					
g606	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRRIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1 ATGTCCAAAT TCATCGCCAA ACAATCGGTC GGC GCGGAAG TTATCGACAC
51 GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCATAT GTTTACGCTG
301 ACGCTGATTG AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCC GAAACAACGA CGGCAGCCAG TCCAGGGAA
401 CTTATTTCCT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCAATACC GCGCCGACGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTC GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTLL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
a606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVNGNDMVTLLTIQGVVNTFVVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVNGNDMVTLLTIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSQGTFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1 ATGCTGCTCG accTgaCCG CTTTTCCTtt tccGTCTTCC TGAAAGAAAT
51 CCGCCTGCTG ACGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTGGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCAGC
251 TTTACGGCGC GGGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGATTTT GGGGATTTTC GGCATGATTT TGATGTGGGC
351 GCGGATTACG CCGTTCGCA ACTGGCTGAC TTTGAGCGAT TATGTGAAG
401 gcacAatggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGCGGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCCGTA TGCCCGCTTT GGGTGGCGCA

```



```

601  GGTTCGCGCG  TGGCGACAAT  GGCGGTGTTT  TGGTTCAGCG  CGCTGGCATT
651  GTGGATTAT  ATCGCCAAGG  AAAAATTCTT  CCGCCCCTTC  GGACTGACAG
701  CGAAATTCGg  caaACCGGat  tGGgcGGTGT  TCAAACAGAT  TtGGAAAATC
751  gGcgcgCCCA  TCGGGCTGTC  TTATTTTGTG  GAAGccaGcg  cGTTTTCGTT
801  TATCGTGTTT  TTGATTGCGC  CTttcggCGA  GGATTATGTG  GCGGCGCAGC
851  AGGTCGGCAT  CAGTTTGTCT  GGGATTCTCT  ATATGATTCC  GCAAAGCGTC
901  GGCTCGGCAG  GGACGGTGCG  CATCGGCTTT  TCGCTTGGGC  GGCGCGAATT
951  TTCGCGGGCG  CGTTATATTT  CAGGAGTGTC  GCTGGTGTCG  GGCTGGGTGC
1001 TCGCCGTGAT  TACCGTGCTT  TCCTTGGTAT  TATTCGGTTC  GCCGCTGGCA
1051 AGCATGTACA  ACGATGaTCC  GGCAGTTTTA  AGCATCGCCT  CCACCGTCCT
1101 GCTGTTTCGCC  GGCCTGTtcc  aACCGGCAGA  CTTACCCCAA  TGTATCGCGT
1151 CCTATGCCCT  GCGCGGCTAC  AAAGTCACCA  AGGTGCCGAT  GTTCATCCAC
1201 GCCGCCGCCT  TCTGGGGCTG  CGGCCTGCTG  CCGGGCTATC  TGCTCGCCTA
1251 CCGTTTCGAT  ATGGGCATT  ACGGCTTCTG  GACGGCATTG  ATTGCCTCGC
1301 TCACCATCGC  AGCCGTGCGC  TTGGTGTGGT  GCTTGAAAA  ATACAGTATG
1351 GAGTTGGTCA  AATCACACAA  GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1  MLLDLDRFSF  SVFLKEIRLL  TALALPMLLA  QVAQVGIGFV  DTVMAGGAGK
51  EDLAAVALGS  SAFATVYITF  MGIMAALNPM  IAQLYGAGKT  GEAGETGRQG
101 IWFGILIGIF  GMILMWAAIT  PFRNWLTLSD  YVEGTMAQYM  LFTSLAMPAA
151 MVHREALHAYA  SSLNRPRLLIM  LVSFAAFVLN  VPLNYIFVYG  KFGMPALGGA
201 GCGVATMAVF  WFSALALWIY  IAKEKFFRPF  GLTAKFGKPD  WAVFKQIWKI
251 GAPIGLSYFL  EASAFSFIVF  LIAPFGEDYV  AAQQVGISLS  GILYMIPQSV
301 GSAGTVRIGF  SLGRREFSRA  RYISGVSLVS  GWVLAVITVL  SLVLFERSPLA
351 SMYNDPDAVL  SIASTVLLFA  GLFQPADFTQ  CIASYALRGY  KVTKVPFMFIH
401 AAAPFWCGLL  PGYLLAYRFD  MGIYGFWTAL  IASLTIAAVA  LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1  ATGCTGCTCG  ACCTCAACCG  CTTTTCCTTT  CCCGTCTTCC  TGAAAGAAGT
51  CCGCTGCTG  ACCACTCTTG  CCCTGCCCAT  GCTGTGGCG  CAGGTGCGGC
101 AGGTGGGCAT  CGGTTTTGTC  GATACTGTGA  TGGCGGGCGG  TGCGGGCAAG
151 GAAGACTTGG  CGGCGGTGGC  TTTGGGCAGC  AGCGCGTTTG  CCACGGTTTA
201 TATTACCTTT  ATGGGCATTA  TGGCGGCGCT  GAACCCGATG  ATTGCCCAGC
251 TTTACGGCGC  GGGTAAAACC  GACGAAGTGG  GCGAAACGGG  GCGGCAGGGG
301 ATTTGGTTTC  GGCTGTTTTT  GGGCGTGTTT  GGCATGGTCT  TGATGTGGGC
351 GCGGATTACG  CCGTTCGCCA  ACTGGCTGAC  CTTGAGCGAT  TATGTGGAAG
401 GCACGATGGC  GCAGTATATG  TTGTTACCA  GCTTGGCGAT  GCCGGCGGCA
451 ATGTTACACC  GCGCGCTGCA  CGCTACACT  TCCAGCCTGA  ACCGCCCGCG
501 CCGTATTATG  TTGGTCAGCT  TTGCGGCGTT  TGTGTGAAC  GTGCCGCTGA
551 ACTATATTTT  CGTTTACGGC  AAATTCGGTA  TGCCCGCTTT  GGGCGGCGCA
601 GGCTGCGGAC  TGGCGACGAT  GCGGTGTTT  TGGTTCAGCG  CGCTGGCATT
651 GTGGATTAT  ATCGCCAAGG  AAAATTCTT  CCGCCCATTC  GGACTGACGG
701 CGAAATTCGG  CAAACCGGAT  TGGGCGGTGT  TCAAACAGAT  TTGGAAAATC
751 GCGCACCCCA  TCGGGCTGTC  TTATTTTGTG  GAAGCCAGCG  CGTTTTCGTT
801 TATCGTGTTT  TTGATTGCGC  CTTTCGGCGA  GGATTATGTG  GCGGCGCAGC
851 AGGTCGGCAT  CAGTTTGTCT  GGGATTCTCT  ATATGATTCC  GCAAAGCGTC
901 GGCTCGGCGG  GGACGGTGCG  CATCGGCTTT  TCGCTTGGGC  GGCGCGAATT
951 TTCGCGGGCG  CGTTATATTT  CGGGCGTGTC  ACTGGTGTTA  GGATGGATGC
1001 TCGCCGTGAT  TACCGTGCTT  TCCTTGGTAT  TATTCGGTTC  GCCGCTGGTA
1051 AGTATGTACA  ACAATGATCC  GCGCGTTTTA  AGCATCGCCG  CCACCGTCTT
1101 ACTGTTTCGCC  GGCTTGTTCC  AACCAGCAGA  CTTACCCCAA  TGTATCGCCT
1151 CCTACGCCCT  GCGCGGCTAC  AAAGTACAA  AGGTGCCGAT  GTTCATCCAC
1201 GCCGCCGCCT  TTTGGGGCTG  CGGCCTGCTG  CCGGGCTATC  TGCTCGCCTA
1251 CCGTTTCAAT  ATGGGCATT  ACGGCTTCTG  GACGGCATTG  ATTGCCTCGC
1301 TCACCATCGC  CGCCATCGCC  TTGGTGTGGT  GCTTGGAATT  GTGCAGTAGG
1351 GAGATGGTCA  GATCGCATAA  GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1  MLLDLNRFSF  PVFLKEVRLL  TTLALPMLLA  QVAQVGIGFV  DTVMAGGAGK
51  EDLAAVALGS  SAFATVYITF  MGIMAALNPM  IAQLYGAGKT  DEVGETGRQG

```

```

101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRLAHAYT SSLNRPRLIM LVSFPAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFPSPLV
351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMTFIH
401 AAAPWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
451 EMVRSHKAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng)
from *N. gonorrhoeae*:

m607/g607

m607.pep	10	20	30	40	50	60
	MLLDLNRFSFPVFLKEVRLTTTLALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLAAVALGS					
g607	MLLDLDRFSFVSFLKEIRLLTALALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVMWAAIT					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGILGIFGMILMWAAT					
	70	80	90	100	110	120
m607.pep	130	140	150	160	170	180
	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRLAHAYTSSLNRPRLIMLVSFPAFVLN					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRLAHAYASSLNRPRLIMLVSFPAFVLN					
	130	140	150	160	170	180
m607.pep	190	200	210	220	230	240
	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
m607.pep	250	260	270	280	290	300
	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV					
	250	260	270	280	290	300
m607.pep	310	320	330	340	350	360
	GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFPSPLVSMYNNDDPAVL					
g607	GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMLAVITVLSLVLFPSPLASMYNNDDPAVL					
	310	320	330	340	350	360
m607.pep	370	380	390	400	410	420
	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMTFIHAAAFWGCGLLPGYLLAYRFN					
g607	SIASTVLLFAGLFQPADFTQCIASYALRGYKVTKVPMTFIHAAAFWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
m607.pep	430	440	450	460		
	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSKAVX					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMELVKSHKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTGGGCGAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACCC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTCGCGAC TGGCGACGAT GCGGCTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAATAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTCGCC GGCTTGTTCC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSF SVFLKEVRLT TALALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRLHAYA SSLNRPR LIMLVSF AAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFSPPLV
351 SMYNDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFIH
401 AAAPWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCSR
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLTTTALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFVSFLKEVRLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
	70	80	90	100	110	120
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRLHAYTSSLNRPR LIMLVSF AAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRLHAYASSLNRPR LIMLVSF AAFVLN					
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRLHAYTSSLNRPR LIMLVSF AAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRLHAYASSLNRPR LIMLVSF AAFVLN					
	190	200	210	220	230	240

970

```

m607.pep      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a 607          VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
                190      200      210      220      230      240

                250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMPIQSV
a 607          WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMPIQSV
                250      260      270      280      290      300

                310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFRSPLVSMYNNDDPAVL
a 607          GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFRSPLVSMYNNDDPAVL
                310      320      330      340      350      360

                370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPFIIHAAAFWGCGLLPGYLLAYRFN
a 607          SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPFIIHAAAFWGCGLLPGYLLAYRFD
                370      380      390      400      410      420

                430      440      450      460
m607.pep      MGIYGFWTALIASLTIAAIALVWCLELCSREMRVRSKAVX
a 607          MGIYGFWTALIASLTIAAIALVWCLELCSREMRVRSKAVX
                430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

```

g608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTCCGCA ACAGCGCGAT
201 ACGGAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCTCGGC ATGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTCCCGCG CATCGGacgA ATTGGCACGG ATTTCCGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCaTCaaa CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTGGAACGCG
551 ACATTTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

```

g608.pep
1   MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPGAGD IRLEGDILIG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRRLDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

```

m608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGGCG CCTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTCCGCA ACAGCGCGGT
201 ACAGAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCTCGGC ATGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTCCCGCG CATCGGACGA ATTGGCACGG ATTTCCGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCG ACATCGGACA CGGCATCAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

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501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACCGC
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLLIG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	:					
g608	MSALLPIINRLILQSPDSRSELTSEAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPEGAGDIGLEGLLIGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	:					
g608	TFRNSAIRKILQGGEPEGAGDIRLEGLLIGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGTT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGCG GCGAACCCGG GCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG
301 CGTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACCGC
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLLIG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

```

m608.pep  MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
a 608      MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
           10      20      30      40      50      60

           70      80      90      100     110     120
m608.pep  TFRNSAVQKILQGGEPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a 608      TFRNSAVQKILQGGEPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
           70      80      90      100     110     120

           130     140     150     160     170     180
m608.pep  RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a 608      RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
           130     140     150     160     170     180

           189
m608.pep  LERDIWIDX
a 608      LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51 TCGGTTGTGC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CCCCGTCTTT CATTTACCCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRV FV GLFGNVFFIG
51 AFEQAVELAA RLRFHIIIDNF LDTDFGIGSQ ADGNVRTLM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51 TCGGTTGTGC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CCCCGTCTTT GATTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRV FV GFPGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

           10      20      30      40      50      60
m609.pep  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGFPGNVFFIGAFEQAVELAA
           10      20      30      40      50      60
g609       MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60

           70      80      90      100     110     120
m609.pep  RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRVAVLGNFFGTTRAKRGYGNHDLHTVAVCPVF
           70      80      90      100     110     120

```

g609 RLRFHIIIDNFLDITDFGIGSQADGNVRTLIMRAILGNFFGTRAKRGYGNHDLHTVAVCPVF
70 80 90 100 110 120

m609.pep DFARETDIIIQX
|:|:|:|:|:|:|
g609 HFTREADIIIIQX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1935>:

```
a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACTCTTGA
51  TGCCTTTGTC GGCAATCAGC GAAGTACGCA CATCGCGCAC CATATCTTCC
101 ACGAATTTCG GGGTTTTCGTA GGCTTTTTCG GTACAGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCATAT TGGGAAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGTTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CACCGTCTTT CATTTCGCCC GTGAGGCTGA CATCATAATC CAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1936; ORF 609.a>:

a609.pep

1	MVVDRLLEILA	LDDETLDAFV	GNQRSSDIAH	HIFHEFRVFEV	GFFGNVFFIG
51	AFEQAVELAA	RLRLHIIDDF	LDTDFGIGSQ	ADGNVRTLVV	RAILGNFFGT
101	RAKRGYGNHD	LHTVAVCTVF	HFAREADIII	Q*	

m609/a609 96.9% identity in 131 aa overlap

		10	20	30	40	50	60
m609.pep		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGGFNVFFIGAFEQAVELAA					
a609		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGGFNVFFIGAFEQAVELAA					
		10	20	30	40	50	60
		70	80	90	100	110	120
m609.pep		RLRLHIIDDFLD TDFGIGSQADGNVRTLVVRV LGNFFGTRAKRGYGNHDLHTVAVCPVF					
a609		RLRLHIIDDFLD TDFGIGSQADGNVRTLVVRV LGNFFGTRAKRGYGNHDLHTVAVCTVF					
		70	80	90	100	110	120
		130					
m609.pep		DFARETDIIIQX					
a609		HFAREADIIIQX					
		130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 1937>:

```

g610.seq
1  ATGATTGGAG  GGCTTATGCA  ATTTCTTAC  CGCAATGTTC  CGGCTTCGCG
51  TATGCGCCGT  ATGCGCAGGG  ATGATTTTTC  ACGCGCGCTG  ATGCGCGAGC
101  ATATGCTGAC  CGCCGATGAT  TTGATTATC  CGGTGTTCGT  ATTGGAGGGG
151  CGCGCGCGCG  AGGAGGATGT  GCCTTCTATG  CGGGCGGTGA  AGCGTCAGAG
201  TTTGGACAGG  CTGCTGTTTA  CGCCGGAGA  CCGCGGTAGG  TCCGGTATTC
251  CGATGTTGGC  ACTATTTCCT  GTGGTTACGG  CAAACAAAC  CGGCGCTGCG
301  CAGGAGGCGT  ACATATCCCA  AGGACTCGTG  CCGTCAACTG  tccgagcctT
351  GCGCGAGAGG  TttcCgaac  gggggattat  gacggtgtc  gcgctcgATc
401  cttatacgtt  gacCGGTGAC  GAGCAGCATG  CGGACgaaa  cggttaCGTG
451  ATGAatcGATg  aaacCGGTAGA  AGTCTTGGTG  AAACAGGCTT  TATGCTCATG
501  AGAGGCGGGC  ACGCAGGTCG  TTGCTCCTTC  CGATATGATG  GAGGGCGGTA
551  TCGGCGCCAT  CCGCGAGGCT  TTGGAGATG  CGGCACATAT  CCATACGGCG
601  ATTATGGCAT  ATATCGGCCAA  ATATGCTTCT  GCATTCTACG  GCCCTTTCCG
651  TGATGCGGTG  GGCAGTTCGG  GCAATTTGGG  AAAGGCAGAT  AAAAAAGACCT
701  ATCAGATGGA  TCCTGCAAA  ACCGATGAGG  CGCTGCATGA  GTTGGCGCTC
751  GATATTACAG  AAGGTGCGGA  TATGGTGATG  GTGAAGCCCG  AGTTGCGGTA

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801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGC GGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

g610.pep

```

1  MIGGLMQFPY RNVFASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51  AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG QVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLOAAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

m610.seq

```

1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CCGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTG ATGCGCGAAC
101 ACACGCTGAC CGCGATGAT TTGATTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGGC
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CCGACGAAA CCGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTGCACGA AGTGGCGTTG
751 GACATTACGG AAGGTGCGGA TATGTAATG GTCAAGCCCG GTTGGCGGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGC GGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

m610.pep

```

1  MIGGLMQFPY RNVFASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AOVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLOAAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*

```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNVFASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNVFASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM					
g610	FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGTQVAPSDMM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIRESLEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLKGADKKTYQMDPAN					

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```

g610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240
           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTIAYQVSGEYAMLQAAIAN
           |||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTIAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300
           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           |||
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTCCCC GTGGTACGG CAAACAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAA CGGTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGCCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1  MIGGLMQFPY RNVSASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTIAYQVSGE YAMLQAAVAN
301 GWLDGGKVVV ESLLAFKRAG ADGILTYAI EAAKMLKR*

m610/a610  99.4% identity in 338 aa overlap

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||
a610      MIGGLMQFPYRNVSASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
           130     140     150     160     170     180

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```

m610.pep      FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
|||||
a610          FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
                130      140      150      160      170      180

                190      200      210      220      230      240
m610.pep      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
|||||
a610          DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
                190      200      210      220      230      240

                250      260      270      280      290      300
m610.pep      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
|||||
a610          TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
                250      260      270      280      290      300

                310      320      330      339
m610.pep      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
|||||
a610          GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
                310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGC GG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCGAG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tatectTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctgA
251 TcgcgGTCTa tggtttCCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTCTCGGAA
401 ATGTTTTGCG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGtc gCTCATgcCG TAGCGCGTTA
501 CCATTTCCGC TGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51 RRVI FRRVRI LAQVVAVILG RAGLFARHNF QYLIAYVGFP FHQGFARHNF
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGC GG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCGAG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTCGCCC CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTCGCGG TTTTCATCGA GGATTTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCGTCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTtac GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTG GCTCATGCCG TAGCGCGTTA
501 CCATTTCCGC CGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51 RRVI FRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGFH FHQGFARHNF
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLLGCRSGVCRGRFCGFFPSRSVRRVIFRRVRI
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRFCGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIAVDGFPPHQGFAHRFHLVAVFIEDFVGNLILLVQNP
g611          LAQVVAVILGRAGLFARHNFQYLIAVYGFPPHQGFAHRFHLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFARHLGCAFKVV
g611          ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1   ATGCCGTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTT CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTCGCGG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTCG GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCGC AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GCTCATGCCG TAGCGCGTTA
501 CCATTTTCGG CGCCATTGCG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1   MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIAVDGF F HQGFAHRFH
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAFV AHAVARYHFA RHLGCAFKVV *

m611/a611    98.9% identity in 180 aa overlap

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLLGCRSGVCRGRFCGFFPSRSVRRVIFRRVRI
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLLLGCRSGVCRGRFCGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIAVDGFPPHQGFAHRFHLVAVFIEDFVGNLILLVQNP
a611          LAQVVAVIFGRAGLFARHDFQYLIAVDGFPPHQGFAHRFHLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFARHLGCAFKVV
a611          ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAFVAHAVARYHFARHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X

```

a611

X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

g612.seq

```

1 ATGGGcttcg gcgcaatat tgcAAAAAG CTGGCcgGg taGATGAAAT
51 AGCCTttgac ttgacggcA TCGTCTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CCGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCATTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

g612.pep

```

1 MGFGGNIACK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NAAVAGLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRFFY GHSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

m612.seq

```

1 ATGGGCTTCG GCGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTAAC TTTGACGGCA TCGTCTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCATTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

m612.pep

```

1 MGFGGNIACK LAGVDEIAFN FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRFFY GHSN*

```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIACKLAGVDEIAFN	FDGIVDFDGRDDAVRHSGV	INTAVACLHIVGEVFADKAVE			
g612	MGFGGNIACKLAGVDEIAFD	FDGIVDFDGRDDAVRHSGV	INAAGLHIVGEVFADKAVE			
	10	20	30	40	50	60
m612.pep	KCAENVLFKVP	PAIHRAAYFVGNFPNLAVQL	GALLHFGHHRNPYXKLNKSK	SPDIFRFFY		
g612	KCAENVLFKVP	PAIHRAAYFVGNFPNLAVQL	GALLHFGHHRNPYIKLNKSK	SPDIFRFFY		
	70	80	90	100	110	120
m612.pep						
g612						
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

a612.seq

```

1 ATGGGCTTCG GCGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTGAC TTTGACGGCA TCGTCTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTT.AC GGCATTCAA ATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVFDGFR DDAVRHSGVI NTAVACLHIV
  51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
 101  NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

m612.pep      10      20      30      40      50      60
MGFGGNIAKKLAGVDEIAFNFDGIVFDGFRDDAVRHSGVINTAVACLHIVGEVFADKAVE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          10      20      30      40      50      60
MGFGGNIAKKLAGVDEIAFDGIVFDGFRDDAVRHSGVINTAVACLHIVGKVFADKAVE

m612.pep      70      80      90     100     110     120
KCAENVLFKVPAlHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          70      80      90     100     110     120
KCAENVLFKVPAlHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX

m612.pep      GHSNX
               ||||
a612          GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
  51  GCGCAGTCTG CTTATTTTCGT CGaggcagtc ggcaagggct tcgttgccgg
 101  tgtttGcgGA CTCGGGTTCG CGGGAAATC CGCCGATTG TTCGGCGATG
 151  TTCCTGCCGA TTTgtttGAt GCCGTGTCG ATGTCGGTGG CACGgctgcc
 201  gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTegtCC GATGCGCGGG
 251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCC
 301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCCTT GGAGGATTTT
 351  CCGTATCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
 401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCCG
 451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
 501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGCGCG
 551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTTGTGTCT GTTGCCGCTT
 601  ATTTTACAGG CTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
  51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERLPSR DSTAMPRMRS
 101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
 151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
 201  ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
  51  GCGCAGTCTG CTTATTTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
 101  TGTTTGCGGA CTCGATTTCG CGGGAAATC CGCCGATTG TTCGGCGATG
 151  TTCCTGCCGA TTTGTTTGAT GCCGTGTCG ATGTCGGCGG CACGGCTGCC
 201  GATGCTGCC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
 251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCC
 301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
 351  CTGTACCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
 401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCCG
 451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
 501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGCGCG
 551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTTGTGTCT GTTGCCGCTT
  
```

980

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```
m613.pep
  1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
 51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSPMSAPAG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201  ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLSRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSAPAGSPPWRIFCTA					
	:					
g613	MSVARLPMPACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSAPAGSPPWRIFRIA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPPFAESKPSVSMRPASFSPPAMFRVSVLPKAASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPPFAESKPSVSMRPASFSPPAMFRVSVLPKAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```
a613.seq
1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTTGCGGA CTCGGGTTTC GGGGAAATC TGCCGATTG TTCGGCGATG
151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201 GATGTCTGCC TGCCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301 CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCGCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCGGA AGGTGATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCC GCCAG TTCAACCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCG AAGGCGGCAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGACAGG TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGACGCTT
601 ATTTTACAGG CTAA
```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

a613.pep	1	MSRSSRSRRS	LRRSTPSRSL	LISSRQSARA	SLPMFADSGS	RENLPICSAM
	51	FLPICLMPCP	MSAARLPMSA	CVPKIRANSS	DARERRLPSR	DSTAMPRMRS
	101	PSSPMSAPAG	SPPWRIFCTA	LLRKVISVSA	KPFFAESKPS	SVMRPFASFNP
	151	AMFRVSVLPA	KAASSERLSG	LCRIRRLMMG	RRADIFSDRG	GECLLLLLTL
	201	ILQA*				

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENLPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSAPAGSPPWRIFCTA					
a613	MSAARLPMSACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSAPAGSPPWRIFCTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPPFAESKPSVSMRPASFSPPAMFRVSVLPKAASSERLSGLCRIRRLMMG					
a613	LLRKVISVSAKPPFAESKPSVSMRPASFSPPAMFRVSVLPKAASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

g614.seq

```

1   AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acgggcaaat
51  cgaaTATTCT CAGTTCATCC GACAGGTCAG CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCCTTGGATG ACAACCTGAT
201 TCAAACCTTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCAGAGCGC GCTGACTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCCTa
501 tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCctgCtg gcgGgcagcc
551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC
601 GTGCCGTTCT TCAGCATTTT CCGTTCCGAT TTTGTGAAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAACG
701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
751 GCGCAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGACA TCCGGGGGCG
951 CGAACAGatn ttGAACGTCC ATTCTaaaAGTGCcttTG gacgaATCTg
1001 tggatTTATT GTCCCTCGCG CGCGGCACGC ccggtttTtc cggcgcggtat
1051 tTggcgaaac tgggtcaacga agccccctg tttgcccggc gccgcaacaa
1101 agtgaagtc gatcaaagcg atttGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGA CGCCGAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep

```

1   MAAFNALD GK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFETNA PLDDNLIQTL LKNKNVRVKVT PEEKPSALTA LFYSLLPVLL
101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQX LNVHSHKVPL DESVDLLSLA RGTGPGFSGAD
351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq

```

1   ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATACTCT CAGTTCATCC AACAGGTCAG CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACTTTCTT CACCAACGCG CCTTTGGACG ACAACCTAAT
201 TAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCAGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTCTA CTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCCTa
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCTGCTG GCGGGCAGCC
551 CCGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCGAC TTTGTGAAA TGTTCTGTCG
651 TGTCGGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAACG
701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTGTCCCC CTGCCGACA TCCGAGGGCG
951 CGAACAGATT TTGAACGTCC ATTCTAAAA AGTGCCTTTG GACGAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGA CGCCGAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

m614.pep
 1 MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
 51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
 101 LIGAWFYFMR MQTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
 151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
 201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
 251 GAGLGGGND REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
 301 GRFDRQVVV LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTPGFSGAD
 351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
	PLDDNLIKTL LDKNVRVKVTPEEKPSALALFYSLLPVLLLIGAWFYFMRMQTGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVTPEEKPSALTALFYSLLPVLLLIGAWFYFMRMQAGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
	AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL					
g614	AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAIAEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQT VIVIAATNRPDVLDPALQRP					
g614	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQT VIVIAATNRPDVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
	GRFDRQVVVPLDIRGREQILNVHKKVPLDESVDLLSLARGTPGFSGADLANLVNEAAL					
g614	GRFDRQVVVPLDIRGREQXNVHKKVPLDESVDLLSLARGTPGFSGADLAKLVNEAPL					
	310	320	330	340	350	360
m614.pep	370	380	390			
	FAGRRNKVKVDQSDLKTPKTSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

a614.seq
 1 ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51 CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGACG ACAACCTGAT
 201 TAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
 251 AACCAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG

```

301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTCTC TCAGCATTTT AGGTTCCGAC TTTGTCGAAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCCGTTTC ACCGCCAAGT GGTGTCTCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 GTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGKGG AFSFGKSRR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND EQLNQLLV EMDGFESQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKVPL DKSVDLLSLA RGTGPGSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

m614/a614 99.7% identity in 391 aa overlap

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFTNA					
a614	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG					
a614	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
	AFSFGKSRR LLDKDANKVT FADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
a614	AFSFGKSRR LLDKDANKVT FADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
a614	AGSPGTGKTL LAKAAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
	DEIDAVGRQR GAGLGGGNDEREQLNQLLV EMDGFESQTVIVIAATNRP DVLDPALQRP					
a614	DEIDAVGRQR GAGLGGGNDEREQLNQLLV EMDGFESQTVIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
	GRFDRQVVVPLPDIRGREQILNVHSHKVPLDKSVDLLSLARGTGPFGSGADLANLVNEAAL					
a614	GRFDRQVVVPLPDIRGREQILNVHSHKVPLDKSVDLLSLARGTGPFGSGADLANLVNEAAL					

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC  GCGGCGGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACCAC  AATGCCGAAa  gcaggCtgaa  gcGGTTgcgC
101 GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACgtttGgca  gattttggac
151 aggcgcAGga  ATTTGCcgCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201 cacttcttcg  gcggaacggTG  ctctgtcgat  gctgCATTCG  TACagcagga
251 aatcgagggt  ttcttcgatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301 ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351 gAaagggctt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401 cctcttccca  tttgcCGGAA  AtgATGTCGg  gtacggcctg  cAGGGATttg
451 gCGACGGcat  cgtcgatttg  ccgGcggtgc  ttCcgcgctc  ggtttGTTca
501 agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGTggtcC  GATGCCGAGG
551 CGCAGGCGGt  aatagtcctgC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601 GCCGTGTGTG  CcgccGttgc  cgcCGCCGAG  TTTGAATTTg  ATCCGTCCGC
651 AAGGGATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCCTC  GGGTTTGATT
701 TTGTAGAACT  GTCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801 CAACTTCGCC  GAAGAATTTT  TTTCTCTCTT  TAAACGAAGC  CTTCCATTTC
851 CACGCCAGTT  CGTCGAGGAA  CCAAAAGCCC  GCATTGTGGC  GGGTCTGTTC
901 GTATTCTTTG  CCCGGGTTCG  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951 acatgataTT  TtccgtgTTT  CTgTCGaatg  cggTCtgAG  GCTTCAGacg
1001 gcatggTtaT  TCTTCTTgaT  TTtgaACgcg  tgtgcggCGC  GCTTCTTTGG
1051 GGTGATCA  CAGCGGCGG  TACACTTCGA  TGCGGTGCGC  GTCGCGCAGC
1101 GCGGTGTCGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCAATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSFMTVIR  KSGKCRKLKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151 ATASSICRR  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVVSAVAAAE  FEFDPsARDV  EFVVDDEDF  GFDFVELCKR  GNRLSGTVHE
251 RGRFEQPNIA  VGQGGAGNFA  EEEFFFKRS  LPFPQFVEE  PKARIVAGLF
301 VFFARVAQAD  NHFDCVRHDI  FRVSVECLG  ASDGMVILL  FERVCGALLW
351 GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1  ATGCGGAAAA  GCGGTTGCGC  CGGTTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101 GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGGAT
151 AGGCGCAGGA  ATTTTCCGCC  GCGTGCAGCC  AGCATATCGC  GCCAAACGGC
201 AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTCT  TAGAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTCCGTTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCAATT  GCTGTGCAGG  AAGCGGGTTG
401 CTTCTTCCCA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTG
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTAAGT  GGTTTGTTCa
501 GGACATAGCC  GACGACGAGG  TTGCGGTGCG  CCGGGTGGCC  GATGCCGAGG
551 CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601 GCCGTGTGTG  CCGCCGTTCG  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCCTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGACCGGG

```

```

801 CGACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTGCGGCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGGCGG TACACTTCGA TCGGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNA CKPQCREQDK AVAWQIHACS SSSHVWHSLD
51 RRRNFPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDPAGNV EFVVDDEDF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTGDF EEEEEFFKXS LPFRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHD FRVSVECCLK ASDGMVILL FERVCGALLW
351 GRSTAGTTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNA	CKPQCREQDKAVAWQIHACS	SSSHVWHSLD	RRRNFPRAA		
		:	:	:	:	:
g615	MWKRRRRRGVGSFEEQRIDA	AGKPGKQAEAVARQLHAAS	SSSHVWQILD	RRRNLPRAA		
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISRQTAISSAEGASSMLHS	XSRKSRVSSMTGMDSVWIS	CLSSVMTVRIWKSGTCRLKGL			
	:					
g615	SMSRHCATSSADGASSMLHS	YSRKSRVSSMTGMDSVWIS	CLSSFMVTRIRKSGKRLKGL			
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHL	PARMSGMACRDLATASSIC	RRCXRTGFVQDIADDEVAVARVA			
			:			
g615	QTALDYLLCRKRVASSHL	PEMMSGTACRDLATASSIC	RRCFRARFVQDVADDEVAVAGVA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQ	AVVSAVAAAEFEFDPAGNV	EFVVDDEDFGFDFVELCKR			
			:			
g615	DAEAQAVIVCRAEFCLNVFQ	AVVSAVAAAEFEFDPASRD	VEFVVDDEDFGFDFVELCKR			
	190	200	210	220	230	240
	250	260	270	280	290	300
m615.pep	GNCLSGTVHERGRFEQPNV	AVGQGGTGDFAEFFFFFKX	SLPFPRQFVEE	PKTRIVACLF		
g615	GNRLSGTVHERGRFEQPN	IAVGQGGAGNFAEFFFFFK	SLPFPRQFVEE	PKARIVAGLE		
	250	260	270	280	290	300
	310	320	330	340	350	360
m615.pep	VFFARVAQADNHFDCVXHD	IFRVSVECCLKASDGMVILL	DFERVCGALLWGRSTAGGTLR			
g615	VFFARVAQADNHFDCVRHD	IFRVSVECGLKASDGMVILL	DFERVCGALLWGRSTAGGTLR			
	310	320	330	340	350	360
	370					
m615.pep	CGRRRAAACRLX					
g615	CGRRRAAACRLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC  GCGCGCGGCG  CGGTGTCGGC  AGCTTTGAAG  AGCAGCGAAT
51  AGATGCCGCC  GGCAAACCAC  AATGCGGAAA  GCAGGCTGAA  GCGGTTGCGC
101 GGCAGCTTCA  TGCCGCCTCC  TCGTCCAGCC  ACGTTTGGCA  GATTTTGGAC
151 AGGCGCAGGA  ATTTGCCGCC  GCGTGCAGCA  AGTATGTCGC  GCCATTGTGC
201 CACTTCTTCG  GCGGATGGTG  CGTCGTCGAT  GCTGCATTTC  TACAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTGGGTTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCATTT  GCTGTGCAGG  AAGCGGGTTG
401 CCTCTTCACA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGATTTTG
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTG.  TTCCGTAATG  GGTTTGTTCA
501 GGACATAGCC  GACGACGAGG  TTGCGGTTCG  CCGGTGGGCC  GATGCCGAGG
551 CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCGTGA  TGTCTTTCAA
601 GCCGTTGTGT  CCACCGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701 TTATAAACT  GCGCAAGGGC  GGCAACTGCC  TGTCGGGAAC  GGTTCATGAA
751 CGTGGTTCGC  TTGAGCAGCC  AGACATCGCC  GTCGGGCAGG  GTAGCACGGG
801 CGACTTCGCC  GAAGAATTTT  TTTTCTTCTT  TAAATGAAGC  CTTCCATTTT
851 CACGCCAGTT  CGTCGAGGAA  CCAAAAACCC  GCATTGTGGC  GTGTCTGTTT
901 GTATTCTTTG  CCCGGGTTGC  CCAAGCCGAC  AACCATTTTG  ATTGTGTTTG
951 ACATGATATT  TTCCGTGTTT  CTGCCGAATG  CCGTCTGAAG  GCTTCAGACG
1001 GCATGGTTAT  TCTTCTTGAT  TTTGAACGCG  TTTGCGGCGC  GCTTCTTTGG
1051 GGTCGATCAA  CAGCGGGCGG  TACACTTCGA  TCGGTCGCC  GTCGCGCAGC
1101 GCGGTGTCGT  CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSVMTVRIW  KSGTCRLKGL  QTASGHLLCR  KRVASSHLPA  RMSGMACRDL
151 ATASSICRRX  FRTFGVQDIA  DDEVAVARVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVVSTVAAAE  FEFDPAGNV  EFVVDDEDF  GFDIFIKLRK  GNCLSGTVHE
251 RGRLEQPDIA  VQGSGTGDA  EEEEEFFK*S  LPFRQFVEE  PKTRIVACLF
301 VFFARVAQAD  NHFDCV*HDI  FRVSAECLRK  ASDGMVILLD  FERVCGALLW
351 GRSTAGGTLR  CGRRRAAACR  L*
```

m615/a615 90.3% identity in 371 aa overlap

```

10      20      30      40      50      60
m615.pep MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHSIDRRRNFPRAA
||||| || ||||| :||| ||| :| :||| ||||| :||| |||||
a615      MRKRRRRGVGSFEEQRIDAAGKPQCGKQAEAVARQLHAASSSSHVWQILDRRRNLPRAA
10      20      30      40      50      60

70      80      90      100     110     120
m615.pep SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL
|:|:| | |||:||||| ||||| ||||| ||||| ||||| ||||| |||||
a615      SMSRHCATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL
70      80      90      100     110     120

130     140     150     160     170     180
m615.pep QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGTFVQDIADDEVAVARVA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a615      QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXFRTFGVQDIADDEVAVARVA
130     140     150     160     170     180

190     200     210     220     230     240
m615.pep DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPAGNVFVVDDEDFGFDVELCKR
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a615      DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPAGNVFVVDDEDFGFDIFIKLRK
190     200     210     220     230     240

250     260     270     280     290     300
```

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVGQGSGDFAEEFFFFFKXSLPFPQFVEEPKTRIVACLF
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615      GNCLSGTVHERGRLEQPDIAVGQGSGDFAEEFFFFFKXSLPFPQFVEEPKTRIVACLF
          250      260      270      280      290      300

          310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDVCVXHDIFRVSVECLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615      VFFARVAQADNHFDVCVXHDIFRVSACRLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          310      320      330      340      350      360

          370
m615.pep  CGRRRAAACRLX
          |||||
a615      CGRRRAAACRLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CGCCCTGCC CGACGGCGAT GTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGGAC GGATCAAATT CAAACTCGGC GgcggcaacG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCTCGG CATCGgccac CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAACa aaccgagcgc gGaagcaccg Ccgcaaatc gacgatgCCG
501 TCGccaaATC CCTgcaggcc gtaccCGACA TcaTTCCGg caaatgggaa
551 gaggcaacgc gcTTCTTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttccc atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCAccgt ccgccgaaga
751 agtggcacaa TGgcgcgaca tactTGccgc acgcgGcgGC AAATtcCTGc
801 gcctgtccaa aatctgcCaa aCGTGGCtGG ACgAGGAGGC GGCatgAAgc
851 tGCCGcgcaA CCgcttcaGc ctgctTTCCG CATTGTGGTT TGCCGCGGc
901 atctAtTCgc tgctettcaA AGCTGccgaC ACCGCGCCGC CGCCGTTTCC
951 ACATTTcgac AAAGCAGCAC ACCTTGCCCT GTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAAA ACCGGAaAAC TTCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGGCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGccc
1201 gactaa

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This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSAEAP PANRRCRROI PAGRTRHHR OMGRGNALPA QQIIQCRLKP
201 FQTAFSRFPY PNSHRTQAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPRNRF LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QILELAKAFK TGKLPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGSIGDV LADLTGAALA LFAARSACRP
401 D*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CGCCCTGCC CGACGGCGAC GTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGAT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGGCGGAC GGATCAAATT CAAACTCGGC GCGCGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCCG CAAATGGGAA

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551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701 GATTTCTGCT TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGCGCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCC
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPALRM QHRRCLPLRR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRG TSMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPFHD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMFVLCFAL FSECAQAWFT ATRTGSGLDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
	MSNTIKMVVGLG	NPGKEYEQTRHN	AGFWFLDELAWK	WKASFKEEKKFF	GEVARAALPDGD	
g616	MSNTIKMVVGLG	NPGKEYEQTRHN	AGFWFLDELAWK	WKASFKEEKKFF	GEVARAALPDGD	
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRS	QQAVALAQFYKI	KPEEILVVHDEL	DIPCGRIKFKLG	GNGGGHNLK	
g616	VWLLKPATFMNRS	QQAVALAQFYKI	KPEEILVVHDEL	DIPCGRIKFKLG	GNGGGHNLK	
m616.pep	130	140	150	160	170	180
	DIQAKLGTADYY	RLRLGIGHPGDR	NLVVGYVLNKP	STEXPPTDXRCR	RQIPASHTRHPCR	
g616	DIQAKLGTADYY	RLRLGIGHPGDR	NLVVGYVLNKP	STEXPPTDXRCR	RQIPASHTRHPCR	
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQM	TRCRLKPFQTAC	SRFPYPNSHRTQ	AAAYPNRIHPRH	RNRNPRFPALRM	
g616	QMGRSNPLPAQM	TRCRLKPFQTAC	SRFPYPNSHRTQ	AAAYPNRIHPRH	RNRNPRFPALRM	
m616.pep	250	260	270	280	290	300
	QHRRCLPLRRRNC	RLARYAGTRRKI	PAPIQTMPDMAX	RGTSMNLPRNRF	ILLSALWFAGS	
g616	QHRRCLPLRRRNC	RLARYAGTRRKI	PAPIQTMPDMAX	RGTSMNLPRNRF	ILLSALWFAGS	
m616.pep	310	320	330	340	350	360
	IYSLLFKAAETAP	PPFPFHDKVAHL	ALFFAQIWLTKA	FRTDNRPIPYRS	LMVFALCFAL	
g616	IYSLLFKAAETAP	PPFPFHDKVAHL	ALFFAQIWLTKA	FRTDNRPIPYRS	LMVFALCFAL	
m616.pep	370	380	390	400		
	FSECAQAWFTATR	TGSGLDVLADLT	GAAALFTARAAC	RDPDX		
g616	FSECAQAWFTATR	TGSGLDVLADLT	GAAALFTARAAC	RDPDX		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq
1 ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51 ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAGTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTCGGCGAA
151 GTCGCCCGTG CTACCTGCGC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCCG GACAGGAGT TGCCGCCCTT GCGCAGTTT
251 ATAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTGCGGAC GGATCAAAAT CAACTCGGC GGCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTGAGG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTGAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTC
701 GATTTCCTGC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGGCACA TGGCGCGACA TACTTGCCG ACGCGGCGGC AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGCTT TGCCGGCGGC
901 ATCTATTGCG TGCTCTTCAA AGCTGCCGAC ACCGCGCCG CGCCGTTTCC
951 GCATTTGCGA AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAAA ACCGGAACAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTGCGCGATA
1151 TGGCAGGTAC GGTTCCTGCA CTCTTTGCCG CCCGCGCCG CGACCGCCCG
1201 GACTGA

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARATLPDGD VLLKPTTFM NRSGQAVAAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QQMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPVRM QHRRRTIRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPNRNFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPHFD KAAHLALFFA QIWLTLKAFK TGLPLIPYRS
351 LMVFALCFAL FSECAQA*FT ATRTGSIGDV LADMAGTVLA LFAARAADRP
401 D*

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLG	NPGKEYEQTRH	NAGFWFLDEL	AWKWKASFKE	EKKFFGEVAR	AALPDGD
a616	MSNTIKMVVGLG	NPGKEYEQTRH	NAGFWFLDEL	AWKWKASFKE	EKKFFGEVAR	ATLPDGD
	70	80	90	100	110	120
m616.pep	VLLKPATFMNR	SGQAVAAAL	AQFYKIKPEE	ILVVHDELDI	PCGRIKFKL	GGGNGGHNGLK
a616	VLLKPTTFMNR	SGQAVAAAL	AQFYKIKPEE	ILVVHDELDI	PCGRIKFKL	GGGNGGHNGLK
	130	140	150	160	170	180
m616.pep	DIQAKLGTADY	YRLRLGIGH	PGDRNLVVG	YVLNKPSTEX	PPTDXRCRR	QIPASHTRHPCR
a616	DIQAKLGTADY	YRLRLGIGH	PGDRNLVVG	YVLNKPSTEX	PPTDXRCRR	QIPASHTRHPCR
	190	200	210	220	230	240
m616.pep	QMGRSNPLPA	QQMTRCRLK	PFQTACSRFP	YPNSHRTQAA	YPNRIHPRH	RNRNPRFPALRM
a616	QMXRGNPLPA	QQMTRCRLK	PFQTACSRFP	YPNSHRTQAA	YPNRIHPRH	RNRNPRFPVRM
	250	260	270	280	290	300

m616.pep	QHRRCP L R R R N C L A R Y A G R T R R K I P A P I Q T M P D M A X R G T S M N L P R N R F I L L S A L W F A G S : : : : : : : : : : : : : : :
a616	QHRRRTIRRRSGTMAHRTCTRRQIPAPVQNLPNVAGRGGMKLPNRNFSLLSALWFAGG 250 260 270 280 290 300
m616.pep	310 320 330 340 350 360 IYSLLFKA AETAPPPFP HFDKV AHLA LFFAQIWLLTKAFRTDNRFIPYRSLMVFALCFAL : : : : : : : : : : : : :
a616	IYSLLFKAADTAPPPFP HFDKAAHLA LFFAQIWLLTKAFKTGKLPIPYRSLMVFALCFAL 310 320 330 340 350 360
m616.pep	370 380 390 400 FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX : : : : : : : : : : : : :
a616	FSECAQAXFTATRTGSLGDVLADMAGTVLALFAARAADRPDX 370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

g619.seq

1	ATGCCGCTCTG	AAAAAATAT	CGGTTTTATG	GCAGGAAGCA	GCCGTCGGTT
51	CGGGGTCGCC	TTTGGCGTGT	TGCTGGTTTC	CTGCATCTGT	TTTATGACGC
101	TCAACGCTCAA	AGGAGATTGG	GACTTTGCT	TGCACCTCG	CCTGACCAAG
151	CTTGCCGCGC	TGCTGATGGT	CGCCTATGCG	GTCGGCGGTG	CCACTCACT
201	PTTCCAAACG	CTGACCAACA	ACCGAATGCT	GACCCCTFCG	ATTTTGGGTT
251	TCGATTTCGCT	GTATGTGTTT	TTGCAGACCT	TGCTGgtGTT	TACGTtcgGC
301	GGCGTGGGCT	ATAcatccct	gcggttgagc	gGCAAAATTCG	GCTTTGAACAT
351	GGTGTGTATG	ATGGGCGCGT	CGCTGCTCGT	GTTTTACACG	CTCATCCGTC
401	AGGGCGGGCG	CGATTGGCCG	CACATGATTT	TAATCGGCGT	GATTTTCGGG
451	ATTTTGTTC	CGAGCCTTTC	CTCGCTGCTT	TCGCGCATGA	TAGACCCGTA
501	AGAATTTACC	CGCGCGCAGG	CGAATATGTT	TGCCGGATTC	ATACCCGTC
551	GCAGCGAGCT	TTTAGGCATA	GGCGCGCTGG	TCCTGCTCGT	CAGCGCGCGC
601	GTGCTTTGGC	ACAAGCGTCA	CCGCTCGGAC	GTACACCTTT	TGGGGCGCGA
651	CCAAGCCGTC	AATTGTGGCA	TCAGCTACAC	CGCGAACACC	TTATGGATAC
701	TGCTTTGGAT	TGCCGCAATT	TGGCGCAGCG	CGACCGCCGT	TGTCGGCCCC
751	GTGAGCTTTT	TCGGGCTTTC	CGCGCCGCTCG	CTTGCGAACAC	ACTTTTCCCC
801	gtCCGTGGCG	CATTCCGTCC	GCTTCGcgat	gacggtttGC	gtcgGcgGCA
851	TCTCTTGgt	cggCggacaA	ACCGTATTCG	AACACTTCTT	GGGCATGAag
901	gCggTATTAA	CGCTGGTGGT	cgaAATTTCG	ggcggactcG	TTTTCTCTA
951	TCTCGTTTTA	AGCATCAAAA	AATGA		

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

g619.pep

1	MPSEKNIGFM	AGSSRPLRVA	FALLVSCIL	FMTLNVKGDW	DFVLHLRLTK
51	<u>LAALLMVAYA</u>	VGSTQLFQT	LTNNPILTPS	<u>ILGFDLSLVF</u>	<u>LQTLLVFTFG</u>
101	GVGYTSLPLT	GKGFQFLVMV	MGGSLLEFY	LIRQGRDLRP	HMILIGVIFG
151	<u>ILFRSLSSLL</u>	SRMIDPEEFT	AAQANLFAFT	NTVRSELGLI	<u>GATVATVLSAA</u>
201	<u>VVWHERYRSD</u>	VHLLGRDQAV	NLGISYTRNT	<u>LWILLWIRAL</u>	<u>VALATAVVGP</u>
251	<u>VSFFFGLLAAS</u>	LANHFFSPSR	HLRMLPTMVC	<u>VGGIILVGGQ</u>	<u>TVFEHFLGMK</u>
301	AVLSVVVEFA	GLGVFLYLVL	KHKK*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```
m619.seq
1  ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCGCGTT
51  GTGGGTGCGCC TTGCGCGTGT TGCTGGTTTC TCGCGTCTGT TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTGTGTT TGCAACTCGC GCTGACCAAA
151 CTTGCGCGCG TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAACG CTGACCAATA ATCCGATTGT GACCCCTTCA ATTTTGGGTT
251 TCGATTTCGCT GTATGTGTTT TTGCAGACCT TCGTGGTGTG TACGTTTCGC
301 GGCCTGGGCT ATGCTTCCCT GCCGTGACG GGCAAATTCG GCTTTGAAC
351 GGTCTGTCAT ATGGCGCGCT CGCTGCTGCT GTTCTACAGC CTCATCAAC
401 AGGGCGGACG CGATTGTGCG CGCATGATT TAATCGGCGT GATTTTCGG
451 ATTTTGTTC CGACCTGTC GTCGCTGCT TCGGCGATGA TCGATCCGA
501 AGAATTTACC GCGCGCGAG CGCAATAGTT TGCCGGATT CAAACCGTCC
551 ACAGCGAGCT TTTGGGCATA GGCATCGCTG TCTGTCTGCT CAGCGCGGCC
601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTTTACCTTT TGGGCGTGA
651 CCAAGCCGCT AATTTGGGCA TCAGCTACAC CGCACAACC TTATGGTATC
701 TGCCTTTGGAT TCGCCGATTG GTGGCGACGG CGACCGCGGT GGTGCGCCCC
751 GTAAGCTTTT TCGGGCTTCT GC CGCGCTCG CTTGCCAACC ACTTTCCCC
801 GTCGGTCAAA CATTCGCTTC CGCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCCTCTTGGT CCGCGGACAG ACCGTGTTGC AACACCTGCT CGGTATGCA
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901 GCAGTGTGA GCGTAGTAGT AGAATTTGCC GCGGACTCG TTTTCCTCTA
951 TCTCGTTTA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep

1 MPSEKNIGFM AGSSRPLWVA FALLVSCVL FMTLNKGDW DFVLQRLTK
51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
101 GVGYSILPLT GKFGFELVVM MGGSLLLFYT LIKQGGRLDS RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ
301 AVLSVVVEFA GGLVFLYLVL KHKX*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLVSCVLFMTLNKGDWDFVLQRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLVSCILFMTLNKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYTSPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	130	140	150	160	170	180
	MGGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGGRLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVHSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHLLGMK					
	250	260	270	280	290	300
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKX					
g619	AVLSVVVEFAGGLVFLYLVLKHKX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq

1 ATGCCGCTCG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCGGTT
51 GTGGGTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTTC TGCACCTGCG CCTGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTTT CGACCCAGCT
201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAATTCG GCTTTGAACT
351 GGTCTGTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
401 AGGGCGGGCG CGATTGCGG CGTATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCGA
501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGGATTG AATACCGTCC
551 ACAGCGAGCT TTTAGGCATA GCGCGCTGTA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTCGGCCCG

993

751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
 801 GTCGGTCAAA CATTCCTGCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
 851 TCCTCTTGGT CGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
 901 GCGGTATTA GCGTGGTGGT CGAATTGCG GCGGACTCG TTTTCCTCTA
 951 TCTCGTTTA AGACACAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

a619.pep

1 MPSEKNIGFM AGSSRPLWVA FALLVSCIL FMTLNVKGDW DFVHLRLTK
 51 LAALLMVAYA VGVSTQLFOT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
 101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGRLP RMILIGVIFG
 151 ILFRSLSSL SRMIDPEEF AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
 301 AVLSVVVEFA GGLVFLYVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA					
a619	MPSEKNIGFMAGSSRPLWVAFALLVSCILFMTLNVKGDWDFVHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
m619.pep	70	80	90	100	110	120
	VGVSTQLFOTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
a619	VGVSTQLFOTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	130	140	150	160	170	180
	MGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLSRMIDPEEFATAQANMFAGF					
a619	MGSLLLFYTLIKQGGRLPRMILIGVIFGILFRSLSSLSRMIDPEEFATAQANMFAGF					
	130	140	150	160	170	180
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
a619	NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
a619	VATATAVVGVPVSFFGLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYVLKHKXX					
a619	AVLSVVVEFAGGLVFLYVLKHKXX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

g620.seq

1 ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gttTTCGCCT TAAGTGCCTG
 51 CCGGCaggcg gaAGaggcac cgcgcCCTTt ACCCCGGCAG AtTAGCGacc
 101 gttcgtcg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
 151 aaagcccaga ttttttgaa cGGCAAAccc GATCAGCCCG TTTGGTTCTC
 201 CACCGTcaag cagatgttcg GCTATACCAa GCTGCCCGAA GAGCCCAaAG
 251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCCT
 401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
 451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

```
g620.pep
1  MKKTLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

```
m620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

```
m620.pep
1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLAIVAVFALSACRQAEAEPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKIRVIYVTDGNVTDWTPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFGYTKLPEEPKIRVIYVTDGNVTDWTPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

```
a620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

995

m620/a620 100.0% identity in 164 aa overlap

```

      10      20      30      40      50      60
m620.pep MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
|||||
a620      MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
      10      20      30      40      50      60

      70      80      90     100     110     120
m620.pep DQPVWFSTIKQMFQYTKLPEEPKGIIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS
|||||
a620      DQPVWFSTIKQMFQYTKLPEEPKGIIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS
      70      80      90     100     110     120

      130     140     150     160
m620.pep GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX
|||||
a620      GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta cgcgtgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAG ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTTCCG CGTTGCCTGC
301 GGCTTGGATT CGATGGTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAAACTCA
401 ATGCCCTGTT CCRAAAAACC TTTTCCGTTG CTAAGAAGT CCGTACCGAT
451 ACCGCTGTCG GCGAAAATTC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GCGCGAACAG ATTTTTCCTG ACATCGGCGA TTTGAACGTA TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAT
601 CCGCGGTGTA TGACGGTTCG CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GCGAGCCAG
751 CTTCGGATAG TCGGCAAAGG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTGAAC GATGCGTATC TTTATACGGT GGACGATATG
901 GTCAACATCG TCCAAAGCGg caaggaggca aggcagaaag ccgccgcCgc
951 cgcgaaacg ctggTGTCGG AAAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GagggttcCG CTGATTAAGG CCTTGCGGGA CGAGGGCGAG
1051 AAGCGCGCA AGCAGGTGTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaacGGCG GAAGaggttt TGgaacggct gtcggtcCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCAACT CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGatttGG TTCATGCCgt cGCGCAGAtt tatcatttGG ACAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDME TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEQUESM AKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEO IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGLN DAYLYTVDDM
301 VNIQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAGAG CTGGCGTTTG CCGCCGCCGC CCTGCCATAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTCCG CGTCGCCTGC

```

```
301 GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGTATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAATT
501 GGCAGAACAG ATTTTCCCG ACATCGGCGA TTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTGC CGCCAAAAGT
601 CCGCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTTG TCGGCAAAGG CATGGTGGAG CGTGCAATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTGATTTGGC AGTGCCGCGT GACATTGAAG
851 CGGAAGTCGG CGATTTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCGAAGACG CTGGTGTCCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGCAGGCA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AACAGGTGTT GGAATATGCC ATGAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGCGGG GGAAGAAAGT
1201 AAAGATTTGG TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```
1 MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51 NRTELYCVGD SEEIIRWLAD YHSLPIEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMPL FMLDLAVPR DIEAEVGLND DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPLIKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*
```

m622/g622 98.8% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	SEEIIRWLADYHSLPIEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	SEEIIRWLADYHSLPIEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	130	140	150	160	170	180
	RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEQESMGAKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
m622.pep	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRMLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
m622.pep	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
	250	260	270	280	290	300
m622.pep	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
m622.pep	370	380	390	400	410	
	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCGTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGTTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCTGTG CTAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAATC GGTTCATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCG ACATCGGCGA TTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTCTTCAAC GGCAAGCCAG
751 TTGCCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCTG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAAATCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGTTG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLP EAVRNLA RSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHA FRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQE QESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLA EQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV P LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

```

      10      20      30      40      50      60
m622.pep MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLA RSNAATEAVILSTCNRTELYCVGD
|||||
a622      MQLTAVGLNHQTAPLSIREKLAFAAACLP EAVRNLA RSNAATEAVILSTCNRTELYCVGD
      10      20      30      40      50      60

      70      80      90     100     110     120
m622.pep SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHA FRVACGLDSMVLGEPQILGQIKDAV
|||||
a622      SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHA FRVACGLDSMVLGEPQILGQIKDAV
      70      80      90     100     110     120

     130     140     150     160     170     180
m622.pep RVAQE QESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLA EQIFPDIGDLNV
|||||
a622      RVAQE QESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLA EQIFPDIGDLNV
     130     140     150     160     170     180
```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq
 1 ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
 51 GATAATCGGC ATTTTTCGCG CGCTGTTGCC GACACGCCG TTCGTACTAC
 101 TCTCCGCCG CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG
 151 CACcgGCacc gCTATTTCGG CCCGATGGT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AGATTTCGCG CATCAGCATG AtaaccgcAt
 251 cctgcctcat gatctTTtgg CattTTCCcc aacnctggtg ggtcGGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTTGTCacC ATacggatgt gGcacAGacC
 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep
 1 MIRYLLIACG GISLLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFHRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIEW HFPQXWWVGA
 101 VSSVFCSLVT IRMWRPES*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq
 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTCCCG TACTGTTGGG
 51 TATCATCGGC ATTTTTCGCG CGCTGTTGCC GACACGCCG TTCGTACTGC
 101 TCTCCGCCG CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
 151 CACCGGCACC GCTATTTCGG CCCGATGGT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AAATATTCGCG CATCAGTATG ATGACCGCAT
 251 CCTGCCTGAT AATGTTTGG CAGTTTCCCC AACGCTGGTG GGTCGGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTTGTCGCC ATATGGATGT GGCGCAGGCC
 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep
 1 MIRYLLIACG CISLLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFYRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLMIEW QFPQRWWVGA
 101 VSSVFCSLVA IWMWRPES*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACG CISLLLGIIG IFPLPLPTTP FVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACG GISLLLGIIG IFPLPLPTTP FVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
g624	HNWEQNGAVPRKAKIFAISMITASCLIMFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624.seq
1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCT TGCTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTGG CAGTTTCCCC AACGCTGGTG GGTCCGGGCG
301 GTTTCATCGG TTTTGTGTC CTTGTGCGC ATATGGATGT GCGCAGGCGC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624.pep
1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRRHYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRRHYFGPMV					
a624	MIRYLLIACGCISLLLGIIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRRHYFGPMV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
a624	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625.seq
1  ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtCTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGtCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625.seq
1  atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtcTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttcc CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gTAA
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625.pep
1  MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAPVVPVME ASAVPTASRA
```

1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AACTGAACG GGATGAGGAA GAGCAATGTC CAAAAGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFW LAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCGGGCC TTTGGAAACC CGAACACCCG GGATTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTATCCTG ATTACATTGA
101 CCGCCGTATC TATGGCAATC ACGCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGTTTCAG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GCGGGCGGC GATGCCAAG
401 CCTTAATGAC GGGTCCCCTG TTTCATTcgc TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gCAACgcac cgaactTCAT